GENE   PRECURSOR-SEQUENCE P-SEQID GENE-SEQ   G-SEQID FOLDED PRECURSOR

======== ==================== ======= ========== =======

==

GAM15 ACCTCTTTCTGATGGAGTCG 1   TGATGGAGTC 350   TTTCT- T TC   AAG   CT TC TCTTC
T CTCACAA

      TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   C   GA GGAG GTAAAA TTTTAT CTT TC   GA
GGT   A

      CTCTCTTCGATGGTCTCACA   TTTA | || ||||| |||||| |||||| ||| || || |||
      AAAATATTAAACCTCTTTCT   G   CT TCTC TATTTT AAAATG GAG AG   CT CCA   A
      GATGGAGTCGTAAAAAGTT   CTTCCT T --   GAA   CT GT TCTTT - AATTATA
      TTATCTTTCTCCTTCGAT
      GGT

GAM16 ACCTCTTTCTGATGGAGTCG 2   TGATGGAGTC 351   TTTCT TG TC   AAG   CT TC TCTTC
T CTCACAA

      TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   TC   GA GAG GTAAAA TTTTAT CTT TC   GA
GGT   A

      CTCTCTTCGATGGTCTCACA   TTTA || || ||| |||||| |||||| ||| || || |||
      AAAATATTAAACCTCTTTCT   AG   CT TTC TATTTT AAAATG GAG AG   CT CCA   A
      GATGGAGTCGTAAAAAGTT   CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
      TTATCTCTTTCTCTCTTCGA
      TGGT

GAM17 ACCTCTTTCTGATGGAGTCG 3   TGATGGAGTC 352   TTTCT TG TC   AAG   CT TC TCTTC
T CTCACAA

      TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   TC   GA GAG GTAAAA TTTTAT CTT TC   GA
GGT   A

      CTCTCTTCGATGGTCTCACA   TTTA || || ||| |||||| |||||| ||| || || |||
      AAAATATTAAACCTCTTTCT   AG   CT TTC TATTTT AAAATG GAG AG   CT CCA   A
      GATGGAGTCGTAAAAAGTT   CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
      TTATCTCTTTCTCTCTTCGA
      TGGT

GAM18 ACCTCTTTCTGATGGAGTCG 4   TGATGGAGTC 353   TTTCT TG TC   AAG   CT TC TCTTC
T CTCACAA

      TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   TC   GA GAG GTAAAA TTTTAT CTT TC   GA
GGT   A

      CTCTCTTCGATGGTCTCACA   TTTA || || ||| |||||| |||||| ||| || || |||
      AAAATATTAAACCTCTTTCT   AG   CT TTC TATTTT AAAATG GAG AG   CT CCA   A
      GATGGAGTCGTAAAAAGTT   CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
      TTATCTCTTTCTCTCTTCGA
      TGGT

GAM19 ACCTCTTTCTGATGGAGTCG 5   TGATGGAGTC 354   TTTCT TG TC   AAG   CT TC TCTTC
T CTCACAA

      TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   TC   GA GAG GTAAAA TTTTAT CTT TC   GA
GGT   A

      CTCTCTTCGATGGTCTCACA   TTTA || || ||| |||||| |||||| ||| || || |||
      AAAATATTAAACCTCTTTCT   AG   CT TTC TATTTT AAAATG GAG AG   CT CCA   A
      GATGGAGTCGTAAAAAGTT   CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
      TTATCTCTTTCTCTCTTCGA
      TGGT

GAM20 ACCTCTTTCTGATGGAGTCG 6   TGATGGAGTC 355   TTTCT TG TC   AAG   CT TC TCTTC
T CTCACAA

```
        TAAAAAAGTTTTATCTCTTT      GTAAAAAGT      TC  GA GAG GTAAAA  TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA      TTTA          ||   ||  |||  ||||||  |||||| ||| ||    || |||
        AAAATATTAAACCTCTTTCT                    AG   CT TTC TATTTT  AAAATG GAG AG    CT CCA     A
        GATGGAGTCGTAAAAAAGTT                    CTTCT CT  TC    GAA    CT GT TCTTT -  AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM21  ACCTCTTTCTGATGGAGTCG 7     TGATGGAGTC 356    TTTCT TG  TC    AAG   CT TC TCTTC
T  CTCACAA
        TAAAAAAGTTTTATCTCTTT      GTAAAAAGT      TC  GA GAG GTAAAA  TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA      TTTA          ||   ||  |||  ||||||  |||||| ||| ||    || |||
        AAAATATTAAACCTCTTTCT                    AG   CT TTC TATTTT  AAAATG GAG AG    CT CCA     A
        GATGGAGTCGTAAAAAAGTT                    CTTCT CT  TC    GAA    CT GT TCTTT -  AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM22  ACCTCTTTCTGATGGAGTCG 8     TGATGGAGTC 357    TTTCT TG  TC    AAG   CT TC TCTTC
T  CTCACAA
        TAAAAAAGTTTTATCTCTTT      GTAAAAAGT      TC  GA GAG GTAAAA  TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA      TTTA          ||   ||  |||  ||||||  |||||| ||| ||    || |||
        AAAATATTAAACCTCTTTCT                    AG   CT TTC TATTTT  AAAATG GAG AG    CT CCA     A
        GATGGAGTCGTAAAAAAGTT                    CTTCT CT  TC    GAA    CT GT TCTTT -  AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM23  ACCTCTTTCTGATGGAGTCG 9     TGATGGAGTC 358    TTTCT TG  TC    AAG   CT TC TCTTC
T  CTCACAA
        TAAAAAAGTTTTATCTCTTT      GTAAAAAGT      TC  GA GAG GTAAAA  TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA      TTTA          ||   ||  |||  ||||||  |||||| ||| ||    || |||
        AAAATATTAAACCTCTTTCT                    AG   CT TTC TATTTT  AAAATG GAG AG    CT CCA     A
        GATGGAGTCGTAAAAAAGTT                    CTTCT CT  TC    GAA    CT GT TCTTT -  AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM24  ACCTCTTTCTGATGGAGTCG 10    TGATGGAGTC 359    TTTCT TG  TC    AAG   CT TC TCTTC
T  CTCACAA
        TAAAAAAGTTTTATCTCTTT      GTAAAAAGT      TC  GA GAG GTAAAA  TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA      TTTA          ||   ||  |||  ||||||  |||||| ||| ||    || |||
        AAAATATTAAACCTCTTTCT                    AG   CT TTC TATTTT  AAAATG GAG AG    CT CCA     A
        GATGGAGTCGTAAAAAAGTT                    CTTCT CT  TC    GAA    CT GT TCTTT -  AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM25  ACCTCTTTCTGATGGAGTCG 11    TGATGGAGTC 360    TTTCT TG  TC    AAG   CT TC TCTTC
T  CTCACAA
        TAAAAAAGTTTTATCTCTTT      GTAAAAAGT      TC  GA GAG GTAAAA  TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA      TTTA          ||   ||  |||  ||||||  |||||| ||| ||    || |||
        AAAATATTAAACCTCTTTCT                    AG   CT TTC TATTTT  AAAATG GAG AG    CT CCA     A
        GATGGAGTCGTAAAAAAGTT                    CTTCT CT  TC    GAA    CT GT TCTTT -  AATTATA
```

```
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM26   ACCTCTTTCTGATGGAGTCG 12   CGTAAAAAAG 361    TTTCT TG  TC     AAG     CT  C TTC--
T  CTCACAA
        TAAAAAAGTTTTATCTTTCT       TTTTATCTTT    TC  GA GAG GTAAAA  TTTTAT TTCT TC   GA
GGT    A
        CTCTTCGATGGTCTCACAAA       CTCT         ||  || ||| |||||| ||||||| |||| ||   || |||
        AATATTAAACCTCTTTCTGA                    AG   CT TTC TATTTT AAAATG GAGG AG   CT CCA
A
        TGGAGTCGTAAAAAAGTTTT                    CTTCT CT  TC    GAA    CT  T TCTTT -  AATTATA
        ATCTCTTTCTCTCTTCGATG
        GT
GAM27   GATGGAGTCGTAAAAAAGTT 13   TGATGGAGTC 362    T  TC     AAG    --  T TCCTTC T
CTCACAA
        TTATCTCTTTCTCCTTCGAT       GTAAAAAGT     GA GGAG GTAAAA TTTTAT CTCT TC    GA GGT
    A
        GGTCTCACAAAAATATTAAA       TTTA         || |||| |||||| |||||| |||| ||    || |||
        CCTCTTTCTGATGGAGTCGT                   CT TCTC TATTTT AAAATG GAGG AG   CT CCA    A
        AAAAAAGTTTTATCTCTTTC                   T  --   GAA    CT  T TCTTT- -  AATTATA


GAM28   GATGGAGTCGTAAAAAAGTT 14   TGATGGAGTC 363    T  TC     AAG    --  T TCCTTC T
CTCACAA
        TTATCTCTTTCTCCTTCGAT       GTAAAAAGT     GA GGAG GTAAAA TTTTAT CTCT TC    GA GGT
    A
        GGTCTCACAAAAATATTAAA       TTTA         || |||| |||||| |||||| |||| ||    || |||
        CCTCTTTCTGATGGAGTCGT                   CT TCTC TATTTT AAAATG GAGG AG   CT CCA    A
        AAAAAAGTTTTATCTCTTTC                   T  --   GAA    CT  T TCTTT- -  AATTATA


GAM29   GATGGAGTCGTAAAAAAGTT 15   TGATGGAGTC 364    T  TC     AAG    CT  TC TCTTC T
CTCACAA
        TTATCTCTTTCTCTCTTCGA       GTAAAAAGT     GA GGAG GTAAAA TTTTAT CTT TC    GA GGT
    A
        TGGTCTCACAAAAATATTAA       TTTA         || |||| |||||| |||||| ||| ||    || |||
        ACCTCTTTCTGATGGAGTCG                   CT TCTC TATTTT AAAATG GAG AG   CT CCA    A
        TAAAAAAGTTTTATCTCTTT                   T  --   GAA    CT  GT TCTTT -  AATTATA
        C

GAM30   GATGGTCTCATAAAAAAAGT 16   ATAAAAAAG 365     G  TCATAAAA  TTTTAC         ATTCT-
CTCTCTT  TG
        TTTACAAAAATATTTTTATT       TTTTACAAAA    AT GTC    AAAG    AAAAATATTTTT    CTTT
TGA  G
        CTCTTTCTCTCTTTGATGGT       ATAT         || |||     ||||   ||||||||||||    ||||     |||
        CTCATAAAAAAGTTTTACA                    TG TAG    TTTC   TTTTTATAAAAA    GAAA    ACT /
        AAAATATTTTTATTCTCTTT                   G  TTTCTCTC  TCTTA-       CATTTT  AAAAT-- CT
        CTCTCTTTGATGGTC

GAM31   GGAGTCATAAAATATTTTTA 17   TAAAATATTT 366     TC    A    T- T TCTCTTC T CTCACAA
        TTCTCTTTCTCTCTTCGATG       TTATTCTCTT     GGAG ATAAAAT TTTTTAT CTCT TC    GA GGT
A
```

```
        GTCTCACAAAAATATTAAAC    TCTC            |||| ||||||| |||||| |||| ||      || |||
        CTCTTTCTGATGGAGTCGTA           TCTC  TATTTTG AAAAATG  GAGG AG     CT CCA     A
        AAAAAGTTTTATCTCT                --     A     CT   T  TCTTT-- -  AATTATA


    GAM32  TTAAACCTCTTTCTGATGGA 18    TGATGGAGTC 367   CTTTCT TG  TC     AAG    -- T  TCCTTC
    T  CTCACAA
        GTCGTAAAAAGTTTTATCT           GTAAAAAGT       GA GAG GTAAAA  TTTTAT CTCT TC    GA
    GGT    A
        CTTTCTCCTTCGATGGTCTC        TTTA             || ||| ||||||  ||||||  |||| ||     || |||
        ACAAAAATATTAAACCTCTT              CT TTC  TATTTT  AAAATG  GAGG AG     CT CCA     A
        TCTGATGGAGTCGTAAAAAA              TCTTTC CT  TC     GAA     CT   T TCTTT-  -  AATTATA
        GTTTTATCTCTTTCTCCTTT
        CTCACAAAAA
    GAM33  TTAAACCTCTTTCTGATGGA 19    TGATGGAGTC 368   CTTTCT TG  TC     AAG    -- T  TCCTTC
    T  CTCACAA
        GTCGTAAAAAGTTTTATCT           GTAAAAAGT       GA GAG GTAAAA  TTTTAT CTCT TC    GA
    GGT    A
        CTTTCTCCTTCGATGGTCTC        TTTA             || ||| ||||||  ||||||  |||| ||     || |||
        ACAAAAATATTAAACCTCTT              CT TTC  TATTTT  AAAATG  GAGG AG     CT CCA     A
        TCTGATGGAGTCGTAAAAAA              TCTTTC CT  TC     GAA     CT   T TCTTT-  -  AATTATA
        GTTTTATCTCTTTCTCCTTT
        CTCACAAAAA
    GAM34  TTTTTCTTTGGTACAAAATT 20    TCTTTGGTAC 369       T      TT CACAA    ----   CA  A
        TCACACAAGTTTTTATACAG         AAAATTTCAC     TTTTTCTT GGTACAAAA TCA     GTTT   TATA
    GACAA T
        ACAAATTCTTGTCCATATAT        ACAA          ||||||| |||||||| |||   ||||   |||| |||||
        TTTAAACATTGACTTTTGT             AAAAAGAA TCATGTTTT AGT    CAAAA   ATAT CTGTT T
        ACTAAGAAAAA                     -      C- TA---    TTTT   AC    C


    GAM35  AGAGATAAAACTTTTTTACG 21    TGAGACCATC 370        --      AC ------   A A AAGA   A  T
        ACTCCATCAGAAAGAGGTTT         GAAGGAGACT      AGAGATA AAACTTTTTT GA    CTCC TC GA
    GGTTT ATA T
        AATATTTTTGTGAGACCATC        CCAT          ||||||| |||||||||| ||    |||| || ||   ||||| |||
        GAAGGAGACTCCATCAGAAA              TTTTTAT TTTGGAGAAA CT    GAGG AG CT   CCAGA
    TGT T
        GAGGTTTAATATTTTT                AA      GA ACCTCA   A - A---    G  T


    GAM36  ATAAAAATATTTTTGTAAAA 22    AATATTTTTG 371           AAAA      A-- GA
        CTTTTTTTATGAGACCATCA         TAAAACTTTT     ATAAAAATATTTTTGT  CTTTTTTT  TGA C
        AAGAGAGAAAGAGAATAAAA        TTTA          ||||||||||||||  |||||||| |||
        ATATTTTTGT                      TGTTTTTATAAAAATA  GAAAGAGA  ACT /
                                    AGA-       GAA  AC


    GAM37  ATAAAAATATTTTTGTAAAA 23    AATATTTTTG 372           AAAA      A-- GA
        CTTTTTTTATGAGACCATCA         TAAAACTTTT     ATAAAAATATTTTTGT  CTTTTTTT  TGA C
        AAGAGAGAAAGAGAATAAAA        TTTA          ||||||||||||||  |||||||| |||
```

```
        ATATTTTTGT                    TGTTTTTATAAAAATA   GAAAGAGA   ACT /
                                      AGA-       GAA   AC


GAM38   ATGGATTTTACTAGATCATT 24    TTATACGATC 373      -  TTT -     ATTT-   ACC
     TATATACCAAAAAATATTAT        TACGTTTTAT        ATG GAT  AC TAGATC   ATAT  A
     ACGATCTACGTTTTATTATA        TATA           ||| |||   || |||||||   ||||
     T                          TAT TTA  TG ATCTAG    TATA  A
                               A  TTT  C    CATAT   AAA


GAM39   CTTTTTTACGACTCCATCAG 25    CATCAGAAAG 374     A CTCCA  G   G  T  A   G  GACCA  -
     AAAGA
        AAAGAGGTTTAATATTTTTG        AGGTTTAATA       T CGA    TCA AAAGA GTT AAT TTTTT TGA    TCG
AAGAGAG    G
        TGAGACCATCGAAGAGAGAA        TTTT           | |||    ||| ||||| ||| ||| ||||| |||   ||| |||||||
        AGAGATAAAACTTTTTTACG                   A GCT    AGT TTTTT TAA TTG AGAAA ACT    AGC TTTTTTC
     A
        ACTCCATCAGAAAGAGGTTT                   - ACCAG  G   A  T  G   G ACCTC  A     AAAAT
        AATATTTTTGTGAGACCATC
        GAAGAGAG
GAM40   CTTTTTTACGACTCCATCAG 26    CATCAGAAAG 375     A CTCCA  G   G  T  A   G  GACCA  -
     AAAGA
        AAAGAGGTTTAATATTTTTG        AGGTTTAATA       T CGA    TCA AAAGA GTT AAT TTTTT TGA    TCG
AAGAGAG    G
        TGAGACCATCGAAGAGAGAA        TTTT           | |||    ||| ||||| ||| ||| ||||| |||   ||| |||||||
        AGAGATAAAACTTTTTTACG                   A GCT    AGT TTTTT TAA TTG AGAAA ACT    AGC TTTTTTC
     A
        ACTCCATCAGAAAGAGGTTT                   - ACCAG  G   A  T  G   G ACCTC  A     AAAAT
        AATATTTTTGTGAGACCATC
        GAAGAGAG
GAM41   CTTTTTTACGACTCCATCAG 27    CATCAGAAAG 376     A CTCCA  G   G  T  A   G  GACCA  -
     AAAGA
        AAAGAGGTTTAATATTTTTG        AGGTTTAATA       T CGA    TCA AAAGA GTT AAT TTTTT TGA    TCG
AAGAGAG    G
        TGAGACCATCGAAGAGAGAA        TTTT           | |||    ||| ||||| ||| ||| ||||| |||   ||| |||||||
        AGAGATAAAACTTTTTTACG                   A GCT    AGT TTTTT TAA TTG AGAAA ACT    AGC TTTTTTC
     A
        ACTCCATCAGAAAGAGGTTT                   - ACCAG  G   A  T  G   G ACCTC  A     AAAAT
        AATATTTTTGTGAGACCATC
        GAAGAGAG
GAM42   CTTTTTTACGACTCCATCAG 28    CATCAGAAAG 377     A CTCCA  G   G  T  A   G  GACCA  -
     AAAGA
        AAAGAGGTTTAATATTTTTG        AGGTTTAATA       T CGA    TCA AAAGA GTT AAT TTTTT TGA    TCG
AAGAGAG    G
        TGAGACCATCGAAGAGAGAA        TTTT           | |||    ||| ||||| ||| ||| ||||| |||   ||| |||||||
        AGAGATAAAACTTTTTTACG                   A GCT    AGT TTTTT TAA TTG AGAAA ACT    AGC TTTTTTC
     A
        ACTCCATCAGAAAGAGGTTT                   - ACCAG  G   A  T  G   G ACCTC  A     AAAAT
        AATATTTTTGTGAGACCATC
```

GAAGAGAG

GAM43   CTTTTTTACGACTCCATCAG 29   CATCAGAAAG 378   A CTCCA G   G T A   G GACCA -
    AAAGA

    AAAGAGGTTTAATATTTTTG   AGGTTTAATA   T CGA   TCA AAAGA GTT AAT TTTTT TGA   TCG
AAGAGAG   G

    TGAGACCATCGAAGAGAGAA   TTTT | |||| ||| ||||| ||| ||| ||||| ||| ||| ||||||
    AGAGATAAAACTTTTTTACG   A GCT   AGT TTTTT TAA TTG AGAAA ACT   AGC TTTTTTC
    A

    ACTCCATCAGAAAGAGGTTT   - ACCAG G   A T G   G ACCTC A   AAAAT
    AATATTTTTGTGAGACCATC
    GAAGAGAG

GAM44   CTTTTTTACGACTCCATCAG 30   CATCAGAAAG 379   A CTCCA G   G T A   G GACCA -
    AAAGA

    AAAGAGGTTTAATATTTTTG   AGGTTTAATA   T CGA   TCA AAAGA GTT AAT TTTTT TGA   TCG
AAGAGAG   G

    TGAGACCATCGAAGAGAGAA   TTTT | ||| ||| ||||| ||| ||| ||||| ||| ||| ||||||
    AGAGATAAAACTTTTTTACG   A GCT   AGT TTTTT TAA TTG AGAAA ACT   AGC TTTTTTC
    A

    ACTCCATCAGAAAGAGGTTT   - ACCAG G   A T G   G ACCTC A   AAAAT
    AATATTTTTGTGAGACCATC
    GAAGAGAG

GAM45   CTTTTTTACGACTCCATCAG 31   CATCAGAAAG 380   A CTCCA G   G T A   G GACCA -
    AAAG

    AAAGAGGTTTAATATTTTTG   AGGTTTAATA   TT CGA   TCA AAAGA GTT AAT TTTTT TGA   TCG
AAGAGAG   A

    TGAGACCATCGAAGAGAGAA   TTTT || ||| ||| ||||| ||| ||| ||||| ||| ||| ||||||
    AGATAAAACTTTTTTACGAC   AA GCT   AGT TTTTT TAA TTG AGAAA ACT   AGC
TTTTTTC   T

    TCCATCAGAAAGAGGTTTAA   - ACCAG G   A T G   G ACCTC A   AAAA
    TATTTTTGTGAGACCATCGA
    AGAGAG

GAM46   GTGTGCCTGAATCGTTCGAT 32   TGAATAGAGT 381   C   TTCGAT C C   CAA
    TAACCCTACTCATCCAATTT   TATCGATTCA   GTGTG CTGAATCG   TAAC CTA TCATC T
    CAGATGAATAGAGTTATCGA   GACA ||||| ||||||| |||| ||| |||||
    TTCAGACACAC   CACAC GACTTAGC   ATTG GAT AGTAG T
                A   T----- A A ACT

GAM47   TCAGAAAGAGGTTTAATATT 33   AGAGGTTTAA 382   AAA GTTT--   GAGACCA- GA
    TTTGTGAGACCATCGAAGAG   TATTTTTGTG   TCAG GAG   AATATTTTGT   TC A
    AGAAAGAGAATAAAAATATT   AGAC |||| ||| ||||||||||| ||
    TTATGACTCCATTGA   AGTT CTC   TTATAAAAATA   AG /
                AC- AGTATT   AGAGAAAG AG

GAM48   TTTTATGAGACCATCAAAGA 34   AGAGAGAAAG 383   ACCA AAG   AGA-   AAAA   A-
- GA

    GAGAAAGAGAATAAAAATAT   AGAATAAAAA   TCA AGAGAAAG   ATAAAAATATTTTTGT
CTTTTTTT TGA C

    TTTTGTAAAACTTTTTTTTAT   TATT ||| ||||||| ||||||||||||||| |||||||| |||

GAGACCATCAAAGAGAGAAA   AGT TTTTTTC TGTTTTTATAAAAATA GAAAGAGA
ACT /
        GAGAATAAAAATATTTTTGT   CCAG A--   AAAA   AGA-   GAA AC
        AAAACTTTTTTTATGAGACC
        ATCAAAGAGAG
GAM49   TTTTATGAGACCATCAAAGA 35   GAAGAGAGAA 384   ACCA AAG   AGA-   AAAA---
- A
        GAGAAAGAGAATAAAAATAT   AGAGAATAAA   TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTTG TG G
        TTTTGTAAAACTTTTTTTGT   AATA ||| ||||||| ||||||||||||| ||||||||| ||
        GAGACCATCGAAGAGAGAAA   AGT TTTTTTC TGTTTTTATAAAAATA
GAGAGAAGC AC A
        GAGAATAAAAATATTTTTGT   CCAG A--   AAAA   AGAGAAA   T C
        AAAACTTTTTTTATGAGACC
        ATCAAAGAGAG
GAM50   TTTTTCTTAGTACAAAAGTC 36   TCAATGTTTT 385   A-   G- AT--- AAAA   G
        AATGTTTTAAAATATATGGA   AAAATATATG   TTTTTCTT GTACAAAA TCA   GTTTT
TATATGGACAA A
        CAAGAATTTGTCTGTATAAA   GACA ||||||||| ||||||||| ||| ||||| |||||||||||
        AACTTGTGTGAAATTTTGTA   AAAAAGAA CATGTTTT AGT   CAAAA   ATATGTCTGTT A
        CCAAAGAAAAA   AC   AA GTGTT   ----   T

GAM51   ATGTAGTAATCGTTGTCGTG 37   ATGGTTCTTT 386   C TG GTGTTCC-- TCC TTCTCC   -
    T TTCT
        TTCCTGTTTCCTACTTCTCC   CCGTACAACA   AT GT TC   TGTT TAC   AATCAT
ATAGATATT TCT   A
        AATCATATAGATATTTTCTT   TACT || || || |||| ||| |||||| ||||||||| |||
        TCTATCATGGATAATATTTG   TA TA AG   ACAA ATG   TTGGTA TGTTTATAA AGG   /
        TAATGGTTCTTTCCGTACAA   - GT ATTTGTCAT C--   CCTTTC   A   T TACT
        CATACTGTTTAGATGATATT
        GCGCAT
GAM52   GAATGACTCGTCCCTTAATA 38   TGACTCGTCC 387   GA G   TAATA AGTAG   - TCT
        GGCAGTAGGCTAGTATCTTT   CTTAATAGGC   GAAT CTC TCCCT   GGC   GCTA GTA T
        TTTACGTAGTAATCGTCGTA   AGTA |||| ||| ||||| ||| |||| |||
        GGGAGAGAATTC   CTTA GAG AGGGA   CTG   TGAT CAT /
                        A- - TG--- CTAA- G TTT

GAM53   GAGATTGTATCAGTTTCGTA 39   GATTGTATCA 388   -- - T TA   TGA   G T
        GTCTTGAGTATTGGTATTAC   GTTTCGTAGT   GAGATTGTA TC AGT TCG GTCT GTATTG TAT A
        TATATAGTATATAGATGTCG   CTTG ||||||||| || ||| ||| |||| |||||| |||
        ACGCTAGATATACAGTCTC   CTCTGACAT AG TCG AGC TAGA   TATGAT ATA C
                        AT A C TG TA-   - T

GAM54   GGCAAATCTTATCATTGGTC 40   TAACATCGAT 389   CTT   - ---   TG- TTGCTTT
        GGTGTTTGGTCTTGCTTTGT   TCCCATATGA   GGCAAAT ATCAT TGG TCGGTGTT GTC   G
        GACTTTGATAATAACATCGA   TGTT ||||||| ||||| ||| ||||||||| |||
        TTCCCATATGATGTTTGTT   TTGTTTG TAGTA ACC AGCTACAA TAG   /

```
                        ---    T  CTT      TAA  TTTCAGT


GAM55   AGTATGTTGTACGGAAAGAA 41    TGATTGGAGA 390        --    A GAAAGAA ATTACAAA  A-  TG--
-  AAGA
        CCATTACAAATATTATCCAT      AGTAGGAAAC     AGTA TGTTGT CG     CC      TATT TCCA
ATAGA   A
        GATAGAAAGAAAATATCTAT      AGGA          |||| |||||| ||    ||     |||| ||||    |||||
        ATGATTGGAGAAGTAGGAAA                   TCAT GCAACA GC     GG     ATGA AGGT    TATCT  /
        CAGGAACACGACAACGATTA                   TA    - ACAA--- ACAAAGG- AG   TAGTA    ATAA
        CT


GAM56   AAAATCGATTCCGTCCAAGA 42    TCGATTCCGT 391        C      CCAAG     AAAAACA
        TGATAAAAACATTTACCGGC      CCAAGATGAT     AAAAT GATTCCGT ATGAT    T
        ATCATAAACACGGAGTTTAT      AAAA          ||||| |||||||| |||||
        TTT                      TTTTA TTGAGGCA  TACTA    T
                                 T    CAAA-  CGGCCAT


GAM57   CATGGAGATACTTTATTACT 43    TAATGTCCTG 392        ------------ T          TAAATA
        CCATTAAATAATTTATCATG      TTTCATTGT      CATGGAGAT     AC TTATTACTCCAT    A
        GAGTGATAATGTCCTGTTTC      TTCC          |||||||||     || ||||||||||||
        ATTTGTTTCCATG            GTACCTTTG      TG AATAGTGAGGTA   /
                                 TTTACTTTGTCC  T      CTATTT


GAM58   ACTGTATGCTCCTAGCGGAG 44    TGTATGCTCC 393        A  - A      AATCCTTCG  T
        TTAATCCTTCGTTGTTTCTA      TAGCGGAGTT     ACTGT TGCTC CT GCGGAGTT      TTGT T
        CAAAGTCTCTCGACTCCGCG      AATC          ||||| ||||| || |||||||||      ||||
        AGAGAGTAACAGT            TGACA ATGAG GA CGCCTCAG       AACA C
                                 -  A G     CTCTCTGA-  T


GAM59   ATACGGAATATCTACGTCCA 45    TCATCGGGTG 394        C    C-------- GT - T T
        TGTCATTATTGTCATCGGGT      TATTCTCATT     ATA GGAATAT     TAC CC ATG CA T
        GTATTCTCATTCATATTCTC      CATA          ||| |||||||     ||| || ||| ||
        TAT                      TAT TCTTATA      ATG  GG TAC GT A
                                 C     CTTACTCTT  TG C  T T


GAM60   GCAATACTTCTGGTCTCGGA 46    TTCTGGTCTC 395        ACTTC       A ---------- C
        TTAGGCGTCGTTACGTATAT      GGATTAGGCG     GCAAT  TGGTCTCGGATT GG     CGT G
        ATCCACCAATCCGAGACCAT      TCGT          |||||  |||||||||||| ||     |||
        TGATTGC                  CGTTA  ACCAGAGCCTAA CC     GCA T
                                 GTT--      - ACCTATATAT  T


GAM61   GCTTTGCAAATTGTATATTA 47    ATCGATCATA 396        TT  ATT    TAT  C  C CCGC  AAT    A
TTT
        TTGACATCGACCGCGTAATA      TCTATATCAT     GCT GCAA  GTATAT  TGA AT GA  GT  ATAGT
GAG   T
```

```
TAGTAGAGTTTTATTCTCAT        CCAT          ||| |||| |||||| ||| || ||  ||  |||| |||
TATCGATCATATCTATATCA                TGA CGTT  CATGTA  ACT TA CT   TA  TATTA CTC  /
TCCATGTACTTGCTTAGT                  TT  ---    CCT  A T ATAC GC-   - TTA


GAM62  GTCGTTCTCGTTCAGAATCT 48    TTGAAGACTC 397     T GTTC A  TCG   -    G  G
       TTCGCAGCATAAGTAGTATG        TTCCAGAGAC     GTCGT CTC  AGA TCTT  CAGC ATAAGTA TAT T
       TCGATATACTTATCGTTGAA    GAT          ||||| |||   ||| |||| |||| ||||||| |||
       GACTCTTCCAGAGACGAT                TAGCA GAG   TCT AGAA  GTTG TATTCAT ATA C
                             - ACCT  C  ---  C    - G


GAM63  TAACAATATATTATTAGTTT 49   TTAATAATAT 398       ------------       TA
       ATATTACTGAATTAATAATA       AAAATTCCCA      TAACAA       TATATTATTAGTTTA T
       TAAAATTCCCAATCTTGTTA    ATCT        ||||||       |||||||||||||
                     ATTGTT       ATATAATAATTAAGT T
                     CTAACCCTTAAA          CA


GAM64  TCTCAATAAGAAGATTAACG 50   TGGGGTTACT 399     C   AA   AACGAT--     CTA
       ATTTCCATGTCTACATTATA       CTAAATCGCT      TCT AATAAG GATT     TTCCATGT  C
       TGGGGTTACTCTAAATCGCT    TGTT          ||| |||||| ||||     ||||||||
       TGTTTAGA                AGA TTGTTC CTAA      GGGGTATA  /
                     T   G-  ATCTCATT     TTA


GAM65  TGTATTCAGTCAGACAATGT 51   TTAGTAGCGT 400     A   -  AA  TGACGTCG    G   C  G
       CTGACGTCGGCCACGGTATT       GGCAATGACA      TGT TTCAGT CAGAC  TGTC     GCCACG TATT
AGG A
       CAGGGAGTCCTTAGTAGCGT    GGGT          ||| |||||| |||||  ||||     |||||| |||| |||
       GGCAATGACAGGGTCTGAAC             ACA GGGTCA GTCTG  ACAG     CGGTGC ATGA TCC G
       TGGGCACA                  C    A   GG  TAA-----   G   T  T


GAM66  TTGATATTACTTATAATAAC 52   TTAATTGTAA 401     T   T---  CG  - TG   --  TT  T
       GATTTGTTTAATTTTTAGTT       ATGATATTAT      TTGATA TACTTA  AATAA AT T TTTA ATT TAGT T
       TATACTATTAATTGTAAATG    TATT          |||||| ||||||   |||||  || | |||| ||| ||||
       ATATTATTATTTTTTTAAGT             GACTAT ATGAAT   TTATT  TA A  AAAT TAA ATCA A
       ATTATCAG                 T    TTTT   AT T GT   GT TT  T


GAM67  TTTAAACTTTGGCATATACA 53    AGATAACATA 402      CTT  CATATACAA--    ACT
       AGTCTATACTTTTAGTAGAT        CCACACCATT       TTTAAA TGG       GTCTAT  T
       AACATACCACACCATTTTTT    TTTT          |||||| |||        ||||||
       AAA                 AAATTT  ACC       TAGATG  /
                     TTT  ACACCATACAA     ATT


GAM68  TTTCTTTTCACGATGCATCT 54   ATAAGTGGAC 403      TC- GA-   ------- GA  CGT
       TATTGAATGACGTTTTCTCA       ATATAGATGC      TTTCTTT AC TGCATCT    TATT ATGA T
```

```
TAAGTGGACATATAGATGCA      AGAA            ||||||| || ||||||||    |||| ||||
GAAGTAATGAAGAAA                       AAAGAAG  TG  ACGTAGA     GTGA  TACT  /
                          TAA  AAG     TATACAG  A-   CTT


GAM69   TCGATGATACATGTATTAAA 55    TGATACATGT 404      A---     TGTA    T  TCC
        ATACTTTCCGAATAAGTCTT         ATTAAAATAC    TCG   TGATACA  TTAAAA ACTT  G
        TTAAATATTGTATTAATTAT     TTTC          |||   ||||||||   |||||| ||||
        GA                         AGT   ATTATGT   AATTTT TGAA  /
                                   ATTA    TATA    C   TAA


GAM70   TGATAATACTTAAAAAAATA 56    TAAAAATTAA 405      A  AAAAAA     ATCATTTAC  AA   A
        ATAATATCATTTACAATTAA         ACAAATCGTT     TGATA TACTT   ATAATAAT      AATT  TAGT  T
        TAGTATAAACTAAAAATTAA     ATTA          |||||| |||||    ||||||||     |||| ||||
        ACAAATCGTTATTATAAGTA         ACTAT ATGAA      TATTATTG       TTAA  ATCA  A
        ATATCA                       A  ------    CTAAACAAA  AA   A


GAM71   AGCAGCGAACAACAACATCA 57    ATGGATTCTG 406      AACAAC  T  TAT     CA
        GATATTTCATCGACATTTTT         TGTTTATGCT        AGCAGCG    AACA CAGA  TTCATCGA  T
        GATGGATTCTGTGTTTATGC     GTT          |||||||    |||| |||| ||||||||
        TGTT                         TTGTCGT    TTGT GTCT  AGGTAGTT  /
                          AT----   -  T--      TT


GAM72   TAACAAGATTGGGAATTTTA 58    TAATATAAAC 407      GATTGGGAAT-       AA
        TATTATTAATTCAGTAATAT         TAATAATATA        TAACAA       TTTATATTATT  T
        AAACTAATAATATATTGTTA     TTGT          ||||||        ||||||||||||
                          ATTGTT         AAATATAATGA  /
                          ATATAATAATC         CT


GAM73   TACATGCTGACATCTAATGC 59    TCTCTAGCGT 408      C  ATCTAATGCC   AA    --   C-  T
AATA
        CTGTATAACCATGAGAGCAT         GGATACAGTC     TACATG TGAC      TGTAT CCATG AGAG  ATC
AC   C
        CTACAATACATACCGTCGAT         ACCG          |||||| ||||       ||||| ||||| |||| ||| ||
        ATCTCTAGCGTGGATACAGT             ATGTGC ACTG      ACATA GGTGC TCTC  TAG TG   A
        CACCGTGTA                    C  ----------   --  GA   TA  C  CCAT


GAM74   TCCGTTTTTATCAGTATGTA 60    TATCAGTATG 409      T--------     TGTA- C  AT    T
        TATCTATATTAACGTCGTCG         TATATCTATA        TCCGTTTT       ATCAGTA  TAT TAT  TAACG  C
        TTGTAGTGAATAGTAGTTAT     TTAA          |||||||      |||||||    ||| ||| |||||
        TGATCTATTATATGAAACGG             AGGCAAG       TAGTTAT   ATA GTG  GTTGC  G
        A                         TATATTATC    TGATG  A  AT    T


GAM75   TGCTAAATATGCGATGTATC 61    TATTATACAA 410      A-   - T TCTAT A    T-    AACAATAC
```

```
       TATGTTATTTGTATTTATCT      AAATTTTTTA     TGCT AATATGC GA GTA    GTT TTTGTAT TATCTA
  C
       AAACAATACCTCTACCTCTA     TTTC          |||| ||||||| || |||    ||| ||||||| |||||
       GATATTATACAAAAATTTTT              ATGA TTATACG CT TAT    TAA AAACATA ATAGAT      /
       TATTTCAGCATATTAAAGTA              AA    A T TTTT- -    TT    CTCCATCT



   GAM76   TTTTGATTACGATGTTATAA 62    TATAACATCG 411              ATGT TTAATT TG  GAT
       GAATGTAGTTAATTGATGTA      TAATCAAAA      TTTTGATTACGATGTTATAAGA  AG   GA TAT  G
       TGATGTTAATGTGTCCTCTT          ||||||||||||||||||| ||   || |||
       TCCTCTTATAACATCGTAAT          AAAACTAATGCTACAATATTCT   TC    CT GTA /
       CAAAA                         CCTT TC---- GT  ATT



   GAM77   GATTTTGTGATTTTTCTTCC 63    ATAGTTAGAT 412      TTTT  TTT  TC  A    A
       TAAACTGTTTACGTAAATAG      AGAATATTCA      GA   GTGA  TTCT CTAA CTGTTT C
       TTAGATAGAATATTCATTAG      TTAG          ||  |||| |||| |||| ||||||
       TTC                       CT   TACT  AAGA DATT GATAAA G
                                 TGAT  TAT  TA  -   T



   GAM78   GCGTCAAATATTTCCCGTTT 64    TGGTATGTTC 413      CAA-   CC TTA-     GTCAAGA
       AATATCGCATTTGTCAAGAT      ACGATAAGTA      GCGT  ATATTT CGT  ATATCGCATTT    T
       AATAATAGAGTGTGGTATGT      TAAT          ||||   |||||| |||  ||||||||||
       TCACGATAAGTATAATAACG               CGCA   TATGAA GCA   TATGGTGTGAG     /
       C                                  ATAA    TA  CTTG      ATAATAA



   GAM79   TATCTTTTAAGAATTGTGGA 65    TCTTTTAAGA 414      C   A    GATAT GA  TA
       TATTAGGATATTATTACGTA      ATTGTGGATA      TAT TTTTA GAATTGTG   TAG TAT T
       AACTATTACACAATTCTAAA      TTAG          ||| ||||| |||||||   ||| |||
       ATATA                     ATA AAAAT CTTAACAC   ATC ATG T
                          T   -     ATT-- AA  CA



   GAM80   ATTTAGACTGATGTATGGGT 66    TTCTCATCAT 415      GA   T  T  - GTTT
       AATAGTGTTTGAAGAGCTCG      CAGAATAAAT       ATTTA CTGATG ATGGG AAT AGT   G
       TTCTCATCATCAGAATAAAT               ||||| |||||| ||||| ||| |||
                          TAAAT GACTAC TACTC TTG TCG   /
                          AA    -   - C AGAA



   GAM81   AGCCGCTGAGTGGTAAACAA 67    CCGCTGAGTG 416      C    -----     CAACA- AG
       CAGAACAGATAGTTTATTAT      GTAAACAACA      AGC GCTGAG   TGGTAAA    GAAC A
       CTTTACCAACACCCTCAGCC      GAAC          ||| |||||| |||||| ||||
       GCT                       TCG CGACTC   ACCATTT   TTTG /
                          C    CCACA      CTATTA  AT



   GAM82   GACTAGATCCGTTAGTTTAA 68    CGTTAGTTTA 417         CCGTT  T  T  CATC-  TA
```

TATCCTCAGTCATCTTGTCT   ATATCCTCAG   GACTAGAT   AGTTTAA ATCC CAGT   TTGTC G
AGAATGGCAAATCTAACTGC   TCAT |||||||| |||||||| |||| |||| |||||
GGGTTTAGGCTTTAGTTTAG   TTGATTTG   TCGGATT TGGG GTCA   AACGG A
TT   ATT--   - C ATCTA   TA

GAM83   GGATGTAAAATGTTGATGAT 69   TTGATGATAT 418   AAAAT A   CTACATCGTT   TTT
    ATCTACATCGTTGGATTTT   CTACATCGTT   GGATGT   GTTG TGATAT   TGGAT T
    TATGTATCCACTTTAATAAT   TGGA |||||| |||| |||||| |||||
    ATCATAGCTGTAACATCC   CCTACA   CGAT ACTATA   ACCTA A
                           ATGT-   -   ATAATTTC--   TGT

GAM84   GTCCGTATCCAGTCAACACT 70   TAGCTTTCAC 419   C   CC C CA   TA T
    ATGTTAGCATTTCTGTCGAT   TCATATGAC   GTC GTAT AGT AA CTATGT GCA T
    ATAGCTTTCACTCATATGAC ||| |||| ||| || |||||| |||
    CAG TATA TCA TT GATATA TGT T
     - C-   C TC   GC C

GAM85   TAGCTTTCATAGTTAGATAC 71   CAGAAGTAGG 420   -----   GTCTCA- ---   T   A   CT
AT
    ATGGTCTCAGAAGTAGGATT   ATTATGTAAC   AGTTAG   ATACATG   GAA GTAGGATTA
GTAAC TCAG TCG A
    ATGTAACATCAGCTTCGATA   ATCA |||||| ||||||| ||| |||||||||| ||||| |||| |||
    AAATGACTGGGTTATTTAGT   TCAATT   TATGTAC   CTT CATTCTGAT TATTG GGTC
AGT A
    CTTACACATTCGCTCATACA   GCCAG   ATACTCG ACA   T   - -- AA
    TGTATGACCGTTAACTACAG
    AGTCTA
GAM86   TCGTAAGATACTCCTTCATG 72   TATGAAGTAA 421   A   C--   GAAC   TCA A
    AACATAATCAGTTACAAAAC   AGTATCTACG   TCGTA GATACT CTTCAT ATAA GTT C
    GTTTATATGAAGTAAAGTAT   A ||||| |||||| |||||| |||| |||
    CTACGA   AGCAT CTATGA GAAGTA TATT CAA A
                            -   AAT   ---- TG- A

GAM87   TTCACCGTTTGCATGTTACC 73   CCGTTTGCAT 422   C   C TTACCACTATCA   AA
    ACTATCAACCGCATAATACA   GTTACCACTA   TTCAC GTTTG ATG   ACCGCAT T
    ATGCGGTGTTTCCTTTGTCA   TCAA ||||| ||||| ||| |||||||
    TCAAATTGTGAA   AAGTG TAAAC TAC   TGGCGTA A
                           T   - TGTTTCCTTTG-   AC

GAM88   TTTCAGGAGATGATCTCGCC 74   GCTACAGTTC 423   ------   - C C T TACCA-- A   T
    GTAGCTACCATGATAGTAGA   CTTGTTCGTC   TTTCAG   GAGAT GAT TCG CG AGC   TG
TAGTAGA G
    TGCCTCTGCTACAGTTCCTT   GACA |||||| ||||| ||| ||| || || || ||||||
    GTTCGTCGACATCTATCTTT   AAAGTC   TTCTA CTA AGC GC TTG   AC ATCGTCT C
    GCATTCTGAAA   TTACGT   T C T - TTCCTTG -   C

GAM89   TGATGCATTAATTTTTGTAT 75   TGCATTAATT 424   C   A   A   TTC   CCTAAAA AAAA
AATAAG
        TGATTCTCAATCCTAAAAAC   TTTGTATTGA   TGATG ATTA TTTTTGT TTGA TCAAT   ACT
TATG   T
        TAAAATATGAATAAGTATTA   TTCT ||||| |||| ||||||| |||| ||||| ||| ||||
        AACATAGCGGTGTACTAATT   ATTGT TGAT AAAAATA AATT AGTTA   TGG   ATAC   /
        GATTTAACATAAAAAATAGT   -   A   C   T--   ATCATG- CG--   AAATTA
        TGTTA

GAM90   GTTGTTTTGCGATAGCCATG 76   TGTTTTGCGA 425   TG T   A CCAT----   A   CAG
        TATCTACTAATCAGATCTAT   TAGCCATGTA   GT T TTGCG TAG   GTATCT CTAAT A
        TAGAGATATTATTAATTCTG   TCTA || | ||||| ||| |||||| |||||
        GTGCAATATGAC   CA A AACGT GTC   TATAGA GATTA /
            GT T   G   TTAATTAT   -   TCT

GAM91   ACTGATTCTGGACATAGCTT 77   TAAGTTTGGC 426   T   GACA   T C   G------------   AT
        TCCGACTGGCGCATTTGGTG   AGCTAGCAGA   ACTGA TCTG   TAGCT TC GACT   GCGC T
        TGATGGTTCCCATAAGTTTG   TTCA ||||| |||| ||||| || |||| ||||
        GCAGCTAGCAGATTCAGT   TGACT AGAC   ATCGA GG TTGA   TGTG /
            T   G---   C T   ATACCCTTGGTAG   GT

GAM92   ATATGTGTATTATCAGATAT 78   TCCTCCTAGG 427   T   T   AAAATTTT ATG
        CCAAAATTTTGTATGAAGAA   ATATTTGTAA   ATATG GTATTA CAGATATCC   GT A
        CTCCTCCTAGGATATTTGTA   TATC ||||| |||||| ||||||||| ||
        ATATCTATGT   TGTAT TATAAT GTTTATAGG   CA /
            C   -   ATCCTCCT AGA

GAM93   ATCATCATTTTTTCACCATT 79   TGAGAATACT 428   A TTTTCACCATTAC TC   - CA
        ACTTCTTCCATGTCCAATAT   AAAATTCCTA   ATCATC TT   TTCT CATG TC A
        GATCATGTGAGAATACTAAA   ACGA |||||| || |||| |||| ||
        ATTCCTAACGATGAT   TAGTAG AA   AAGA GTAC AG T
            C TCCTTAAAATCAT   GT   T TA

GAM94   GAAATTGTTGCTCCCATGGA 80   TAATAGTTAC 429   AA T TCC   GAA   CCAA   T
        ATGACCCAATAAGTAGATTT   CACGTGCTGT   GA TTG TGC   CATG TGAC TAAG A
        AATAGTTACCACGTGCTGTA   ACCA || ||| ||| |||| |||| ||||
        CCAAAGTC   CT AAC ATG   GTGC   ATTG   ATTT G
            GA C TC- ACC   ATA-   A

GAM95   TGGTTCTTTCCATAGTACAT 81   TCCATAGTAC 430   TCT   GTACATAG   GGTG
        AGTTGTTGCGGTGCAGAAGC   ATAGTTGTTG   TGGT TTCCATA   TTGTTGC C
        AATAAATACAGAGTGTGGAA   CGGT |||| ||||||| |||||||
        CACCA   ACCA AAGGTGT   AATAACG /

C--   GAGACATA   AAGA

GAM96   TTAATAGTTTACACCTTTTA 82   TAGTAGGACT 431   TTTTA A C TA-- --   CAT CT
GAATTCCA
         GTAGGACTAGTATCGTACAA   AGTATCGTAC   ACACC GT GGA TAG   TCGT ACAATT AG
GTATTTT   A
         TTCATAGCTGTATTTTGAAT   AATT ||||| || ||| ||| |||| |||||| || |||||||
         TCCAATCACGCATAAAAATA   TGTGG   TA CCT ATC AGCA TGTTAA TC TATAAAA
T
         TCTTCCAATTGTTGACGAAG   CCTAC - A CAGA GT   CCT --   ATACGCAC
         ACCTAATCCATCATCCGGTG
         TAATATTAA
GAM97   TTCATCCGATAAACTCCAAT 83   TTTGTGGTAT 432   -   AACT A   G GATA
         AAAAAGATGATATATCTAGT   TGGATAGAA   TTC ATCCGATA CCA TAAAAA AT T
         GTTTTTGTGGTATTGGATAG ||| |||||||| ||| |||||| ||
         AA   AAG TAGGTTAT   GGT GTTTTT TG A
                             A   ---- - G ATCT

GAM98   TTAGTGACAGACCAGACCTA 84   TGACAGACCA 433   T ----------- GA   ---   TC
         GGAGCTATTCTACCATAGCA   GACCTAGGAG   TTAG GACAGA   CCA CCTAGGA GCTAT T
         AATCTTAGGCATGGACATAC   CTAT |||| |||||| ||| ||||||| |||||
         TAATATCTGTCTTAA   AATT CTGTCT   GGT GGATTCT CGATA A
                             - ATAATCATACA AC   AAA   CC

GAM99   AACAAGAAATGGAAATCGT 85   TTGAAATTGT 434   AG   T TAATACC   T
         AATACCAGTTATGTTTAACT   TTTTTATTTT   AACAA AAATGGAAA CG   AGTTA G
         TTGAAATTGTTTTTTATTTT   CTTG ||||| |||||||||| || |||||
         CTTGTT   TTGTT TTTATTTTT GT   TCAAT T
                             CT   T TAAAGTT   T

GAM100   TTCCACTGTCCAAAATGATG 86   TCCAAAATGA 435   ACT   A G - C CCTTTTTA
         CCTCTGCCTTTTTATACATG   TGCCTCTGCC   TTCC GTCCAA AT ATG C TCTG   T
         TTCCAGATGTCATAATATTG   TTTT |||| |||||| || ||| | ||||
         GATTGGGAA   AAGG TAGGTT TA TAC G AGAC   /
                             GT-   A A T T CTTGTACA

GAM101   CTGTGACCAAGATAGAGAGC 87   GTGAATCCAT 436   ACCA   GCTCC-- TGAAT T CTA
  AGTTT
         TCCTTTGGTGAATCCATCTC   CTCTATGTTT   CTGTG AGATAGAGA   TTTGG CCA CT
TGTTTC   A
         TATGTTTCAGTTAACCAAG   CAGT ||||| ||||||||| ||||| ||| || |||||
         AAACAGTCAGCTGGTCTAAA   GACAT TCTATCTCT   AAATC GGT GA ACAAAG   /
         ATTTCCATCTCTATCTAATA   AA--   ACCTTTA T---- C CTG   AACCA
         CAG

GAM102 GTTTCTTTTAGAAGTGATTC 88   GAAGTGATTC 437   T--   GAA   TT- A G
        TTTGATGGTGTCAGCATACG   TTTGATGGTG   GTTTCT TTA GTGATTC TG TG T
        AATTACAATAATGCAGAAAC   TCAG |||||| ||| ||||||| || ||
                              CAAAGA AAT CATTAAG AC AC G
                               CGT AA-   CAT G T

GAM103 TTGATACGATATTTGTTGGA 89   TTTGTTGGAT 438   TACGA-   -   CCTG   TT
        TTCCTGATTATTTACTATAA   TCCTGATTAT   TTGA   TATTTGT TGGATT ATTAT A
        TATAATCTAGACAGATAGAT   TTAC |||| |||||| ||||| |||||
        GATTCGA   AGCT   ATAGACA ATCTAA   TAATA /
                               TAGTAG   G   TA--   TC

GAM104 AATATCGGGCCAATAGTAGC 90   GGCCAATAGT 439   CG   A AG   - C
        TATTACCGTCGACACGTGTA   AGCTATTACC   AATAT GGCCA TAGT CTATTAC CGT G
        GTGGGAACTATGGCCAAATG   GTCG ||||| ||||| |||| ||||||| |||
        TT   TTGTA CCGGT ATCA GGTGATG GCA A
                                  AA - AG   T C

GAM105 AGACTTCTGGCGGTTGCCAT 91   TTATCCCAAT 440   ---- CG   CCAT-   ATA
        AGAATATACGTCGTTCTTAT   TACCAACTAG   AGACTTCT GG GTTG   AGAAT C
        CCCAATTACCAACTAGAAGT   AAGT |||||||| || |||| |||||
        CT   TCTGAAGA   CC TAAC   TCTTG /
                               TCAA AT   CCTAT   CTG

GAM106 GAAGTTTTTGGAGAATAATA 92   GGAATTGGAG 441   GAATAAT   ------------- TATT   CA
ACAA   G
          TGACTCATGATCTATTTCGT   GCGATGATCT   GA   ATGACTCAT   GATC TCGTC TAA
TCTA A
          CCATAAACAATCTAGACATA   TAAT || |||||||||| |||| ||||| ||| ||||
          GGAATTGGAGGCGATGATCT   CT   TGCTGAGTA   CTAG   AGCGG GTT GGAT
C
          TAATTTTGTGCAATGAGTCG   AAC----   ACGTGTTTTAATT T--- AG AA-- A
          TCAATCCTATAACTTC

GAM107 TAATCCCTTTTTCAGATGCC 93   GCGCTCCCCT 442   - TTTTCA GCCTCTTTTA   CA
        TCTTTTAGTTTATCAAAAAT   AGTCGTACTC   TAATCC CT   GAT   GTTTAT A
        AAGCGCTCCCCTAGTCGTAC   AGAG |||||| || ||| ||||||
        TCAGAGGATTA   ATTAGG GA   CTG   CGAATA /
                               A CTCATG ATCCCCTCG-   AA

GAM108 TTAAATAGTTACGCAATATC 94   TTAGCTGTTT 443   TTAC   T C------   T- T
        TCAATAGTTTCATAATTGTT   TCATCAAGAT   TTAAATAG GCAA ATCT   AATAGTT CA A
        AGCTGTTTTCATCAAGATTT   TTGT |||||||| |||| |||| ||||||| ||
        GTACCCTGTTTAA   AATTTGTC TGTT TAGA   TTGTCGA GT A
                                CCA- - ACTACTT   TT T

GAM109 TGCCGTTACTATTATTTATA 95   TATTATTTAT 444   C   AT--- TAA TG   A C
    ACTGATGTAACCCACGTAAC   AACTGATGTA   TGC GTTACTATT   TTA C ATGT AC C
    ATTGGAATTAACTATCGATA   ACCC ||| |||||||| ||| | |||| ||
    GTAATGCA   ACG TAATGATAG   AAT G TACA TG A
                         -       CTATC TAA GT   A C

GAM110 ACACGCGTGTCTAACTAGTG 96   ACGCGTGTCT 445   G   -   A   TCGTCA   T AGTT A
    GAGGTTCGTCAGCTGCTCTA   AACTAGTGGA   ACAC CGTGTC TAACT GTGGAGGT   GCTGC CT
  TGA T
    GTTTGAATCATCATCGGCGT   GGTT |||| |||||| ||||| |||||||| |||||| || |||
    AGTATTCCTACTTTTACAGT   TGTG GCACAG ATTGA CATTTCA   TGATG GG   ACT C
    TAGGACACGGTGT   -   G   -   TCCTTA   C CT-- A

GAM111 CAGCATCCGGCTTATCCGCC 97   CGAGGAGGAA 446   A   T- - G   C TCA
    TCCGTTGTCATAAACCAACG   TATCGTCGGA   CAGC TCCGGC TAT CC CCTC GTTG T
    AGGAGGAATATCGTCGGAGC   GCTG |||| |||||| ||| || |||| ||||
    TG   GTCG AGGCTG ATA GG GGAG CAAC A
                 -   CT A A   - CAA

GAM112 CCATTAATATCTCTATTATA 98   TATACCAGAA 447   ATCTCTATTATAGCT   AC   TC
    GCTTCTGGACATAATTCATC   TTAATGG   CCATTAAT   TCTGG ATAAT A
    TATTATACCAGAATTAATGG |||||||| ||||| |||||
                 GGTAATTA   AGACC TATTA T
                     --------------- A-   TC

GAM113 CTTCATTATGAATTGATTCT 99   TGAATTGATT 448   T   T   --- G TAT-- C--   CA TT   TAG
TT
    TGAGGTATAAACCTAACACA   CTTGAGGTAT   A GAAT GATTCT T AGG   AAAC TAACA AA
ATATTAT AC T
    AATTATATTATTAGACTTTT   AAAC | |||| |||||| | ||| |||| ||||| || ||||||| ||
    CGTATGTAATGTCTTTCATG   T TTTA CTAAGA G TCC   TTTG ATTGT TT TGTAATG
TG /
    TTATAAGTTTTTAATCCTGG   -   T   TAA G TAATT AAT   AC TC   TA- CT
    AATAGAATCTATTTTAATGA
    GG
GAM114 GAAGAGATGTAACGGGAACA 100   ACGGGAACAG 449   --   ACG   CAG   TG
    GGGTTTGTTGATTCGCAAAC   GGTTTGTTGA   GAAGAG ATGTA GGAA GGTTTGT A
    TATTCTAATACATAATTCTT   TTCG |||||| ||||| |||| |||||||
    C   CTTCTT TACAT TCTT TCAAACG T
                         AA   AA- A--   CT

GAM115 GTTAATACGTCTTGCACGTA 101   TGCACGTAAT 450   -   C- CTAT   CC
    ATCTATTATAGATGCCAAGA   CTATTATAGA   GTTAATA CGTCTTGCA GTAAT TATAGATG A

```
TATCTATATAATTATTTTGT     TGCC          ||||||| ||||||||| ||||   |||||||||
AAGATGATGTTAAC                   CAATTGT GTAGAATGT TATTA  ATATCTAT A
                                 A       TT      AT--      AG


GAM116  GTTTTTGATATCGATCTGAT 102    TTCATATTTA 451    ATCG    T  CCTA    A-
ATAACGTGCTC      A  TT
     TGATCCTAGAACTAGATATA      TTAGATACCG       ATCTGAT GAT   GAACT  GATATATTA
ATTAGGC GT  A
     TTAATAACGTGCTCATTAGG     CATT        |||||| |||   |||||  |||||||||       ||||||| ||
CAGTTTATGGCAGCTTGATA               TAGATTA TTA  CTTGA  TTATATGAT      TAGTTCG
CG  /
     ATTAGATATAGTATATTCCA            CA--    T TA--    CC       ATAGATTAA--     A GT
GTTCATATTTATTAGATACC
GCATTGC
GAM117  TAATGGTGACAGGGTTAGCA 103    TATGATCCTC 452      T C    GCA-    CCAATCAATA    TTT
     TCTTTCCAATCAATAATTTT     TCTCATTG      TAATGG GA AGGGTTA  TCTTT      ATTTT  A
     TTTAGCCGGAATAACATCAT          |||||| || |||||||  |||||        |||||
CAAAAGACTTATGATCCTCT              GTTACT CT TCCTAGT   AGAAA       TAAGG  /
CTCATTG                      - C    ATTC   ACTACTACAA    CCG


GAM118  TCGTTTAGATTTTCCATCTG 104    TAGGAGAGTT 453     TTA T TCCATCT   TATCG  A   C CG-
     A
     CCTTATCGAATACTCTTCCG      ACTAGGCCCA    TCGT  GA TT    GCCT   AAT CTCTT CGT
ATGTCT C
     TCGATGTCTACACAGGCATA      ACTG        |||| || ||     ||||    ||| ||||| |||  ||||||
AAATGTAGGAGAGTTACTAG               AGCA  CT AG     CGGA    TTG GAGGA GTA  TACGGA A
GCCCAACTGATTCAATACGA              TAA  T TCAACC-   TCA-- A   T AAA    C


GAM119  TGATGTAGTACTTTGATGAT 105    TAAGTCTTCC 454      AGT  T T  TTCC   CC
     TTTTCCATGGCCCATTCTAT      AAGTTGGCAT      TGATGT ACTT GA GATTT  ATGG  C
     TAAGTCTTCCAAGTTGGCAT      CA         |||||| |||| || ||||| ||||
CA                         ACTACG  TGAA CT CTGAA  TATC  A
                           GT-  C T  T--- TT


GAM120  TTGGTAACTCATTCTATATA 106    TAGAATATAC 455       A TC    -----   G T  GTT
     TGCTTTCCTTGTTGATGAAG      TCAATAGAAT     TTGGTA C ATTCTA   TATAT CT TCCTT  G
     GATAGAATATACTCAATAGA      TTGT        |||||| | ||||||   ||||| || |||||
ATTTGTACCAA                AACCAT G  TAAGAT    ATATA GA AGGAA  /
                            - TT   AACTC    A T   GTA


GAM121  TTTCTAAGATATGGGATTTT 107    TAAGATATGG 456      A--  A G   ACT   T A   TC
     ACTTAATATAATATTATTTC      GATTTTACTT      TTTCT AGAT TGG ATTTT  TAATA AAT TTATT  C
     CCGTAATAAATTTTATTAGA      AATA        |||||  |||| ||| |||||  |||||| ||| |||||
AATGCCAAATCTATAAGAAA              AAAGA  TCTA ACC TAAAG  ATTAT TTA AATAA  C
                       ATA  A  G    ---   T  -   TG
```

GAM122 TCTAGTTATCAATAACAGTT 108   TCAATAACAG 457   GTTA   C--   - TTAG- TA
        AGTAGTTTAGTTATACATTG   TTAGTAGTTT   TCTA TCAATAA AGTTAGTA GT   TTA C
        AATCATACATATTAATTTTT   AGTT |||| ||||||| |||||||| || |||
        TTATTGAGATAGA   AGAT   AGTTATT TTAATTAT CA   AGT /
                              AG--   TTT   A TACTA   TA

GAM123 TCCGCACTATCGATTTGATA 109   TAAAGCTATC 458   CACT   T-   -   - T
        CTTTCTTTTCAGAGTAAAGC   GTCATTGATC   TCCG   ATCGAT TGATA CTTT CTT T
        TATCGTCATTGATCATCGGA   ATCG |||| |||||| ||||| |||| |||
                              AGGC   TAGTTA GCTAT GAAA GAG C
                              TAC-   CT   C   T A

GAM124 TTCTAGAGTAGTAGTCCTAA 110   TCTTATTGTC 459   T   CT CATTCTCT---   TTAT- TCCT
TT ATGT GT
        TCATTCTCTTAAATTTTATG   TGATTTATTT   TAG AGTC AAT   TAAATT   GTA AGT CA
CTC A
        TATCCTAGTTTCAATGTCTC   CTTT ||| |||| ||| |||||| ||| ||| || |||
        GTAATGAGTTTGTGCTGCTC   ATC TCGG TTA   ATTTAG   TAT   TCG GT   GAG /
        TTATTGTCTGATTTATTTCT   - TT CCATTTTCTTT   TCTGT TC-- TC GTTT TA
        TTTACCATTTTGGCTCTATT
        CTGAA
GAM125 GATCTATAGTCTTCGTATCT 111   TGTTACGAAA 460   -   CTTC- CT T AA   TAT   TT
        GTTACGAAAATCAATATATT   ATCAATATAT   GATC TATAGT   GTAT GT ACGA ATCAA
ATTCAGGA A
        CAGGATTATTTTCTGAATCA   TCAG |||| ||||||| |||| || |||| ||||| ||||||||
        CTTGATTCGTCACTAATATA   CTAG ATATCA   TATA CA TGCT TAGTT TAAGTCTT /
        CATAACTATATGATC   T   ATACA   AT C --   CAC   TT

GAM126 TGTACGATTGTATTGCGTTA 112   TTAGTCAATG 461   A TATT   -   AC TAA
        CTAAACGATAAATAATTCTT   CTTTAACGTA   TGTACG TTG GCGTT ACTAA GA A
        AGTCAATGCTTTAACGTACA   CA ||||||| ||| ||||| ||||| ||
                              ACATGC AAT   CGTAA TGATT CT T
                              - TT--   C   -- TAA

GAM127 GCGTATCTACTACTCCAAAT 113   TCCAAATTGC 462   CTACTCCA   A TTC TAT
        TGCAGTTTCTGGTATCCATC   AGTTTCTGGT   GCGTATCTA   AATTGC GT TGG C
        CATACGCGTAATTATCAAAT   ATCC ||||||||| |||||| || |||
        AGATATGT   TGTATAGAT   TTAATG CG ACC /
                              AAACTA--   - CAT TAC

GAM128 TATATCCTACCGCTTTTTAT 114   TAATAAGATG 463   CG TTT C-- --   ATG TTTTATGTTAT
TTA   TTA
        CAACTATGTAATGAGTTTTT   CTAATACATC   CT TAT AACT ATGTA AGT   GTCTT
GTTAGG A

```
ATGTTATGTCTTTTAGTTAG     AGGT           || ||| |||| ||||| |||        ||||| ||||||
GTTAATATTCTAATAAGATG          GA  ATG  TTGG  TACAT  TCG       TAGAA  TAATCT  /
CTAATACATCAGGTTAAAGT          A-  TT-  AAA   AC     AA-  -----------  ---    TAT
ATTAGAATGGGATTATA


GAM129  ATCAGACCATATACTGAGTT 115   TGAGTTGGCT 464     AC TAT    TT   -  ----  -  CGT
        GGCTACTATCTTGTACGTAT     ACTATCTTGT     ATCAG CA ACTGAG GGCTA CTA   TCT TGTA  A
        ATTGCATGGAATCATAGATG     ACGT          ||||| || |||||| ||||| |||   ||| ||||
        GCCTTTTCAGTTGAACTGGT             TGGTC GT TGACTT CCGGT GAT   AGG ACGT  /
                             AA ---   TT   A  ACTA  T  TAT


GAM130  TAGTCACGACTGAAATAACC 116   CGGCATGGTT 465     ACT   AA-- C --     TTT
        GCGTGATTATTTTTGGTAT      TCTGTGACTA     TAGTCACG GAAAT  CCG GT GATTAT  T
        AATTCTACACGGCATGGTTT         |||||||| ||||| ||| || ||||||
        CTGTGACTA                   ATCAGTGT CTTTG  GGC CA TTAATA  T
                          ---  GTAC  A TC   TGG


GAM131  TCATCCAATATTATTGAAAT 117   TGATGGACAG 466  CA   TTGA-   TT   CAG  TACAAATA
A  AC T C
        GACGTTGATGGACAGATGAT     ATGATACAAA     ATATTA  AATGACG GATGGA ATGA     AGA
GGT GG AC T
        ACAAATAAGAAGGTACGGTA     TAAG        ||||||  |||||| |||||| ||||     ||| ||| || ||
        CCTTTGTCCACCATCTCCTC             TGTAAT   TTACTGT TTATCT TACT     TCT CCA CC
TG T
        CAATTCATGCTCTATTTTGT             --  TTCAA   T-  CG-  TAACCTCC A -- - T
        CATTAACTTTAATGTATGA


GAM132  TCGTCGGTATTTTTTATGGC 118   CGGTATTTTT 467    CG     A C  TTTACTCT
        AAACTTTACTCTTCCAGCAT      TATGGCAAAC     TCGT GTATTTTTT TGG AAAC     T
        CCGTTTCTAAAAAAATATTA      TTTA        |||| ||||||||| ||| ||||
        ACGA                  AGCA TATAAAAAA ATC TTTG     C
                          AT     - -  CCTACGAC


GAM133  ACCATTCCAAGTCACTGTGT 119   TATCATAAGC 468    TTCCA   CTG- TA GAT
        GTAAGAAGATTATATTCTAT      TTGACTACAT     ACCA  AGTCA  TGTG AGAA  T
        CATAAGCTTGACTACATTTG      TTGG        |||| ||||| |||| ||||
        GT                    TGGT  TCAGT  ATAC TCTT  /
                          TTACA  TCGA  TA ATA


GAM134  ATATCTTTAACTAAGTCAAT 120   TCAATGATTT 469      AACT    ATTTCATCAACCG--  TC
        GATTTCATCAACCGTTAGAT      CATCAACCGT     ATATCTTT AAGTCAATG         TTAGA T
        CTATTTTAAAGTTAATCATA      TAGA        ||||||||| |||||||||       |||||
        TAGGCATTGATTTTTAAAAG             TATGGAAA TTTAGTTAC        AATTT /
        GTAT                  ATT-     GGATATACTAATTGA  TA
```

GAM135 CAGCCGAAACATATTCTACC 121   CATGGCTCCG 470   CC   ATTCTACC GC   A- T
        ATGGCTCCGTTTAATTTGTT   TTTAATTTGT   CAG GAAACAT   ATG TCCGTTT ATT G
        GATGAAGATGGATTCATCCT   TGAT ||| ||||||| ||| ||||||| |||
        TAAATGTTTTCTCTG   GTC TTTTGTA   TAC AGGTAGA TAG T
                                   TC   AATTCC-- TT   AG   T

GAM136 CCGTTTTTAGACCGAGACTC 122   TAACTCGGAT 471   TTT-   -   ACTCCA   TAAA   CA
        CATCCGTAAAAATGCATACT   CTGCTATATG   CCGT TAGA CCGAG   TCCG AATG T
        CGTTAGTTTGGAATAACTCG   G |||| |||| ||||| |||| ||||
        GATCTGCTATATGG   GGTA GTCT GGCTC   AGGT TTGC A
                                   TATC   A   AATA-- TTGA   TC

GAM137 CGCTTCTATCTTGTTTAGAT 123   TGACTAGATA 472   ----   GTTT   TT TAAA   TCTC--
ACATA
        TTATTTTTATAAAGTTTAGT   AACTATCAGT   TCTATCTT AGATTTATT TA GTTAGTC
CTTCCA   A
        CTCTCCTTCCAACATAATAA   AAGT |||||||| |||||||||| || |||||||| ||||||
        AAGTGGAAGTCATTTGACTA   AGATAGAG TTTGAATGA AT TAGATCAG   GAAGGT
  T
        GATAAACTATCAGTAAGTTT   AAGC   ATAT   CT CAAA   TTTACT   GAAAA
        TATAGAGATAGACGAACAAT
        TAGCG
GAM138 GACATACATACTATCTTTAA 124   ACTATCTTTA 473   C   TT----------   CTCT   C---   AAT--
T
        TAGAACTCTTTTCATCCAGT   ATAGAACTCT   CATA TATCT   AATAGAA TTTCAT CAGTTG
 GGA T
        TGAATGGATTCGTCCTTAAC   TTTC |||| ||||| ||||||| |||||| |||||| |||
        CAACTGATTAATGAGATCTT   GTAT GTAGA   TTATCTT AGAGTA GTCAAC   CCT
C
        CTATTTTATCATTTTCCAGA   A   CCTTTTACTATT   CT--   ATTA   CAATT G
        TGATATGTATGTC

GAM139 TACAAAGGAGATGATTTATC 125   TATGGTATTA 474   ----------   TTATCTAT TT - C   TC
 A
        TATGGTATTAAGAATTCGTT   AGAATTCGTT   ACAAAGGA   GATGAT   GGTA AAG AATT
GTTTT GAC T
        TTTCGACATCCGTCAAAACC   TTTC |||||||| |||||| |||| ||| ||||||| |||
        AATTCCTTTTTGCCTGTATC   TGTTTCCT   CTACTA   CCGT TTC TTAA CAAAA
CTG C
        ATCCAGTTTTCCATCCTTTG   ACCTTTTGAC   TGT----- TT C   C   -- C
        TA

GAM140 TGTCACTTTGTTATTGGCCA 126   TTCCTCGGCC 475   ---   T--   AACC--   TT
        ACCTTTGTTGTACAAATTCC   ATTTTAATAT   TGTCACTT TGTTA TGGCC   TTTG G
        TCGGCCATTTTAATATTTAA   TTAA |||||||| ||||| ||||| ||||
        GTGATA   ATAGTGAA ATAAT ACCGG   AAAC /
                                   TTT   TTT   CTCCTT   AT

GAM141 TTGCTAGACACCTTTTCAAT 127   TTTGATAAAG 476   T ACAC- - T   A   T
    GTTTAATTTTTTTGAAATAA   CCTTCCTCGC   TTGC AG   CTTT TCAA GTTTA TTT T
    GCTTTGATAAAGCCTTCCTC   AA |||| || |||| |||| ||||| |||
    GCAA   AACG TC   GAAA AGTT CGAAT AAG T
                  C CTTCC   T   T   A T

GAM142 CACCGCCTCTAGATATCGCC 128   CGCCTTTATT 477   CG   ATCG-- TTTAT ACATT
AAATCCA
    TTTATTTCCACATTAGATGG   TCCACATTAG   CAC CCTCTAGAT CC   TTCC   AGATGGT
A
    TAAATCCAATAGTGAAACTA   ATGG ||| ||||||||| || |||| |||||||
    TCTTTTTAGGAATGTATGGA   GTG GGAGATTTG   GG   AAGG   TCTATCA   /
    CTCGCGTTTAGAGGAGTG   A-   CGCTCA TATGT ATTTT   AAGTGAT

GAM143 GACACTTTGCCGGCGGTTGT 129   ACATATCCGT 478   CT CC   T--   ATTTATCA
    AGATTTATCATATTTCTCCA   TACAATTTGT   GACA TTG GGCGG TGTAG   T
    CTACATATCCGTTACAATTT   T |||| ||| ||||| |||||
    GTT   TTGT AAC TTGCC ACATC   A
                  TT A-   TAT   ACCTCTTT

GAM144 GAGACTTGATAGATATTAGT 130   TCACCACGTG 479   - -   TAG   TA-   TTGAA
    GATGAATTGAAAATTATTTT   TGTTTCAGGA   GA GA CTTGA ATAT GTGATGAA   A
    TATCACCACGTGTGTTTCAG   TCAT || || ||||| |||| ||||||||
    GATCATC   CT CT GGACT TGTG CACTATTT   A
                  A A   TTG   CAC   TTATT

GAM145 GGCTATTCTGGCGGCTAGAA 131   TGCTATTTCG 480   C   TA   TAAT GA TGT
    TGGCATAATCCGGATGTTGT   GCTGCCAGAG   GG TATTCTGGCGGC GAATGGCA CCG TGT
G
    GTAGTACAAGTGGCTGCTAT   TGTC || |||||||||| ||||||| ||| |||
    TTCGGCTGCCAGAGTGTCC   CC GTGAGACCGTCG TTTATCGT   GGT ACA T
                  T   GC   C--- GA TGA

GAM146 TATATACGATAAGATATGTT 132   TAAGATATGT 481   C   ---   TTT A ------ -- AATT
    TATTCATAAACGCGTCAAAT   TTATTCATAA   TATATA GATAA GATATG ATTC TAAAC   GCG
TCA T
    TTTTCATGAATCGCTAAGGA   ACGC ||||||||| ||||| ||||| |||| ||||| ||| |||
    GTTTAAGAATCTCATGTCAA   ATATAT CTGTT CTGTAC TAAG ATTTG   CGC AGT   /
    ATTGTCCTATATA   C   AAA   TC- A   AGGAAT TA ACTT

GAM147 TCTGGTTCTATGTTCCTCGT 133   TCTATGTTCC 482   TC   ---   TT C TATT
    TTCCTGTATTCTTTTTAAGA   TCGTTTCCTG   TCTGGT TAT GTTCCTCG TC TG   C
    TCGAGGAACGCCATAATATC   TATT |||||| ||| |||||||| || ||

AGA   AGACTA ATA CAAGGAGC AG AT   /
                              TA CCG   T- A TTTT

GAM148 GGAACAAATATAGTATCTGA 134   TATAGTATCT 483   A- G C AA   TTCATA TC
        AATCATATTCATATATCCCG   GAAATCATAT   GGAACAAAT TA TAT TG ATCATA   TA C
        TTAGAGGTCTATGATAATAT   TCAT ||||||||| || ||| || |||||| ||
        ATAGTAGCGTTGTTCC   CCTTGTTTG AT ATA AT TAGTAT   AT C
                                    CG G T AA   CTGGAG TG

GAM149 TTCCTTTTCGTTGATCTCTC 135   TCGTTGATCT 484   CGTT   TCT TA   G
        ATAGATTTAGAAATAAATTC   CTCATAGATT   TTCCTTTT GATC CA GATTTA A
        TTGCGATCCTCCAAAAGGAG   TAGA |||||||| |||| || ||||||
        GAGGAAAA CTAG GT TTAAAT A
                                    CCTC   C-- TC   A

GAM150 ATTGGAATTATAATATAGGT 136   ATGCATCGGT 485   TATA- G   ---- C - G
        GTATTTGCGCACTCGCGACG   AAATATAGCT   ATTGGAAT ATATAG TGTATTGC GCA TCG C
A
        GTTGATGCATCGGTAAATAT   GTAT ||||||| ||||| ||||||||| ||| ||| |
        AGCTGTATCTAATGTTCTAG   TGATCTTG   TATGTC ATATAAATG CGT AGT G C
T   TAATC   G   GCTA - T G

GAM151 GTATATCATCAGCTGAAAAA 137   TTCCTTCGGC 486   CA--------- AAAC   TT
        CTATGTTTTACACGTATTCC   ATTTCTTTTT   GTATATCAT   GCTGAA TATGT T
        TTCGGCATTTCTTTTTAATG   AATG |||||||| ||||| |||||
        ATATAT   TATATAGTA   CGGCTT ATGCA /
                                    ATTTTTCTTTA   CCTT   CA

GAM152 ACAACTATGCCTTTTAGATT 138   TAAGATAAAC 487   A CT-- A   CCTAATT   CACGG
TAT
        ATCTCCTAATTTATAACACG   TAAATCTCGC   ACAACT TGC TTTAG TTATCT   TATAA CCG
A
        GCCGTATACACTTGGAATAC   AAAG |||||| ||| |||| ||||| ||||| |||
        TTGTACAATCTAAGATAAAC   TGTTGA ACG AAATC AATAGA   ATGTT GGT C
        TAAATCTCGCAAAGTTGT   A CTCT A   ATCTAAC   CATAA TCA

GAM153 GGATTTTAGAATTTCCAAAT 139   TGAAATCCAA 488   T AATT AAA---   --- T
        TCACCAGCGATTTATCGGTT   GGATTTATTA   GGAT TTAG TCC   TTCACCAG CGA T
        TTGGTGAAATCCAAGGATTT   ATGT |||| |||| ||| |||||||| |||
        ATTAATGTCC   CCTG AATT AGG   AAGTGGTT GCT T
                                    T ATTT AACCTA   TTG A

GAM154 ATGGTCGAAGTATAGCAGGA 140   TAGCAGGACA 489   ----   A CATT- GCTC CCG TA

CATTGATGCTCTAGACCGTG   TTGATGCTCT   ATGGT   CGAAGTATAGC GGA   GAT   TAGA   TG
T
TATAACAAAATCTACAAATT   AGAC ||||| |||||||||| ||| ||| |||| ||
TTTCATCCGCTATATTTTGT   TATCA   GTTTTATATCG CCT   TTA   ATCT   AC /
TTCACTAT   CTTT   -   ACTTT   AAC-   AAA AA

GAM155 GGTGTTAATCCACTATATGT 141   TCCACTATAT 490   T - -------   -   A---   C ATAACA
CAT
TTCTGTAGCGGCTGATAACA   GTTTCTGTAG   GGTGT AATC CACT   ATATGT TTCTGT GCGG
TG   CAG   C
CAGCATCCAACTGAGCATCC   CGGC ||||| |||| |||| |||||| |||||| |||| || |||
GCGTCCGCAGAGCACATATT   CTACA TTGG GTGA   TATACA GAGACG   CGCC AC
GTC /
TTTAACAGTGAGGTTACATC   - A CAATTTT   C   CCTG   T GA---- AAC

GAM156 GTTAGCAAGAAATTAACATT 142   TTCCGCATAT 491   C A--   CATTG ATTC   A   T   TCCC
GGCATTCGAACACTCTGGAT   TTTAATGACT   GTTAG AAGA ATTAA   GC GAAC CTC GGA   A
CCCAACATTCTCGAGGTTCC   CTTC ||||| |||| ||||| || |||| ||| |||
GCATATTTTAATGACTCTTC   CAATC TTCT TAATT   CG   CTTG GAG TCT   /
TAAC   - CAG   TTATA C---   - C TACA

GAM157 TCAGTGGGTACTCCCGGAGG 143   GAGCTCAACA 492   TACTCCC-- A   ------------ GT
CGGATCCCGTTTAGGGAGCT   CTTACTCCGC   TCAGTGGG   GG GGCGGA   TCCC T
CAACACTTACTCCGCCACCC   CACC ||||||| || ||||| ||||
ATATTTATCTCATTGA   AGTTACTC   CC CCGCCT   AGGG /
TATTTATAC A   CATTCACAACTCG   AT

GAM158 ACACGACTGTGGTAGATTTG 144   TGTGGTAGAT 493   C TG--   A   T   AGA C   T
TTCTATAGAGCCGGTTGCCG   TTGTTCTATA   ACA GAC TGGTAG TTTGT CTAT GC GG T
CAAATAGATAGAACTACCAA   GAGC ||| ||| |||||| |||| |||| || ||
TATGTCTGT   TGT CTG   ACCATC AGATA GATA   CG CC /
- TATA   A   - AA- - G

GAM159 ACAGTTTGAAAAATAACAGT 145   AACAGTATCA 494   AATA   TCATTTAAACAT   TG
ATCATTTAAACATTTAACTT   TTTAAACATT   ACAGTTTGAAA ACAGTA   TTAACT C
GCGGGGTTAATTTCACAACT   TAAC |||||||||| ||||||| ||||||
TTACTGTTTTTAAGCTGT   TGTCGAATTTT TGTCAT   AATTGG /
----   TTCAACACTTT-   GG

GAM160 CCACCTGTTTTAACATATAA 146   TAATATTGAT 495   T-   --   GA T TATCCGTCATTG-   -------
---   TT
TAGGCAGGAGATAGATATCC   AAAATCTCCA   ATAATAG GCAG GA AGA   CAATATT
CCT T
GTCATTGCAATATTCCTTTT   TTCT ||||||| |||| || ||| ||||||| |||

```
        CGTAGGCACACAATCTAATA                    TATTATT CGTC TT TCT        GTTATAA      GGA  C
        TTGATAAAATCTCCATTCTC              TC     TA   TC C  TACCTCTAAAATA     TCTAACACAC  TG
        TTCTGCATTTATTATCTT
        GTTTCGGTGG
GAM161  TACTTTTTCTTTACCTTGAG 147    TGAGAATATC 496        TTTACC  -- T - CGT   TGG
        AATATCCATCGTTTGCTTGG          CATCGTTTGC     TACTTTTTC   TTGA GAA ATC CAT  TTGCT  T
        TCAATAGCGATATGTGATTT         TTGG          |||||||||   |||| ||| ||| |||   |||||
        TTTATCAACCACTCGAAAAA                 ATGAAAAG     AACT TTT TAG GTA  AGCGA  C
        GTA                         CTCACC   AT  T  T  T--   TAA


GAM162  TAGTACTAGACTGACTTCTA 148    TATTAAAGTC 497       TAC   CT   C-- A  A  CTCACCTG
        ACAAACATCTCACCTGCCAT          TTCTATTTCT       TAG  TAGA  GACTT  TA CAA CAT     C
        AAATAAATGCTTGATATTAA         A           |||  ||||  |||||  || ||| |||
        AGTCTTCTATTTCTA               ATC  ATCT  CTGAA   AT GTT GTA      C
                TTT   T-    ATT A  C  AATAAATA


GAM163  AAATTATTCTTATCATGCGT 149    ATTATTCTTA 498     T    TATCAT  TCC   TCC  T
        CCATAGTCCCGTTCCGTATC          TCATGCGTCC       AAA TATTCT   GCG  ATAG  CG T
        TATTATCGTTAGAATATTTT          ATAG         ||| ||||||   ||| |||| ||
                TTT ATAAGA     TGC  TATC  GC /
                T    T----- TAT   TAT  C


GAM164  ACATCCATTTTTAAGTATTA 150    TTTTTAGATA 499        C  TTA       AAA-   TC GTTTA
        TATTAAAATTTAATCAATGT          AAAAATATAA     ACATC ATTT  AGTATTATATT  ATTTAA AAT    T
        TTATTTTTAGTTTTTTAGAT         TATT          ||||| |||| |||||||||||  |||||| |||
        AAAAAATATAATATTATGAG                 TGTAG TGAG   TTATAATATAA   TAGATT TTG    /
        TCGATGT                      C  TA-       AAAA   TT ATTTT


GAM165  ATTTTATTACCGTGTGGGAT 151    TACCGTGTGG 500       TT  G   G ATAAA  C  TCCAT-- A
G
        ATAAAGTCCTTGATCCATT          GATATAAAAG       ATTTTA ACC TGTGG AT   AGTC TTGA      TG
TCTG A
        GATCTGGAAACGGGCATCTC         TCCT          ||||||| ||| ||||| ||   |||| ||||     || ||||
        CATTTAAGACTAGATGCCAC              TAAAAT TGG GCACC TA   TCAG AATT     AC GGGC A
        GGGGTTTAAAAT                  T-  G   G GA---  -  TACCTCT -  A


GAM166  CTATCGGTTTACTATTTATT 152    GTTTACTATT 501       C  T   TTAT    G  A
        GATAACGCAGATGTTTGAGT          TATTGATAAC     CTAT GG TTACTAT  TGATAAC CAG T
        TGTCATCCATGGTAATCCAT         GCAG          |||| || |||||||  ||||||| |||
        AG                    GATA CC AATGGTA   ACTGTTG GTT G
                - T   CCT-    A T


GAM167  GTACATGTGAAAATAGTCAT 153    CATGTGAAAA 502       CA-    T- TCA  - GAT    AA AAAGT
 CT
```

```
     ATTCCTGATTAGGATAATCA        TAGTCATATT     GTA  TGTGAAAA AG  TATT CCT  TAGGAT TC
TAACAA A
     AAGTTAACAACTACTTTGTT       CCTG          |||  |||||||| ||  |||| |||  ||||| ||   ||||||
     ACGGACGATCTTATTAAGGT              CAT  ATACTTTT  TC  ATGA GGA  ATTCTA AG    ATTGTT
/
     AGTACATCTTTTTTTCATAA                TTA   TT TAC  T  ATT   GC GC---    TC
     TTTAC


GAM168  TGAAGAACATATTTAATTCA 154   TGAATACAAC 503     AACATATTTA  GA   AAAAT
     GATCTAAAAAATACATATAT        GAATACTTCA      TGAAG     ATTCA TCTAA   A
     TAGAATGAATACAACGAATA             |||||        ||||| |||||
     CTTCA                     ACTTC       TAAGT AGATT   C
                          ATAAGCAACA   A-   ATATA


GAM169  CAGCTACTTCTACCCAATCA 155   TTAATTGGTT 504    TC   CAA   GTAT    T   TTT---- --
TA
     CCAGGCAATAAATGTATTTT        TAATCGTTTA    CAA ACCAGG  TAAAT   TTTATTTT AATAAAC
CC TTGGCG T
     ATTTTTAATAAACTTTCCTT        TTAA        |||  |||||| |||||   ||||||| |||||||    || ||||||
     GGCGTATTCTTGTTAATTGG              GTT TGGTTC  ATTTA  AAATGAAA TTATTTG    GG
AATTGT T
     TTTAATCGTTTATTAAAGTA                --   A--  ----    -  CTAATTT TT   TC
     AAATTTAACTTGGTTTGACG
     CTAATAGTTG
GAM170  TTGCAAGTTTCTGTTTCTGA 156   TTCCACAGAG 505    C  TC  T A-   CG TCC
     GAGTAAACGAATCCCTGTTT        CACTAATTTC     TTG AAGTT TGTT CTG GAGTAAA AA  C
     TATTTTATTCCACAGAGCAC        CAA         ||| ||||| |||| ||| ||||||| ||
     TAATTTCCAA                 AAC TTTAA ACGA GAC CTTATTT TT  T
                  C  TC  -  AC    TA TTG



GAM171  CCGCTTCTATTTACTCCCGC 157   CCGCAGCACA 506     C--   CTCCCG-- AC   A AA
     AGCACAATGAACCAACACGG        ATGAACCAAC     CCGCTT TATTTA    CAGC AATGA CC C
     GCTCGTTTCGTTGATCACAT        ACGG          ||||||  ||||||    |||| ||||| ||
     TTAGATAAAAAGGCGG                 GGCGGA  ATAGAT    GTTG TTGCT GG  A
                  AAA   TTACACTA   CT   C GC



GAM172  GTTAGGCAATGTATATTTAT 158   CAATGTATAT 507     - CA    TATTTAT
AAATTTAAAACATATT  CT
     CCATCGTCAAATTTAAAACA        TTATCCATCG     GTTA GG ATGTA    CCATCGTC        TGAA T
     TATTTGAACTTAACTTCAGA        TCAA         |||| || ||||||   ||||||||         ||||
     TGATGGTGCATCCATAGC               CGAT CC TACGT     GGTAGTAG         ACTT A
                  A  --   -------     ---------------- CA



GAM173  ACTTTTTATGAAGAGCCGCG 159   TGAAGAGCCG 508     TAT A  CG  A---   C
     TTTAACAATGCTTTATTGTC        CGTTTAACAA     ACTTTT  GA GAGC CGTTT  ACAATG T
     TCCGAACGTAGCTCTCTTAA        TGCT         |||||| || |||| |||||   ||||||
```

GAGT   TGAGAA CT CTCG GCAAG TGTTAT /
                        TT- -   AT   CCTC   T

GAM174 TCGTCATATCCCGTATAGTC 160   TTGAATTTAC 509   TATCCC ---- CA----   A
        AGAGATAGGAATCTTGAATT   TAATCTTGCC   TCGTCA   GTA TAGT   GAGAT G
        TACTAATCTTGCCCTTGTTG   CTTG |||||| ||| |||| |||||
        GCGG   GGCGGT CGT ATCA   TTCTA G
                                     TGTTCC TCTA TTTAAG   A

GAM175 CGCCTAATAGCTTGCGGCAG 161   TCCAATCGCA 510   ----   - CA- TGT
        ATATGTTTTCTTATCCAATC   TAGCTATAAA   CGCCTA ATAGCT TGCGG GATA T
        GCATAGCTATAAATAGGCG   ATAG |||||| |||||| ||||| ||||
                                     GCGGAT TATCGA ACGCT CTAT T
                                     AAAA   T   AAC   TCT

GAM176 GCGCACTAATTGCCAATATA 162   TTGATGTTTT 511   C TAATT   T A   AAGAA
        ATAACAAAGAATATAAGTGT   GGCTGCTTGT   GCG AC   GCCAA ATA TAACA   T
        TGATGTTTTGGCTGCTTGTA   ACGC ||| || ||||| ||| |||||
        CGC   CGC TG   CGGTT TGT GTTGT   /
                                     A TTCGT   T A   GAATA

GAM177 AATACGAGTTATATTTTCGT 163   AGTTATATTT 512   AG--   C-- TATCCAT TTCA
        CTATCCATTGTTTCACATTT   TCGTCTATCC   AATACG TTATATTTT GTC   TGT C
        ACATATTTCGACAAAAAGAT   ATTG |||||| ||||||||| ||| |||
        ATAAAATGCGTATT   TTATGC AATATAGAA CAG   ACA /
                            GTAA   AAA CTTTAT- TTTA

GAM178 GCCGATCTCTGAATGGATAC 164   TCTCTGAATG 513   ATCTCT - ACTA   TA T- TA
        TAGTTTTCTAAGTTCTAATG   GATACTAGTT   GCCG GAAT GGAT   GTTTC AG TC A
        TGATTCTCTGAAAATGTAAA   TTCT |||| |||| |||| |||||| || ||
        TCCAATTCCTCCGGC   CGGC   CTTA CCTA   TAAAAG TC AG T
                            CTC---   A AATG   TC TT TG

GAM179 GCGGTATAATTAGTTTTTTTT 165   TGTGATGGAA 514   GG T   -   C ATT T
        CTCTCAATTTCTATTTTTAG   AAATGACTAA   GC TA AATTAGTT TTTTTCT TCA TCTA T
        ATGTGATGGAAAAATGACTA   TTTT || || |||||||| ||||||| ||| ||||
        ATTTTGTAGC   CG GT TTAATCAG AAAAAGG AGT AGAT T
                            AT T   T   T GT- T

GAM180 GTGGAAACGATAACTGTATT 166   GATAACTGTA 515   ACG-- A   TTAATCAC- CA
        TTTAATCACGTCAGCGGCAT   TTTTTAATCA   GTGGAA ATA CTGTATTT   GT G
        CTAAATTAAATATAGGTATA   CGTC |||||| ||| ||||||||| ||
        TTTATTCCAC   CACCTT TAT GATATAAA   CG /

ATTTA G   TTAAATCTA GC

GAM181 AAATTCATGTGAAACTTTGT 167   TTCATGTGAA 516   T T CTTT   TTCCTACAAACT TAA
        CCTTTCCTACAAACTTGATA   ACTTTGTCCT   AAAT CATG GAAA GTCCT   TGA C
        ACTATTTCATCGGGACTTAT   TTCC |||| |||| |||| ||||| |||
        TTCTATGTGTTT   TTTG GTAT CTTT CAGGG   ACT T
                             T - ATT- CT---------- TTA

GAM182 AATTGTTCGGCTATACTCGA 168   TACTCGATGC 517   TC ATA   CG AG T A T AGA
        TGCGTGAGTCTTGCATTCAT   GTGAGTCTTG   AATTGT GGCT CTCGATG TG TCT GC TTCA
CTCC T
        CTCCAGATATCGGAGTGAGG   CATT |||||| |||| ||||||| || ||| || |||| ||||
        GTCAGATCCAAATATTGAGA   TTAATA CCGA GAGTTAT AC AGA TG GAGT GAGG /
        AGCCTTATAATT   TT A--   AA CT C G - CTA

GAM183 ACCGTCGATACTGCAGAGAT 169   TCGATACTGC 518   T C C-   TC T TA
        TCTAGTAATAATTTTCTTAA   AGAGATTCTA   ACCG CGATA TG AGAGAT TAG AA A
        GATCTTTAACGATATTGTCG   GTAA |||| ||||| || |||||| ||| ||
        GT   TGGC GTTAT GC TTTCTA ATT TT /
                             T   A AA   GA C TT

GAM184 AGGAGATGGAGAATTTTTTT 170   TGGAGAATTT 519   A - TTTTTTTC   TT T AT
        CAGTTGTTTGATGATATTCC   TTTTCAGTTG   AGGAG TGGA GAA   AGTTGT GA G A
        TCTATAACTACTTCTTCTTC   TTTG ||||| |||| ||| |||||| || |
        CACTTCCT   TCCTT ACCT CTT   TCAATA CT C /
                             C   T CTTCA---   T- C TT

GAM185 GGAGAAAGAATTACATTCTC 171   TTAGTTCATC 520   A T T   AG----------- AATAT CG
TCGT
        TGGAGAAGCCATAAATATAT   ATATGGAACT   ATT CAT C CTGGAGA   CCATA ATGA
TGATAGAG C
        GACGTGATAGAGTCGTCAAT   TTTT ||| ||| | ||||||| ||||| |||| ||||||||
        TCCTTTATTAGTTCATCATA   TAA GTG G GATCTCT   GGTAT   TACT ATTATTTC
A
        TGGAACTTTTTCATTGTCTC   - T-   GTTACTTTTTCAA AC--- TG   CTTA
        TAGGTGTGAATTCTATTTCC

GAM186 GGATAAGTTATTCATGACGG 172   TAAGTTATTC 521   T AT--- - - CATAA   CGG GAA
        TAGCATAATGTCTCGGATGA   ATGACGGTAG   GGA AAGTT TCAT GAC GGTAG   TGTCT AT
A
        AAAGAATAATGGATAGCAAA   CATA ||| ||||| |||| ||| ||||| ||||| ||
        CTGCCAGTCGATGATATTAA   CCT TTCAA AGTA CTG CCGTC   ATAGG TA /
        ACTTTCC   - ATTAT G A   AAACG   TAA AGA

GAM187 GTATTTCTTTGACTTGAATA 173   CACTAGTTTA 522   TTCT   C GAAT   TCC CAC
     CTATCCGATCACAAATATCC   GATTCAACAT   GTAT TTGA TT ACTA GAT A
     ACTAGTTTAGATTCAACATA   AC |||| |||| || |||| |||
     C   CATA   AACT AG   TGAT CTA /
                                C--- T ATT- CAC TAA

GAM188 GTTATCTATAGCATCTACTA 174   TCTATAGCAT 523   TA-- CTA AC CAT
     ACTGTACATTTTTTACATCT   CTACTAACTG   GTTATCTA GCAT CTA TGTA T
     AGACCATGTACCTTAGATAA   TACA |||||||| |||| ||| ||||
     T   TAATAGAT TGTA GAT ACAT /
                                TCCA   CCA CT   TTT

GAM189 TCCTTTACCATTTCTAAAAT 175   TGTAAGCTCT 524   TTTCTAA- T CCATG   TCTTTTTG
A   ATGA
     AGTCGTTGCCATGTAAGCTC   TTTTGAAATT   ACCA   AATAG CGTTG TAAGC   AAATTG
TGGAGT   C
     TTTTTGAAATTGATGGAGTA   GATG |||| ||||| ||||| ||||| ||||| |||||
     TGACCTACCACTTCAGCAGT   TGGT   TTATC GCAAT   GTTTG   TTTGAC ACTTCA
C
     TTGTTTGATAGTTAACGCTA   TTTTTCAA   - TGATA --------   G   CCAT
     TTAACTTTTTTGGTGACGGA

GAM190 TAGTGGCTTCTAATCAGATG 176   ATATCATTGA 525   TCTAAT   T TAATAAATATTTTAAA
ATCT   A
     TTCTAATAAATATTTTAAAA   CCATTTGTCT   TAGTGGCT   CAGATG TC   AATGA
TGATT A
     ATGAATCTTGATTAAAAATC   GGCT ||||||||| |||||| || ||||| |||||
     ATATCATTGACCATTTGTCT   GTCATCGG   GTTTAC AG   TTACT ACTAA /
     GGCTACTG   TCT---   C ---------------   AT--   A

GAM191 TTGATTTTCTTTCTAATACT 177   TGGGAATAAA 526   T TC A C ATAT   TC A A TC
     ATATATTTCTCTCGAAGAAG   ATACTACTGT   TTGATTT CTT TA TA TAT   TTCTC GA GA GT T
     TTCTTGCACATCATCTGGGA   TGAG |||||| ||| || || ||| ||||| || || ||
     ATAAATACTACTGTTGAGT   GACTAAA GAG GT AT ATA   AAGGG CT CT CA T
     AAATCAG   T TT C C AAAT   T- A A CG

GAM192 AGGTATCGGTCTCTACTGAA 178   TAGCTTCTAC 527   TAT TCTCT   AATCTA   TC
     TCTACTAACATGTCTCGTAT   AGTCTTTCGT   AGG CGG   ACTG   CTAACATG T
     GTTAGCTTCTACAGTCTTTC   TTCC ||| ||| |||| ||||||||
     GTTTCCT   TCC GCT   TGAC   GATTGTAT /
                                TTT TTC-- ATCTTC   GC

GAM193 CGTCATTATTTTCAGCAGCC 179   TGAGAAAAGT 528   ATTATT   CA- - ---   T A
     TCTCTACCAGAAGGTTGAGA   GTGTTCTGAA   CGTC   TTCAG GC C TCTC ACC G
     AAAGTGTGTTCTGAATCGCA   TCGC |||| ||||| || | |||| ||

```
          CGACG                              GCAG    AAGTC  TG G  AGAG TGG A
                                             CACGCT   TTG  T AAA   T  A


GAM194  GGGTGTAGGATATAGTTTCA 180    TAGGATATAG 529    ------        TTTC      AACAT AT---
CATTTC
     TAATAGGAACATGATATTTT       TTTCATAATA     T   GTAGGATATAG  ATAATAGG   GAT
TTTTTGTAC    A
     TTGTACCATTTCACCAACAA       GGAA        |   ||||||||||  |||||||   |||  ||||||||
     GTATAGAAATGCAAATCTAT            A    CATTTTATGTT  TATTATCT   CTA    AAAGATATG
C
     ATCTATTATTTTGTATTTTA            ATCTAC       T---   ATAT- AACGT      AACAAC
     CCATCTAACCC


GAM195  GAATAGTTACATTTGATTCA 181    TATTACACAC 530    CATT    ATCTTCG TTT    TC ACTAT
CC A   AT
     TCTTCGATGTTTAATGTTCC       GGAACGTTTA     GTTA  TGATTC    ATG  AATGTTCC TG    AT
CC ACGTG  A
     TCTGACTATATCCCCAACGT       TAAC        ||||   ||||||    |||  ||||||||| ||   || || |||||
     GATAATACGCGTAGGTTATT            CAAT    ATTAAG     TAT  TTGCAAGG AC    TA GG
TGCGC  A
     ACACACGGAACGTTTATAAC            T---   ACATCAA  ---    C- ACAT- TT  A    AT
     TACAGAATTATTAACTATTT


GAM196  GCTACCAAGGCGAACAACAA 182    TAACACGCTT 531    C - C--   ACA  A-      CCTGATC
     AGCGATTATTGTTTTACCTG       CTGTTCTCAT     GCTA CA AGG  GAACA  AAGCG TTATTGTTTTA
C
     ATCCCATAATATGGAACAAT       CTAT        |||| || |||  |||||  |||| |||||||||||
     AACACGCTTCTGTTCTCATC            TGAT GT TCT  CTTGT  TTCGC  AATAACAAGGT    /
     TATGATAGT              A A ACT  C--   AC       ATAATAC


GAM197  TCAGGCATTTCGTAATATGA 183    AGGCATTTCG 532        G  --  TATTCTTCC---   CA
     TATTCTTCCTTTAAGCAAAT       TAATATGATA     TCAGGCATTTC TAAT  ATGA         TTTAAG A
     CCTTAAGTACATTCACACCT       TTCT        |||||||||| |||| ||||        ||||||
     CGTTCGTTAAGAAGTGTCTG            AGTCTGTGAAG ATTG  TGCT         GAATTC A
     A                   A  CT  CCACACTTACAT    CT


GAM198  AAGAATATAGAAATAATGAT 184    TATAGAAATA 533     AAATA  TA TC  TCATCG
     AAGTCCATCATCGTGTTTTT       ATGATAAGTC     AAGAATATAG  ATGA AG CA    T
     TTGCCTCTTCATAAGAACTA       CATC        |||||||||  |||| || ||
     TATTTTT              TTTTTATATC   TACT TC GT    G
                         AAGAA   TC C- TTTTTT


GAM199  CTTGATAGTTGTTCCTAGAT 185    TACTAGGTAG 534    T   -  -  A   AAAAT
     ATGTAAAATAATCCAACGTA       CAAATTGTCT     CT GATAGTT GTT CCTAG TATGT   A
     CTAGGTAGCAAATTGTCTAG        AG        || |||||||| ||| ||||| |||||
                         GA CTGTTAA CGA GGATC ATGCA   /
```

T   A T   -   ACCTA

GAM200 TAATATACTTGCGTGTCGTC 186   TTCAATTTAT 535   AT   TGCG   TC   TATAC
TTTCTATAGTTCT   TAT
        GTTCAATTTATACGGATTTC   ACGGATTTCT   TA ATACT   TGTCGTCGT AATT   GGA
CTGT A
        TATAGTTCTCTGTTATATAA   ATAG || ||||| ||||||||| |||| ||| ||||
        TACGGTTTTCCATCATGATT   AT TGTGA ACAGCAGCA TTAG CCT   GGCA T
        AGACGACGACAATAGTGTTC   CT TA--   GA TACTA TTT---------   TAA
        TA

GAM201 GCGGACACGGATACTCGTTT 187   ACTCGTTTAT 536   ACAC - GT--- G - A   GGT
        ATGACACCATAGGCATTGGT   GACACCATAG   GCGG GGAT ACTC   TTAT ACAC CAT GGCATT
T
        TAACGAATGCCGTGAGTGTA   GCAT |||| |||| |||| |||| |||| ||| ||||||
        ATAATTTGAGAGTCATCCTC   CGCT   CCTA TGAG   AATA TGTG GTG CCGTAA A
        GC   ---- C AGTTT A A -   GCA

GAM202 TTTCCTGTTTGGACAAATAA 188   TTTCTAGTTC 537   -   GGAC   AATTC   ATC CT
        TTGGAATAATTCAGAAATAA   TAATTATTTC   TTTC CTGTTT AAATAATTGGAAT   AGAAATA
GTTT T
        TCGTTTCTTTCTAAACATGT   AGAA |||| |||||| ||||||||||| ||||||| ||||
        TTCTAGTTCTAATTATTTCA   AAAG GATAAG TTTATTAATCTTG   TCTTTGT CAAA T
        GAATAGAGAAA   A   AC--   A----   A-- TC

GAM203 CGGGATTGTCCGGCATATCA 189   CATCGTATAC 538   - T C C   C   AGT
        TGTAGATAGTTACCGTCTAC   TCGACCATCT   CG GGAT GTC GG ATAT ATGTAGAT T
        ATCGTATACTCGACCATCTA   ACG || |||| ||| || |||| |||||||||
        CG   GC TCTA CAG TC TATG TACATCTG /
                                  A C C A C   CCA

GAM204 GCCATTATAAAGTGCACGTT 190   TATAAAGTGC 539   ATAAAGTGCA AC TC   GGAG
        TACATATCTACGTTCTGGAG   ACGTTTACAT   GCCATT   CGTTT ATA TACGTTCT G
        GAGTAAGAACGTGACTATTG   ATCT |||||| ||||| ||| |||||||||
        AGACGAATGGC   CGGTAA   GCAGA TAT GTGCAAGA /
                                  ---------- GT CA   ATGA

GAM205 GCTCTTGAAACCAAGGTTTT 191   TGAGAAGTCT 540   CT   CC GT TC A --- TC
        CCAACCGGACTCATTGTCGA   TTTTCATTAG   GCT TGAAA AAG TT CA CCG DAC A
        TCGGTGAGAAGTCTTTTTCA   C ||| ||||| ||| || || ||| |||
        TTAGC   CGA ACTTT TTC AA GT GGC   CTG /
                                  TT   --   TG GA - TAG   TT

GAM206 AATTCAGTAAATAGAGAGAT 192   CCGCACTAGC 541   GT---   ATA AG---   C C CC   C
T TT

```
     ATCAGCCGCACTAGCATCCC      ATCCCCTTTC      AATTCA   AAATAGAGAG  TC   CCGCA TAG AT
CCTTT AA AG  C
     CTTTCAATAGTTCTCCCTTT      AATA          |||||  ||||||||||  ||   ||||| ||| || ||||| || ||
     TTAAAGGTATCTAATGCGGA                    TTAAGT   TTTATCTCTC  AG   GGCGT ATC TA  GGAAA
TT TC  T
     TTTAGAAAACTCTCTATTTC                    AATTC      AAA  ATTTA   A  - T-   T T CC
     TTAATGAATT


GAM207  GAACGTAAACGTAGTAGCCA 193   TGATATACCT 542    C   CG  - GC-  A  CTC A
     TACGTCTCAGAATTCTAAAT      GTTTTTATTT      GAA GTAAA  TAG TA  CAT CGT  AG A
     GATGATATACCTGTTTTTAT      C              ||| |||||  ||| ||   ||| |||  ||
     TTC                      CTT TATTT GTC AT  GTA GTA  TC T
                    -   TT  C ATA  -  AA- T


GAM208  TATTAACGTATCGCATTAAT 194   TAACGTATCG 543    T   TATCGCATTAATACT     TAGCGA-
C C
     ACTGTTTTCTTAGCGAATGA      CATTAATACT     TA TAACG         GTTTTCT    ATGATG AGA C
     TGCAGACCCTTCTACGTCAT      GTTT          || |||||       ||||||      |||||| |||
     CAAAAATAGAAAACTCGTTA          AT ATTGC          CAAAAGA     TACTGC TCT C
     TTA                      T    T--------------  TAAAAAC    A T


GAM209  TCAAAGACTAGACATTTACC 195   ACTAGACATT 544     GAC-  CATTTACCA     TGCT
     ATGGGATGCTAATATTCCCA      TACCATGGGA      TCAAA  TAGA      TGGGA  A
     AACATACATCTATAAATTTG      TGCT          |||||  ||||        |||||
     A                        AGTTT  ATCT       ACCCT   /
                             AAAT  ACATACAA-  TATA


GAM210  ATGTATAGATTGTTTTCAGT 196   TAGATTGTTT 545     -    TCA-  ----  A    G
     GAGATGATTATTAGATTTAA      TCAGTGAGAT      ATGTA TAGATTGTTT  GTGA  GATG TTATTA A
     TAGCATCTCGTTCACGTTTG      GATT          ||||| ||||||||||  ||||   |||| ||||||
     AACAGTTTATTGCGT                      TGCGT ATTTGACAAG  CACT   CTAC GATAAT T
                        T    TTTG  TGCT   -   T


GAM211  TAATGACGCATATTCTACTC 197   ACGCATATTC 546     G  C AT TACTC-   T TAG   ATA
     TTGGAATTAATAGTTTTGAT      TACTCTTGGA      TAAT ACG AT TC    TTGGAA TAA  TTTTG  T
     ATTAGTAAAAAATTTATTTC      ATTA          |||| ||| || ||    |||||| |||  |||||
     TAAAATTTTGATCATCGTAA          ATTA TGC TA  AG    AATCTT ATT  AAAAT  /
     TTA                      A  - CT TTTTAA   T  TAA   GAT


GAM212  TAATGGCGGAAAACTTTTTA 198   TTCGTGTTCC 547     GC-  A TTTTT    GTTATAT
     GAAATGTTATATATAAAAGA      AAACATTA       TAATG GGAA AC   AGAAAT     A
     ATTTTTTCGTGTTCCAAACA          |||| ||| || |   |||||
     TTA                      ATTAC  CCTT TG   TTTTTA   /
                        AAA   G CT---   AGAAAAT
```

```
GAM213  TATATAATCTTTTTCATCTT 199    TATAATCTTT 548        --    TTTC CT TG    CCT    CG  T
        GTGAGTACCCTGGATACGAA        TTCATCTTGT        TATAT AATCTT  AT TG AGTAC  GGATA AAA A
        ATAAATTTATTATCCGTATT        GAGT         ||||| |||||| || || ||||| ||||| |||
        TCCATAATAAGGTTTAGTAT                     ATATG TTGGAA  TA AC TTATG  CCTAT TTT A
        A                           AT     ---- AT CT    ---    TA  A


GAM214  AGATACTATACCGTTGTGTC 200    CGTTGTGTCT 549        TATACCGTT  CT  ACCG-  AT
        TACAACCGCTACATAATCGT        ACAACCGCTA        AGATAC     GTGT ACA    CTAC A
        AGATTCATGTTAACACTCTA        CATA         ||||||    |||| |||   ||||
        CGTATCT                     TCTATG       CACA TGT   GATG  A
                                    CATCT---- AT ACTTA   CT


GAM215  AGCGAGTGCTTCTTCTTTAG 201    TAGGTGCTGA 550        CT    -------------    GG    A
        CGGGCTTAAAGACTGCTTTA        AATAACCACA        AGCGAGTG TCTTCT      TTAGC GCTTAAAG
C
        GGTGCTGAAATAACCACATC        TCTG         ||||||| |||||        ||||| ||||||||
        TGGAAGGCTTACTCGCT                        TCGCTCAT GGAAGG       AGTCG TGGATTTC T
                                    TC    TCTACACCAATAA    --     G


GAM216  GAAGAGATAGATACGTGATT 202    TACGTAACCG 551        GATAGA    ATTAATACATTTATAT  AC
        AATACATTTATATCCAACAT        AATCTTC         GAAGA    TACGTG         CCA  A
        ATGGTACGTAACCGAATCTT                     |||||    ||||||        |||
        C                           CTTCT    ATGCAT         GGT  /
                                    AAGCCA        ---------------- AT


GAM217  TGTCTTAGAAGGAGTGTTTT 203    TAGAAGGAGT 552    TCT  A        T----    CAAA
        CTTGGCAAAAGAATACCAAG        GTTTTCTTGG        TG  TAG AGGAGTGTTT   CTTGG  A
        TGCTTAAATATTTCTACTAC        CAAA         || ||| |||||||||||    |||||
        TTCA                        AC  ATC TCTTTATAAA   GAACC  G
                                    TTC  A        TTCGT    ATAA


GAM218  TACTGAATCCGCCTAAGCGT 204    GGATAATTTA 553        AA-    TAAGC- -  CT----    A
        GTTCTTCTGCATGTGCGGAT        ACTACTATAT        TACTG  TCCGCC    GT GTT    TCTGC T
        AATTTAACTACTATATTGGC        TGGC         ||||| ||||||  || ||     |||||
        GGAGGACGGTA                 ATGGC AGGCGG    CA CAA    AGGCG G
                                    AGG    TTATAT T  TTTAAT    T


GAM219  AATATTTAGTTTATTCATAA 205    TATTTAGTTT 554        GT T  C  T TAA    C ATAG
        TGTTAAGCATATCCTGAATA        ATTCATAATG        AATATTTA T ATT ATAA GT  GCATATC TGA   T
        GTAAAGTTAGATGTGTCATA        TTAA         ||||||| | ||| |||| ||  ||||||| |||
        CTTGTTAGTAGTTAGATATT                     TTATAGAT A TGA TGTT CA  TGTGTAG ATT   /
                                    TG -  T   - TAC    -  GAAA
```

```
GAM220  AGGATGAGTACATTTCACAG 206    TGAAATAGCT 555      TG  ACATTTCAC    ACT  ATTG  ATGT
        A
        AAACACTAGCATTGTTCAAT        CGTTTCTATT    AGGA AGT     AGAAAC  AGC   TTCA
GCTCTTTAC T
        GTGCTCTTTACATGGGTAAG       TGTT       |||| |||    |||||| |||  ||||  |||||||||
        GAGTTGAAATAGCTCGTTTC              TCTT TTA     TCTTTG  TCG   AAGT  TGAGGAATG G
        TATTTGTTCT                     GT  ---------  C-- ATA- ----      G


GAM221  GATGGCGGCGTCGTCGTTTT 207    AGATAATATC 556      G - TC C  TTTG----    TTA
        TTGATCTTTATTAAATTTAG        CTGAACAGCA       GATG CG GCG  GT GTTT    ATCTTTA A
        AGATAATATCCTGAACAGCA        TTGC       |||| || ||| || ||||    |||||||
        TTGCTCGGCGTC                     CTGC GC CGT  CG CAAG     TAGAGAT /
                                    G  T  TA  A  TCCTATAA    TTA


GAM222  GTTATAGCTTTCTGCTATTA 208    TAGTATAGCG 557      GCTT    A T C-  TTCAAA   TT
        TACCCGCTATTTCAAATAGA        TCGTTTAAGA     GTTATA TCTGCT TTA AC CGCTAT    TAGAC A
        CTTATACGTCTAGTATAGCG        GCAG       ||||||  |||||| ||| || ||||||   |||||
        TCGTTTAAGAGCAGATATAT              TAGTAT  AGACGA AAT TG  GCGATA    ATCTG T
        GAT                         AT--   G  T  CT   TG----   CA


GAM223  GTTTTTGAAGTTTCCAAATT 209    TTGAAGTTTC 558      T  AA TTCCAA     T- A    TG
        TTGATAATATAGTCTAGATG        CAAATTTTGA     GTT TTG GT    ATTTTGATAA AT GTCTAGA G
        GAATTTTAGACCATCTTTGT        TAAT       ||| ||| ||   ||||||||||| || |||||||
        CAAAATCGTTTACCGACAAC              CAA AGC  CA    TAAAACTGTT  TA CAGATTT A
                                    C  -- TTTGC-    TC  C    TA


GAM224  AGGATCTAGATAATTAATAA 210    TTCTTTGTAT 559      ---  --- TT  T   T
        TGATGGGTTTTCTATTCTTA        TTTGGCATAT     AGGAT  CTAG  ATAA AATAA GATGGG T
        TTCTTTGTATTTTGGCATAT        CCT        ||||| |||| |||| ||||| |||||
        CCT                         TCCTA  GGTT  TGTT  TTATT TTATCT /
                                    TAC  TTA  TC   C   T


GAM225  CAGAGTTGGGATAGTATTTT 211    TAGTATTTTT 560      -  -  T  T T-  C TATTATAT   G  TC
        T
        TCTAACGTCGGTATTATATT        CTAACGTCGG     CAGA GTTGG DATAG ATTT TC  AACGT GG
TATTA GA  TACGT C
        ATTAGGATCTACGTTCATAT        TATT       |||| ||||| ||||| |||| || ||||| ||     |||||| || |||||
        GTATCATAATATTAATCATC              GTCT CGATT CTATC TAAA AG  TTGCA CC     ATAAT CT
ATGTA A
        CACGTTTTGATAAATCTATC                  T  T  -  T TT  - TACTAATT   A --   T
        TTTAGCTTCTG


GAM226  CGTATAAATTTTAGAAATAA 212    AATTTTAGAA 561      AAA      -- TA   -- AAT
        CATTAGCGAATTGTTGTGCA        ATAACATTAG     CGTAT TTTTAGAA A ACATTA GCG  T
```

```
TTGATGTCGTTATTCTGAAA        CGAA          ||||| ||||||| | ||||| |||
CAGTATG                          GTATG AAAGTCTT T TGTAGT CGT G
                             AC-      AT GC   TA GTT


GAM227 TAGAGTTAAGAGAGATTAGA 213   TGGCTACAAA 562     GTTAA-- ATT     ACATTA A  GTC
     GTTTGTACATTAAGCAACAT       CTTTTCCTTT     TAGA    GAGAG AGAGTTTGT   AGC ACAT  T
     GTCTCTAAATGTGGCTACAA       TCCA     ||||    |||||  |||||||||   ||| ||||
     ACTTTTCCTTTTCCACATCA              ATCT    CTTTT TTTCAAACA   TCG TGTA  C
     TCTA                      ACTACAC  CCT      ------ G  AAT


GAM228 GAGTCATTCGAAGCGTCAAT 214   TTTCCGGCTG 563     CG GCGT    ----- T CT
     AGAATATGTCTCTTAACTAT       TTGTATATTT    GAGTCATT AA  CAATAG   AATA GT C
     TTCCGGCTGTTGTATATTTA       AAAT     ||||||||| || |||||  |||| ||
     AATGACTT                      TTCAGTAA TT  GTTGTC   TTAT CA T
                              AT ATAT   GGCCT  - AT


GAM229 GACTTGACTAGATCGTCAGT 215   TAGCATCGCT 564     --- ----- G  T TA -   CGTC   T
ATCC
        AGTAATTTGTGCATCGTCTA       TTGAGATTCT    ACTTGA CTA   GATC TCAG AG AT TTGTGCAT
TATTC GC   G
        TTCTGCATCCGCTTCGTCGA       CCAT     |||||  |||   |||| |||| || || ||||||||  ||||| ||
        ATAATGTATAGCATCGCTTT              TGAACT  GAT   TTAG AGTT TC TA GATATGTA  ATAAG
TG   /
        GAGATTCTCCATAGCTATCA              ATC  ACCTC  -  - GC C     ----  C CTTC
        AGTC


GAM230 ATAATAGTGGCCGGAGAATC 216   TTCCTCTGGA 565     A G  G AA  A ---   GA    TA
     ATCATCTGGAAATAGATCTT       GATGACACTA     ATAAT GT GCCG AG TCATC TCT  GGAAATA
TCTTCAT A
     CATTAAGTTGTGAGGATATT       CGGC     ||||| || |||| || ||||| |||  ||||||| |||||||
     TCCTCTGGAGATGACACTAC              TATTA CG CGGC TC AGTAG AGG  CCTTTAT AGGAGTG
G
     GGCGGCATTAT              - G  A AC  - TCT   --    TT


GAM231 GATAATGTTTATGACAATAA 217   TATTGTTTAA 566     AT    C-------  A TT ----  TAA
     TAATCACGTTAGTGACGATA       TCGTTTTATA    GATA GTTTATGA     AATAATA TCACG AGT
GACGA  T
     ATTTTTCGTTTTCTACTTTC       GATT     |||| |||||||||    ||||||| ||||| ||| |||||
     GTGATATTGTTTAATCGTTT              CTAT TAGATATT    TTGTTAT AGTGC TCA  TTGCT /
     TATAGATTCTATC              CT    TTGCTAAT   -  TT TCTT  TTT


GAM232 GTTGTTGACGTTGTTCCGAT 218   GGAGGTGGAG 567      T   GATATCAATA CT  A
     ATCAATAACTCTCTACGAAA       TATCGTCAAT    GTTGTTGACG TGTTCC     ACT CTACG A
     CGTAGGAGGTGGAGTATCGT       AAT     ||||||||| ||||||    ||| |||||
     CAATAAT                      TAATAACTGC ATGAGG    TGG GATGC /
```

T   --------- AG   A

GAM233   TAGTATTCTGGTAAAATTAT 219   TATCAGATGA 568   A C   AT TCTAAATTA
ATTTTGTATTAGATC   TC
      CTAAATTATCAGATGATTTT   TTTTGTATTA   AGT TT TGGTAAA TA   TCAGATG
GTTGATT T
      GTATTAGATCGTTGATTTCT   GATC ||| || ||||||| || ||||||| |||||||
      AAGATTAACCACTTCATCCT   TCA AA ACTATTT AT   AGTCTAC   CAATTAG /
      CCAACATCTGAATTCTTTTA   - T   CT TTTCTTA--   AACCTCCTACTTCAC   AA
TCTTTATCATAAACTA

GAM234   ATAAAGTCTTGGTATGACTC 220   ACTACCTTTG 569   CT TA -------- TTT A
      CTTTCTAATATAGTACGGAC   TCACCCAACT   ATAAAGT TGG TGAC   TCC CTA T
      TACCTTTGTCACCCAACTTT   TTAT |||||| ||| |||| ||| |||
      AT   TATTTCA ACC ACTG   AGG GAT /
                            -- C- TTTCCATC CAT A

GAM235   GCTGAAGTAATTAATTTTTC 221   TGAAGTAATT 570   TG -   TTTTTC C TTT   ACTAGTT
      TGCCTCGTTTTTACTACAAC   AATTTTTCTG   GC A AGTAATTAA   TGC TCGTT ACTACA   T
      TAGTTTTCATCAATGTAGTG   CCTC || | ||||||||| ||| ||||| ||||||
      ACGATGTATTGTTTAGTTAC   TG T TCATTGATT   ATG AGCAG TGATGT   /
      TCTTGGT   GT C   TGTT-- T ---   AACTACT

GAM236   GGGTATTAATAATATCTATA 222   ATTCACGTGA 571   AATATCTATATTT G A TAAC   C
      TTTCCAGCGTTAAGTGTAAC   CGTGGTATCA   GGGTATTAAT   CCA CGTTA GTG   ATTAAA
A
      ATTAAACAGTTTTAATTCAC   ATTA |||||||||| ||| ||||| ||| ||||||
      GTGACGTGGTATCAATTAAA   CCCGTAATTA   GGT GCAGT CAC   TAATTT G
TAATTAATGCCC   ATAAATTAACTAT -   G T---   T

GAM237   GTTCTAGTACAATTAGACGT 223   TACAATTAGA 572   TAGTAC   C   TC C   AATTTT-   C
A
      AAGTTCTGCTTGGGAATTTT   CGTAAGTTCT   GTTC   AATTAGA GTAAGT TG TTGGG
TTAACG TAA G
      TTAACGCTAAAGAGTTAACG   GCTT |||| |||||| |||||| || ||||| |||||| |||
      TTAATCGTGCACCCAACGTA   CAAG   TTGATCT CATTTA GC AACCC   AATTGC ATT A
      TTTACATCTAGTTCTTTGAA   TTTC--   A   T- -   ACGTGCT   A G
      C

GAM238   TGATTTTGGTTTACATGTAA 224   TACATGTAAT 573   - TTA   A TT- TG C
      TACATTTTGAACTCTTTGAT   ACATTTTGAA   TGATT TTGGT CATGT ATACA T AA T
      TTTGTATCACATGCGCCGGC   CTCT ||||| ||||| ||||| ||||| | ||
AGTCA   ACTGA GGCCG GTACA TATGT A TT /
                          C   C-- C   TTT GT C

GAM239 ACTACTATTTAATTTTACCA 225   TCGAAAACAA 574   CCAT T   --   ----   GAT   TTTT--
CA
     TATCTTCGAAAACAAAAATA   AAATAGATAT   AATTTTA ATC TCGAA AACAAA   AATA ATTAT
GCAGTA A
     GATATTATTTTTGCAGTACA   TATT |||||| ||| ||||| ||||| |||| ||||| ||||||
     AACTATTGTTTTTATATGGT   TTAAAAT TAG GGCTT TTGTTT TTAT TGGTA
TGTTAT /
     TTATATTCCACTTTGTTCAT   T--- C   AC   CACC   ATT   TATTTT   CA
     TCGGCGATTTAAAATTTTTA
     TTAGT
GAM240 GAAGAGTAATGTATAGAGGA 226   TGTATAGAGG 575   - AAT--   A   CGTTT   T
     CGTTTTGATTCGATCATTTT   ACGTTTGAT   GAAG AGT   GTAT GAGGA   TGAT C
     CCTCATATTAGAAACTACTT   TCGA |||| ||| |||| ||||| ||||
     C   CTTC TCA   TATA CTCCT   ACTA /
                 A AAGAT   - TTT--   G

GAM241 TCCTAGTTTATCTACAGACA 227   TTTATCTACA 576   T   CAGA CT   TTCGT   AATT
     GACTAATAATTCGTTGCATG   GACAGACTAA   TCCTAGT TATCTA CAGA AATAA   TGCATGA
T
     AAATTTCCTATCATGTACTT   TAAT |||||| ||||| |||| ||||| |||||||
     TATTTCTTTGATGGATGTGC   AGGATCG GTAGGT   GTTT TTATT   ATGTACT   /
     TAGGA   T   A--- CT   TC---   ATCC

GAM242 AAAGAATTATACTTTTCTAT 228   TTTGTACAGA 577   TA   T- ATAGCC   TC- AA
     AGCCGCAGAATCTGAAAATC   CTAAGTAATT   AAAGAAT TACTT TCT   GCAGAA TGA A
     TCAAACTTTTGTACAGACTA   CTTT |||||| ||||| ||| |||||| |||
     AGTAATTCTTT   TTTCTTA ATGAA AGA   TGTTTT ACT /
                 -- TC CA----   CAA CT

GAM243 AAGTAAAGATATTGACTTGG 229   AACATCTTTG 578   A TG CTT   GTA   TG
     ATGGTATTTCTGACAGAAA   AAATCTTTAC   AAGTAAAGAT T A GGATG TTTTC A
     ACATCTTTGAAATCTTTACT   TT ||||||||| | | ||||| |||||
     T   TTCATTTCTA A T TCTAC AAAAG /
                 A GT ---   ---   AC

GAM244 CCGTTATAAATGTCTTTGTC 230   TATCCAGAGA 579   -   TCGAT   TCAA TTC
     GATGATATATTCAACGCTTC   TATCTTGTAA   CCGTTATAA ATGTCTTTG GATATAT CGC C
     CAATTGTGATATATCCAGAG   TGG ||||||||| ||||||||| ||||||| |||
     ATATCTTGTAATGG   GGTAATGTT TATAGAGAC   CTATATA GTG A
                 C   -----   ---- TTA

GAM245 TCATCTAATGCCGTAGCCGT 231   TACTTCTTTA 580   T C- GCCGT TAC   TACA
     AAGTACGTGGTTTACAACAT   AAGTACTCGT   TCATCTAA GC GTA   AAG GTGGTT A
     TAGCTACTTCTTTAAAGTAC   TTTG |||||||| || ||| ||| ||||||
     TCGTTTTGGATGA   AGTAGGTT TG CAT   TTC CATCGA   /

```
                        T  CT  GAAAT  TT-    TTAC


GAM246  TGTGATTGATTCCCACTAAT 232   TCTAAATTCG 581      GA   CA - GA--   CCAC
     GAAGATGCCACATATCCATC      GCAGGAAAGT    TGTGATT TTCC CT AAT  AGATG   A
     TCTAAATTCGGCAGGAAAGT      CACA          ||||||| |||| || |||   |||||
     CACA                    ACACTGA AAGG GG TTA  TCTAC  /
                               --  AC  C  AATC   CTAT


GAM247  AATGCTCGCAACATTAACAT 233   ATAAATTTAT 582      CT  C    ACATCT  CCGT  T AA
     CTTGAACCGTTGGTACAATT      AATGTTCGCC    AATG CG AACATTA   TGAA  TGG AC T
     CCGTTCCATAAATTTATAAT      ATT           |||| || ||||||     |||| ||| ||
     GTTCGCCATT                TTAC GC TTGTAAT    ATTT  ACC TG  T
               C-  -     ------ AAAT  T CC


GAM248  ATGGAGATTTTCTATTCTCG 234   TCCCTAATAA 583      TTTC   T TCCATT   ATAT   C
     TCCATTTTAGGATATGCTTT      CTTCGTGAAT    ATGGAGAT TATTC CG   TTAGG  GCTTT A
     CATAAAGTCCCTAATAACTT      AATG          ||||||||  ||||| ||    ||||   |||||
     CGTGAATAATGTTTCTAT            TATCTTG  ATAAG GC    AATCC  TGAAA /
               TA--   T TTCAAT   C---    T


GAM249  TCTTTTTAGCCAGAGATATC 235   GTTTCAGCGT 584     T   CCA-  T  A C---   T
     ATAGCCGCTCTTAGAGTTTC      GATTTTCCAA    TCT TTTAG  GAGA ATCAT GC   GCTC T
     AGCGTGATTTTCCAACCTAA      CCTA          ||| ||||   |||| |||||| ||   ||||
     ATAGA                    AGA AAATC   CTTT TAGTG CG   TGAG /
               T   CAAC   -   - ACTT   A


GAM250  TTGCTTCGCGTTTAGCCTCT 236   TAGCCTCTGG 585      TTCGCG   CT  GC   A A C
     GGCTTTTTATCAGCCTTTGT      CTTTTTATCA    TTGC   TTTAGC CTG  TTTTT TC GC T
     AGAAAAAAATTCAGTTGCTG      GCCT          ||||    |||||| |||  ||||| || ||
     GAATTGCAA                AACG   AGGTCG GAC  AAAAA AG TG T
               TTA---   TT  TT   A A  T


GAM251  ACACCAGAAAAGACGGCTTG 237   TGAGATCAAC 586     A   AAAGAC  T   -  CT  TCTAAT
ATAA      A
        AGATCAACTTTATCTAATGG     TTTATCTAAT    AC CCAGA   GGC TGAGA TCAA TTA     GGTTT
AACGAAGG G
        TTTATAAACGAAGGAGGCC      GGTT          || |||||    ||| ||||| |||| |||    ||||| ||||||||
        TTCGTTCGAAATCTAATTTG       TG GGTCT    CCG ATTTT AGTT AAT     CTAAA
TTGCTTCC /
        ACTTTTACGCCTCTGGCGT                 C   ------  C  C  T-  ------   GC--      G


GAM252  TGTGAGAAGTTTGCCTCGTT 238   TGGAATAGTT 587      GA--   GC  C  T  T --   TTA-----  TT
    T
```

```
    AAGGTCTTCCATTTAAATAT      TTTTACTAGT      TGA  AGTTT CT GT AAGG CT TCCAT      AATA
ATATAAACA T
    TATATAAACATTTGTGTTTG      AAAG           |||   ||||| || || |||| ||  |||||    |||| |||||||||
    TATCTTATTCGTCTTTTATG              ATT   TCGAA  GA CA TTTT GA  AGGTA     TTAT
TATGTTTGT T
    GAATAGTTTTTTACTAGTAA              AACG    AT T T  T TA   TTTTCTGC  TC      G
    AGCTGCAATTACA


    GAM253  ATAGATGCCATGTTAAAAAT 239   GATGCCATGT 588        T AAAAAT- CG- TCGA
    GTCCGCCGTCGACTTTTTGG      TAAAAATGTC      ATAGATGCCA GTT    GTC CCG  C
    AACGATTGATAAAAGCTGGT      CGCC         ||||||||||| |||    ||| |||
    GTTTAT                    TATTTGTGGT CGA    TAG  GGT  /
                             - AAATAGT  CAA  TTTT


    GAM254  ATAGCATCATCTTTAGATCA 240   AGCATCATCT 589       GC   CTTTA  C AA-  TACCTT
    TTAATTGTTACCTTCCCCAA      TTAGATCATT      ATA ATCAT   GAT ATT  TTGT   C
    TACAACCAAATCATCATGAT      AATT          ||| |||||   ||| ||| ||||
    ATAT                      TAT TAGTA    CTA TAA  AACA   /
                             A-  -----  C ACC   TAACCC


    GAM255  CTTTGGCTTATAAAATACAA 241   TAAAATACAA 590        AAT-------------   CCC   TT--  C--   CT
TC
    ATGACATTCCCTTATGTTTA      ATGACATTCC      ATACA            GACATT TTATG   TAAT  TTAAT
TT T
    ATCTTAATCTTTTCTTTAGT      CTTA          |||||          |||||| |||||  |||| ||||| ||
    TATTGAATCGTTACAATTAT              TATGT          TTGTAG AATAT  ATTG AGTTA GA /
    AAAATGATGTTTTTTCCAAA              GAATCCAAAAACCTTTT    TAA   TAAC  CTA   TT TT
    AACCTAAGTGTATTTAAAAT
    AGATGCCATG
    GAM256  TACGACACTGATAAACCGCA 242   ACACTGATAA 591       C T    CGCA    ----G   T
    TTATCTGTGGACATTTTAAT      ACCGCATTAT      TACGA AC GATAAAC   TTATCTG  T GACAT T
    GTTGGTATCTAGATAACAAT      CTGT          ||||| || ||||||||   ||||||||  | |||||
    GTTTATCGTATTGTA                   ATGTT TG CTATTTG   AATAGAT   G TTGTA T
                             A -    TAAC    CTAT G   A


    GAM257  TGTATCCTCAACATAATCAA 243   TTTATTGGGT 592       ---  C     AA-    - AG- AAT
    TGAGCCAGGTAATCAAGACA      AGTGTTGATG      TGT ATC TCAACAT  TCAATGAG CC  GT  C
    TCGGATTTATTGGGTAGTGT      ATTC          ||| ||| ||||||| |||||||| || ||
    TGATGATTCCGCA                   ACG  TAG AGTTGTG  GGTTATTT GG  CA  /
                             CCT  T   ATG     A CTA GAA


    GAM258  GATTTGGCCAAATGTATCCA 244   TAACTAGTGT 593       CC   G   CATCATAA---  GG ATAA  G
GTAAAC      T
    TCATAATCTGGGTTATAAAC      AGAAAACAGA      GG  AAAT TATC      TCTG TT  AC GGT
AAGAATATA G
    GGGTGTAAACAAGAATATAT      GATA          || |||| ||||      |||| || || ||   |||||||||
```

```
GTTTATATTTTTTAACTAGT                    CC TTTG ATAG      AGAC AA  TG TCA    TTTTTATAT T
GTAGAAAACAGAGATAGTAA              TT  -  ATAAATGATAG   AA GATG A  AT----      T
ATAGATAGTTTTTCCAGATC


GAM259  AGCGAAGCTATCATCGTCCA 245   ATATTATCTA 594        TATCAT CC--   C ATT
     ATATCTCATTCCTAGAAATA        CGTCATTGTT       AGCGAAGC   CGT  AATAT TC  C
     TTATCTACGTCATTGTTTTG        TTGT           ||||||| |||  ||||| ||
     TT                          TTGTTTTG   GCA  TTATA AG  /
                                 TTACT- TCTA    A ATC



GAM260  GTGGTATTATACTCATGCCT 246   TATTATACTC 595       A AT- TCAT-- A AA----   - G T
     AGTAATAGTCTCTTTGCGTT        ATGCCTAGTA       GTGGT TT AC   GCCT GT   TAGTCT CTTT CG
T
     GACGGAAAGCAGACTAGAAA        ATAG          ||||| || ||   |||| ||   ||||| |||| ||
     TAACAGGCTAAAATGTTCAG                    TACCA AG  TG   CGGA CA   ATCAGA GAAA GC G
     ACACCAT                     C ACT TAAAAT  - ATAAG    C   G A



GAM261  GGCAAATAATTAATCAGTGA 247   AACGATGTTA 596       TA  AATCA   AG      T AGT
     TAGATTGTTTACATACAGTA        CCAATCGTTT       GGCAAA ATT   GTGAT ATTGTTACA AC  A
     TGTCGTTTGTAAACGATGTT        GCT            ||||| |||   ||||| |||||||||| ||
     ACCAATCGTTTGCT                     TCGTTT TAA   CATTG TAGCAAATGT TG  T
                        GC  C----   --       T CTG



GAM262  GGAATTTTGACAATTCTCTT 248   AGTGAAAAGA 597      A  -  TTC------   GA C  A
     TGAGCCGATAGTATCAGTGA        ATGTAAACTT       GG ATTT TGACAA      TCTTT GC GAT G
     AAAGAATGTAAACTTTGTCA        TGTC           || |||| |||||      ||||| || |||
     TAAGTACC                    CC TGAA ACTGTT      AGAAA TG CTA /
                        A   T    TCAAATGTA   AG A  T



GAM263  ATATTACGCAGCAAGCATAA 249   TTAGGTTTGT 598        A  ---  T  A--- TA
     CCAGCATAATCTGTCTTAGG        TCATTGTCGT       ATATTACGC GCAA  GCA AACC   GCA A
     TTTGTTCATTGTCGTGTGGT        GTGG           ||||||||| ||||  ||| |||| ||| 
     GT                          TGTGGTGTG TGTT  TGT TTGG   TGT /
                        C   ACT  -  ATTC  CT



GAM264  GATAAAAATGTAGTGTAATT 250   TATAGTGTAA 599    -    GTAATT  TAT   AA   ATGC TT
TCG  TG
     GTTATATAGTGTAACACGAA        CACGAATGCA       ATGTAGT   GTTA AGTGT CACGA  AG
TGGGAGTAT  TTG  C
     TGCAGTTTGGGAGTATTCGT        GTTT           |||||||   |||| ||||| |||||  || ||||||||| |||
     TGTGCTACAAATATATTTCC               TATATTA   CGAT  TTACG GTGCT  TC ACCTTTATA
AAC  /
     ATTCTTCGTGGCATTTTTAG        G    AAATAT  TT-  --  ---- TT     TA- AT
     CTATAAAATTATATGGGGTT
     GTC
```

GAM265 TTTTATCGTTTTATCTATTG 251   TTTATCTATT 600   C TT T   T - T TAA
        ATGGTGTATGAACTAATTTA   GATGGTGTAT   TTTTAT GT TA CTATTGA GGT GTA GAAC T
        CGTTCTACAACTTTTAATAG   GAAC ||||||| || || |||||||| ||| ||| ||||
        TGTCGCTGTAAAA   AAAATG CG GT GATAATT TCA CAT CTTG T
                                         T CT -   T A - CAT

GAM266 TATTGGATTGTATATTTTAT 252   TAAAATGCTA 601   TT T T T -   A   ATT
        TTTATATTTTATATTTTATA   ATGTCAAGTT   TATTGGA GTA ATTT AT TTA TATTTTAT TTTTAT T
        TTTTGTAATAAGAATAAAAT   TATT ||||||| ||| |||| || ||| ||||||| |||||
        GCTAATGTCAAGTTTATTCC   ATAACCT TAT TGAA TG AAT GTAAAATA AGAATA T
        AATA   -- T   C T C   - ATG

GAM267 TGTTAATTTTACTAGATCGT 253   TTCCGTAGTC 602   A TACTA GT   TC TA   T
        CATGGGTCATAGAATTTATA   CATGGATCCA   TGTTA TTT GATC CATGGG A GAATT A
        GGTTCCGTAGTCCATGGATC   AACT ||||| ||| |||| |||||| | |||||
        CAAACTAGCA   ACGAT AAA   CTAG GTACCT T CTTGG T
                                          C C---- -- GA GC   A

GAM268 GGAGTATTCCAAGAGTTTTA 254   AAGAGTTTTA 603   A-   CAA   - TT- A---------------- AT
        GTTGTCTAGTATTTAACAAG   GTTGTCTAGT   GG GTATTC GAGTTT TAG GTCT   GT T
        AGAAGAGATTTCAACAGACT   ATTT || |||||| |||||| ||| |||| ||
        GTTTATGAACTCGAATGCCG   CC CGTAAG CTCAAG ATT CAGA   CA /
        CC   GC   ---   T TGT CAACTTTAGAGAAGAGAA AT

GAM269 GTTTTCTAAAGATGTCATTA 255   TGAATGGATT 604   T A   CATTAAACCCTCGATC TG
TATCA   C   TTA
        AACCCTCGATCATGAATGGA   TATCATCATC   TT TCTA AGATGT   A AATGGATT   TCAT
GTTT T
        TTTATCATCATCGTTTTTAT   GTTT || |||| ||||||| | |||||||| |||| ||||
        GTTGGACATGAGCTTAGTCC   AG AGAT TCTACA   T TTGCCTGA   AGTA CAGG
/
        GTTTGTCCACATCTATAGAC   C A   CC-------------- GT   TTCG- - TTG
        GAC

GAM270 TCGGATGACCATATATTTAT 256   GATGACCATA 605   GAT --   A T   TATTA
        TTTCAGTTTTATTATACGCA   TATTTATTTT   TCG GACC ATATATTT TTT CAGTTT   T
        TAAATTGTAAAAAATATGTT   CAGT ||| |||| |||||||| ||| ||||||
        AGGTTTACGA   AGC TTGG TGTATAAA AAA GTTAAA   A
                                      AT- AT   - T TACGC

GAM271 TATAAGGTGATTGGAATGGG 257   TAAGGTGATT 606   AG TT ATGG   TACAACA
        ATAAATACAACAATTATATT   GGAATGGGAT   TATA GTGA GGA GATAAA   A
        TTTTATCATATCCTTCACGC   AAAT |||| |||| ||| |||||
        TATA   ATAT CACT CCT CTATTT   T
                                      CG T- ATA-   TTTATAT

GAM272 ATTCGCGAAGCGACGTCATT 258   ACGTCATTTA 607   G CGTC   AATAAA   TTT
     TAATAAAAAAGTATTTTTT   ATAAAAAAG   ATTCGCGAA CGA   ATTT   AAAAGTATT T
     TTTAATATTTTTCACAAATA   TATT ||||||| || |||| |||||||||
     TCGTTCGCGGAT   TAGGCGCTT GCT   TAAA   TTTTTATAA /
                               - A---   CAC---   TTT

GAM273 TATCTTGGCAATAACTAATT 259   TGGCAATAAC 608   CT   AACT G A   --   A   T
     GAGATATTGATGCGAGTTCG   TAATTGAGAT   TAT TGGCAAT AATT AG TATT GATGCG
GTTCGGTA G
     GTATGCATATCGGACACGTA   ATTG ||| ||||||| |||| || |||| ||||| |||||||
     TCCGAGTACTGATTCCAAGT   ATG ACCGTTG   TTAG TC ATGA CTATGC CAGGCTAT C
     TGCCAGAGTA   AG   AACC - - GC   A   A

GAM274 ATAGATATGATAACAGGAAT 260   GATATGATAA 609   - A   ATAA A TA- T AAATA
     AACATCTTTAGGTTTAAAAT   CAGGAATAAC   ATAGAT ATGAT ACAGGA   C TCTT GGT TA   A
     AATTATATACACCAGTAGGA   ATCT ||||| ||||| ||||| | |||| ||| ||
     GTCTTGTCATCGTCATCTAT   TATCTA TGCTA TGTTCT   G AGGA   CCA AT   /
                          C   C   ---- - TGA C ATATT

GAM275 GAGTCGTCCATATTTTATTC 261   CGTCCATATT 610   TC CATATT   - CC -------- A
     TGAGGCCTAATAGACCTCTG   TTATTCTGAG   GAG GTC   TTATTCT GAGG TA   ATAG C
     TACATAAAATATTCCTCTAG   GCCT ||| ||| |||||| |||| || ||||
     AATAGTAGACATCTC   CTC CAG   GATAAGA CTCC AT   TGTC C
                          TA AT----   T TT AAAATACA T

GAM276 GGATATTCTTGATACATTCT 262   TATGGCAAAT 611   T T T TTCTTTTT   A   TACAT- ------
 - CA
     TTTTATACAGTGAATTGCAT   CTGCAATCAC   ATA TCT GA ACA   ATACAGTGA TTGCA   CC
 GATA G
     ACATCCGATACAGCATTATC   TGTA ||| ||| || ||| ||||||||| ||||| || ||||
     CATATATGGCAAATCTGCAA   TGT AGA TT TGT   TATGTCACT AACGT   GG   CTAT
C
     TCACTGTATTGTTTTTAGAT   T T T --------   - CTAAAC TATATAC   TA
     TGTCC

GAM277 GTAGTCACCGTAAATTTATC 263   CACCGTAAAT 612   A   AA T TCACC A A
     ACCAGAAATACTAATATCTA   TTATCACCAG   GT GTCACCGT AT TA   AGA AT C
     TCTTTATGTCCATGGTGATC   AAAT || |||||||| || || ||| ||
     AC   CA TAGTGGTA TG AT   TCT TA T
                          C   CC T TTCTA A A

GAM278 TATCTATCAGATTATTATGT 264   TAAGGTACTT 613   ------ AT   AT-- GG - -   ATAAA
     GTTATAAGGTACTTTTTCTC   TTTCTCATAA   TATCTATCA   GATT TATGTGTT AA TACT TTTT
CTCATA   C

```
         ATAATAAACTAGAGTATGAG        TAAA                ||||||||    ||||  ||||||||   ||  ||||  ||||  |||||||
         TAAGATAGTGTTTTTCAAAA                GTAGGTAGT    CTAA  ATATACAA   TT  GTGA  AGAA
GAGTAT    /
         CATATAAATCTAAAATTGAT                      TAAAAT   --     AACT  TT   T   T    GAGAT
         GGATG


GAM279  AAAGTATTGGTAATCGTGTC 265    TTTGTTCTAT 614         -  TAATCGT  CA   TA   TAAAAAG
TTATTTTT     TA
         ATATTAGTATAAAAGTGAT      CAACTACCTA        AAAGTATT  GG    GT  TAT  GTA      TGAT
ACAAAAT  T
         TTATTTTTACAAAATTATGT        TAAA          |||||||| ||    ||  |||  |||     ||||       |||||||
         ATTTTGTTCTATCAACTACC                TTTCATAA CC    CA  ATA  CAT     ACTA        TGTTTTA  /
         TATAAAACTTTCCAAATACT                A  TTT----  AA  TC   CA-----   TCT-----      TG
         TT


GAM280  ATGGCAGATCCAATTTGTAA 266    ATCCAATTTG 615      CA  -  AA   TAAAA  C    ----     GAA
         AAAATCAGCGGTTGAAAGAA        TAAAAAATCA       ATGG  DAT CC   TTTG    AAT AGCGGT   TGAAA  T
         TATATTTCACGTTATCGTTA      GCGG           |||| ||| || ||||    ||| ||||||   |||||
         GTTAGGCTCAAAGGTATCCC              TACC  CTA  GG  AAAC    TTG  TTGCTA   ACTTT  /
         AT                       --  T --   TCGGA  A    TTGC    ATA


GAM281  CGTGAAGATATCATTTCCCA 267    TCATTTCCCA 616       AA    TC      CA----  -  TT  TT
         TGTATTTTTTTTATGATTGT       TGTATTTTT       CGTG  GATA  ATTTCC    TGT  AT  TT  T
         AGCAGTTTATGGAAATTTTA       TTAT          |||| |||| ||||||    ||| || ||
         TCACGCG                  GCGC  CTAT  TAAAGG    ACG  TG  AG  /
                                  A-   TT     TATTTG  A  TT  TA


GAM282  CTTGGTATAATTATCAAAAT 268    TGGAATTGGG 617          TTATCAAAATA  GA-  CG--    C
         ACAAGACGTCGCTTTTAGCA       CTCCTTATAC       CTTGGTATAA      CAA  CGT   CTTTTAG  A
         GCTAAAAGAATAATGGAATT     CAAG           |||||||||    |||  |||   |||||||
         GGGCTCCTTATACCAAG                GAACCATATT       GTT  GTA   GAAAATC /
                                  CCTCGG-----  AAG  ATAA      G


GAM283  TACCTTATCAAATGATCCTG 269    TATCAAATGA 618       TT-  A-  G  C   T   CA  T  TA
         TTGGGCATTTTCTACATTGA       TCCTGTTGGG        TACC  ATC  AAT AT CTG  TGGG   TT TC  C
         TGACATCCATTAGAATAATT     CATT           |||| ||| ||| || ||| |||| || ||
         GGGATTGTGGTA                    ATGG  TAG  TTA TA DAT ACCT  AG AG  A
                                  TGT   GG   A  A  T   AC  T  TT


GAM284  TCGCTACTTGGTTAGTGTAT 270    TTAATAATTA 619       CTACTT  T   T   C  TGA
         TATTCAGTATGAAGACCTAT       CTTATCTTTT       TCG    GGT AGTG ATTATT AGTA  A
         TAATAATTACTTATCTTTTG     GACG           |||   ||| |||| |||||| ||||
         ACGA                    AGC    CTA TCAT TAATAA TTAT  G
                                  AGTTTT  T   -   -  CCA
```

GAM285 TTTTGGTAATCTATTATTAT 271   TATTATTATT 620   CT TATT   CTCT-   ACCG
    TGGCTCTGATCACCGCATCT   GGCTCTGATC   TTTTGGTAAT AT   ATTGG   GATC   C
    AGATCTACACCTAATCTATT   ACCG ||||||||| || |||||| ||||
    AATTACCAAGA   AGAACCATTA TA   TAATC   CTAG   A
                             AT TC--   CACAT   ATCT

GAM286 TTTGGTCGATGTAAAATTTT 272   TGTAAAATTT 621   CGA   AAATTTTT   -   AAA
    TGTCGATAAAAATTAAAAAA   TTGTCGATAA   TTTGGT TGTA   GTCGATAA AAATTAA A
    TAACTTAATTTATTATTGAT   AAAT |||||| |||| |||||||| |||||||
    CTCGTGTGTACAACCGAA   AAGCCA ACAT   TAGTTATT TTTAATT T
                             ---   GTGTGCTC   A   CAA

GAM287 GATTCTCGTCGTACCCACCG 273   TCGTACCCAC 622   T   C-   CC   G T TAA
    AGAGCGTGTGCGTAAAACAT   CGAGAGCGTG   GAT CTCGT GTAC ACCGAGA CGTG GCG A
    CGCCATGATTTCGGTTGTAC   TGCG ||| ||||| |||| ||||||| |||| |||
    ACACGAGATC   CTA GAGCA CATG TGGCTTT GTAC CGC A
                             -   CA T-   A - TAC

GAM288 CGTATTATACGCATTATAAC 274   TTCGTTGTAT 623   CGCAT   T C   GTA
    TGACAGCGTCGTAAATAGAT   ATAGTACG   CGTATTATA   TATAAC GA AGCGTC A
    GTTTCGTTGTATATAGTACG ||||||||| |||||| || ||||||
                    GCATGATAT   ATGTTG CT TTGTAG /
                             -----   - -   ATA

GAM289 GGTAGCAATTTATGGAACTT 275   TAACGGAGAT 624   ---   T AAC   GGTCATT   CAC
GAACAA
    ATATTGGTCATTATTTTTGT   TAAAAATATG   GGT AGCAATT ATGG TTATATT   ATTTTTGT
AG   A
    CACAGGAACAAACTAATACT   ACGC ||| |||||| |||| ||||||| |||||||| ||
    ATAACGGAGATTAAAAATAT   CCG TTGTTAA TACC AGTATAA   TAGAGGCA TC   /
    GACGCCCATAATTGTTAACG   CAA   - CGC   AAAT---   ATA ATAATC
CC

GAM290 GTATCATAATTTTCAAAGAT 276   GTTGTTGTTT 625   T AAT A- A   TTA-   TACTTCC
    GGTCGTTTAGACAATAGTAC   GCGACTGCTT   GTA CAT TTTC AAG TGGTCGT   GACAATAG
A
    TTCCATTATTATTTTGTTGT   CCGA ||| ||| |||| ||| ||||||| |||||||||
    TGTTTGCGACTGCTTCCGAA   CAT GTA   AAAG TTC GTCAGCG   TTGTTGTT   T
    ATACATGTAC   - CAT CC - TTTG   TTATTAT

GAM291 TGTTCTCTATAGTTACATTA 277   TGTGACACCC 626   TA---------   - TTA
    ATTAAAATTTTATATGTGAC   ATTCATCTGG   TGTTCTCTA   GTTACAT TAA A
    ACCCATTCATCTGGAGAATA   AGAA |||||||| |||||| |||
                    ATAAGAGGT   CAGTGTA ATT A
                             CTACTTACCCA   T TTA

GAM292 CATCTTTTACCAACACAAAG 278   TCTTTTACCA 627   CT   ACACAAA   ATATTT TT   -
GATAAT   ACA
       GGTGGATATTTGTTCATTGG   ACACAAAGGG   AT TTTACCA   GGGTGG   G CATTG GAGTT
  AATAC   C
       AGTTGATAATAATACACACA   TGGA || ||||||| |||||| | ||||| ||||| |||||
       AAGTATTTGGATTCACGGTG   TA AGATGGT   TCCATC   T GTGGC CTTAG   TTATG
/
       GGTTACGACTACCTCAGACT   AG   CAGAC--   AGCAT- GG   A   GT----   AAA
       GGTAGAGAATG

GAM293 GTACGCGTGTCGATTCATCA 279   TGAGGCTACC 628   --   ------   A-- AT
       AGGTATATAAACCTGGGGAT   TCGACATACG   GTACGCGT GTCGA   TTCATC AGGT A
       GAGGCTACCTCGACATACGT   TGTG ||||||||| ||||| ||||||| ||||
       GTGC   CGTGTGCA CAGCT   GAGTAG TCCA T
                                  TA   CCATCG   GGG   AA

GAM294 TAATTTTTTATAAACTAACA 280   TAACATGTTA 629   TT AAAC   T A-- G
       TTGTTAATTGAAAAGGGATA   CAGAATATAA   TAATTT TAT   TAACAT GTTA TT A
       ACATGTTACAGAATATAAAT   ATTA |||||| ||| ||||||| |||| ||
       TA   ATTAAA ATA   ATTGTA CAAT GA A
                                  T- AGAC   - AGG A

GAM295 AACACGGCAGAATATCGCCC 281   TGAGATATTC 630   --------------   GC-------- TACT
       ATATACTTTATTTATGGATT   TGAGCGCTAA   AACACGG   CAGAATATC   CCATA T
       TGAATGAGATATTCTGAGCG   CCTT ||||||| |||||||||| |||||
       CTAACCTTATCCGTGTT   TTGTGCC   GTCTTATAG   GGTAT   /
                                  TATTCCAATCGCGA   AGTAAGTTTA   TTAT

GAM296 AGTAGCATACGGATGCTCGA 282   TGTACAAATT 631   GCA   ----   - T C   ATAT GT GT
TATT--- GT
       TGTACAAATTGATATGGTCG   GATATGGTCG   GTA TACGG   ATGC TCGA GTA AAATTG   G C
CG   CA C
       TCGTATTCAGTCAATGTTAC   TCGT ||| ||||| ||| |||| ||| |||||| | | || ||
       AGTCGGTGGTCCAATTTTTA   CAT ATGCC   TACG AGCT CAT TTTAAC C G GC   GT
/
       CTTCGACGCATAGTCCCGTA   AAC   CTGA   C   T T   ---- TG TG TGACATT AA
       CAATACT

GAM297 CCCTATTTTCAATCCCCATG 283   CATGGAGTAG 632   AT TCAA CCA   - TCA T A C
TA
       TTTCCTCTTCAGTCTTCTCA   ATGATAGAGG   CCCT TT TCC TGTTCC TCT GTCT CTC CAT
GTC A
       CATCGTCTAATAGACATGGA   GGAA |||| || ||| ||||||| ||| |||| ||| ||| |||
       GTAGATGATAGAGGGGAACA   GGGA AA   AGG   ACAAGGG AGA   TAGA GAG GTA CAG
/

GAAGGACTATAATCAGGG   CT TATC AAG   G TAG T - - AT

GAM298 GAAAAGACGTGGGTACTAAA 284   AAGTTGGCTG 633   - C AA T C CA- A T
        GTTGGCTGTCATCTTACCAA   TCATCTTACC   GAAAAGACGTG GGTA TA GT GG TGT TCTT
CCAAT G
        TTGCAATTGGAAGAACAACG   AATT |||||||||| |||| || || || ||| |||| |||||
        ACCTGCACTAATACCACATG   CTTTTTTGTAC CCAT AT CG CC GCA AGAA GGTTA C
TTTTTTC   A A CA T A ACA - A

GAM299 GTCGTTAAAAGCGCTTCTAT 285   AATTATAGAT 634   C A CT   TC CAT
        ATCTCTCATTAGCTAGAATT   ACGCTATTAA   GT GTTAA AGCG TCTATA TCT T
        ATAGATACGCTATTAATTAT   TTAT || ||||| |||| |||||| |||
                    TA TAATT TCGC AGATAT AGA A
                     T   A AT   TA TCG

GAM300 TGGTCGTGTAGCGCGATAGA 286   TTAGATATCC 635   C A C AGAGATA   T
        GATAGTCTAATATTAATATT   GTAACACTAC   TGGT GTGT GCG GAT   GTCTAATA T
        AGATATCCGTAACACTACCA   CA |||| |||| ||| ||| ||||||||
                    ACCA CACA TGC CTA   TAGATTAT A
                     T A - -------   A

GAM301 GACATGGTAAGATTACTGGC 287   TGGTAAGATT 636   T-- G ACTG - TCTAA
        TCGTTTTCTAACTCCATGAA   ACTGGCTCGT   GACA GGTAA ATT GC TCGTTT   C
        TGATGCAAAATATTACCCTT   TTTC |||| ||||| ||| || ||||||
        TGTC   CTGT CCATT TAA CG AGTAAG   /
                    TTC   A AA-- T TACCT

GAM302 AAGGGTGGAATGCGATACAT 288   AAGAATTTAT 637   GAATG ACAT C   ---   ACACA
        TGATCTATGTAGTTTTAAAA   ATAAATCATT   AAGGGTG CGAT TGAT TATGTAG TTTTAAA
C
        CACACGCAAACTTTGAAGAA   CCAT ||||||| |||| |||| |||||||| |||||||
        TTTATATAAATCATTCCATC   TTCCTAC GCTA ACTA ATATATT GAAGTTT G
        GATACATCCTT   ATA-- CCTT A   TAA   CAAAC

GAM303 ACTGTATGCTCCTAGCGGAG 289   TGTATGCTCC 638   A - A   AATCCTTCG T
        TTAATCCTTCGTTGTTTCTA   TAGCGGAGTT   ACTGT TGCTC CT GCGGAGTT   TTGT T
        CAAAGTCTCTCGACTCCGCG   AATC ||||| ||||| || ||||||||| ||||
        AGAGAGTAACAGT   TGACA ATGAG GA CGCCTCAG   AACA C
                    - A G   CTCTCTGA- T

GAM304 ATAATTCAGTAATAATAATT 290   TCAGTAATAA 639   - A ATAATTC T   AAA
        CAGTAATGTATATAAAAATG   TAATTCAGTA   ATAATT CAGTA TA   AGTAA GTATATAA T
        CATTGTATATTTACTCCAAT   ATGT ||||| ||||| || ||||| |||||||

```
      ACTACTGTAGTTGT                          TGTTGA GTCAT AT     TCATT TATATGTT  /
                           T    C AACC---   -     ACG


      GAM305  ATAGAGTCTACATTTATATG 291    TCTACATTTA 640         CTACATTT    TCT   --   AGAT
           TTCTCTATCGGTGAGATACA         TATGTTCTCT      ATAGAGT    ATATGT CTATC GGTG  A
           AATACCTAGATAGTCGCGTA         ATCG        ||||||      ||||| ||||| ||||
           TCTTCATCCATTCTAT                        TATCTTA      TATGCG GATAG CCAT  /
                              CCTACTTC    CT-   AT    AAAC


      GAM306  ATATCTTCAGTACATCGTTT 292    TACAAATAGC 641      T T G   C---     A A
           GTAAAGTAATTATTATACAA         AGTGTAGTGC      ATA CT CA TACAT   GTTTGTA AGT A
           ATAGCAGTGTAGTGCAGTAT        AGTA         ||| || || |||||   ||||||| |||
                              TAT GA GT ATGTG   TAAACAT TTA T
                        - C  G   ACGA      A  T


      GAM307  ATTGCACGAAGTTCTTCGGC 293    ATTGTCCCAC 642        C C TTTCAT-- G     A AA
TTTAATG  TC CG
           GGTTTTCATGGAGTCATTTC        GGAAGTGAAT     GTTCTT GG GGT    GGA TCATTCTG TG ACA
 ATC CA C
           TGATGAAACATTTAATGATC        CCTT        |||||| || ||||     ||| |||||||| || |||    ||| ||
           TCCACGCAATTGTCGATATT             CGAGAA CC CCA     CCT AGTGAAGGC AC TGT    TAG
GT A
           GTCCCACGGAAGTGAATCCT               A A CTCAACTT A     - CC TA----- CT TA
           TCAACTCACCACCAAAGAGC
           TCCGTTGCAT
      GAM308  CCACATCCTTTATTAATAAT 294    TGAGAAAGAC 643     A  TT   ATAATAA AA   TCTAT
           AATTTAACAATCTCTATATC        CAGTAGTATT     CC CATCC TATTA    TTT CAATC  A
           TATGGTTGAGAAAGACCAGT        GGAT        || ||||| |||||    ||| |||||
           AGTATTGGATGGG                GG GTAGG ATGAT    AAA GTTGG  /
                        -   TT   GACCAG- GA   TATCT


      GAM309  GAAGGTAGTAATGTTAGTAG 295    TAGTTTATCA 644        GTA TTA   A  TAT  G
           ACAATTTTATCTGTGAAAA         TATACCTTT        GAAGGTA ATG  GTAGAC ATTTT  CTGT A
           CAGGAAATAGTTTATCATAT         ||||||| ||| |||||| ||||| ||||
           ACCTTT                      TTTCCAT TAC  TATTTG TAAAG  GACA A
                        A-- ---   A   ---   A


      GAM310  GCAATACTTCTGGTCTCGGA 296    TTCTGGTCTC 645         ACTTC        A ----------  C
           TTAGGCGTCGTTACGTATAT        GGATTAGGCG       GCAAT   TGGTCTCGGATT GG      CGT G
           ATCCACCAATCCGAGACCAT        TCGT        |||||  ||||||||||| ||      |||
           TGATTGC                     CGTTA  ACCAGAGCCTAA CC      GCA T
                        GTT--      - ACCTATATAT  T


      GAM311  GGCCTTTTTTATCGTTATCG 297    CCTTTTTTAT 646      C TT- CG  CG - -  TCACCTGG
```

GTTTTCTACACTCACCTGGT   CGTTATCGGT   GGC TT TTAT TTAT GT TTTC TACAC   T
TTATAAACGTGTGCGAGACA   TTTC ||| || |||| |||| || |||| |||||
CAAATAATAATAATGTAACG   TCG AA AATA AATA CA AGAG GTGTG   /
CT   C TGT AT AA C C CAAATATT

GAM312 TCATAATATTAGAATATATT 298   TAGAATATAT 647   ATT TATATTTTAAAGGA   TTA TAT
        TTAAAGGACTTATCGTTATT   TTTAAAGGAC   TCATAAT AGAA   CTTATCG TTA T
        ATATTTTTTTAACTCGGTGA   TTAT ||||||| |||| ||||||| |||
        GGTATCTTCTTAACTTTCTC   AGTATTA TCTT   GAGTGGC AAT T
        GAATTATGA   AGC TCAATTCTTCATG   TC- TTT

GAM313 TTCTGAAAGAGATGAGAAGC 299   TCTATGGGTC 648   GAAAG A AA   CCC
        CTGTAGAGAGACCCTGCGCT   CATCTATGAG   TTCT AGATG G GCCTGTAGAGAGA T
        TTCTCTATGGGTCCATCTAT   AA |||| |||||| | ||||||||||||
        GAGAA   AAGA   TCTAC C TGGGTATCTCTTT G
                               GTA--   - --   CGC

GAM314 TTTCTTTTCACGATGCATCT 300   ATAAGTGGAC 649   TC- GA- ------- GA CGT
        TATTGAATGACGTTTTCTCA   ATATAGATGC   TTTCTTT AC TGCATCT   TATT ATGA T
        TAAGTGGACATATAGATGCA   AGAA ||||||| || ||||||| |||| ||||
        GAAGTAATGAAGAAA   AAAGAAG TG ACGTAGA   GTGA TACT /
                                TAA AAG   TATACAG A- CTT

GAM315 TTTTTATAAACATGAAACCA 301   TGTCTAAATG 650   --- AAACCACT- AAA TAATTA   G
 T
        CTGTCTAAATGTAATTATGA   TAATTATGAT   TTTTTATA AACATG   GTCT TG TGATCTT
ATT A
        TCTTGATTTATAGATGAAGA   CTTG ||||||| |||||| |||| || ||||||| |||
        TCAGCCTTTAGAGGATTTTA   AAAAGTAT TTGTAT   TAGG AT   ACTAGAA TAG T
        ACCAGTATGTTTAATATGAA   AAT   GACCAATTT AG- TTCCG-   G A
        AA

GAM316 ATGTAGTAATCGTTGTCGTG 302   ATGGTTCTTT 651   C TG GTGTTCC-- TCC TTCTCC   -
  T TTCT
        TTCCTGTTTCCTACTTCTCC   CCGTACAACA   AT GT TC   TGTT TAC   AATCAT
ATAGATATT TCT   A
        AATCATATAGATATTTTCTT   TACT || || || |||| ||| |||||| |||||||| |||
        TCTATCATGGATAATATTTG   TA TA AG   ACAA ATG   TTGGTA TGTTTATAA AGG /
        TAATGGTTCTTTCCGTACAA   - GT ATTTGTCAT C-- CCTTTC   A   T TACT
        CATACTGTTTAGATGATATT
        GCGCAT
GAM317 GAATGACTCGTCCCTTAATA 303   TGACTCGTCC 652   GA G TAATA AGTAG - TCT
        GGCAGTAGGCTAGTATCTTT   CTTAATAGGC   GAAT CTC TCCCT GGC   GCTA GTA T
        TTTACGTAGTAATCGTCGTA   AGTA |||| ||| ||||| ||| |||| |||
        GGGAGAGAATTC   CTTA GAG AGGGA   CTG   TGAT CAT /
                                A- - TG--- CTAA- G TTT

GAM318 GAGATTGTATCAGTTTCGTA 304   GATTGTATCA 653   -- - T TA TGA   G T
    GTCTTGAGTATTGGTATTAC   GTTTCGTAGT   GAGATTGTA TC AGT TCG GTCT GTATTG TAT A
    TATATAGTATATAGATGTCG   CTTG ||||||||| || ||| ||| |||| |||||| |||
    ACGCTAGATATACAGTCTC   CTCTGACAT AG TCG AGC TAGA TATGAT ATA C
                          AT A C TG TA-   - T

GAM319 GGCAAATCTTATCATTGGTC 305   TAACATCGAT 654   CTT   - ---   TG- TTGCTTT
    GGTGTTTGGTCTTGCTTTGT   TCCCATATGA   GGCAAAT ATCAT TGG TCGGTGTT GTC   G
    GACTTTGATAATAACATCGA   TGTT ||||||| ||||| ||| |||||||| |||
    TTCCCATATGATGTTTGTT   TTGTTTG TAGTA ACC AGCTACAA TAG   /
                          --- T CTT   TAA TTTCAGT

GAM320 ACCTCTTTCTGATGGAGTCG 306   TGATGGAGTC 655   TTTCT- T TC   AAG   CT TC
TCTTC T CTCACAA
    TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   C   GA GGAG GTAAAA TTTTAT CTT TC   GA
GGT   A
    CTCTCTTCGATGGTCTCACA   TTTA | || |||| ||||| ||||| ||| || || |||
    AAAATATTAAACCTCTTTCT   G   CT TCTC TATTTT AAAATG GAG AG   CT CCA   A
    GATGGAGTCGTAAAAAAGTT   CTTCCT T -- GAA   CT GT TCTTT - AATTATA
    TTATCTCTTTCTCCTTCGAT
    GGT
GAM321 ACCTCTTTCTGATGGAGTCG 307   TGATGGAGTC 656   TTTCT TG TC   AAG   CT TC
TCTTC T CTCACAA
    TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   TC   GA GAG GTAAAA TTTTAT CTT TC   GA
GGT   A
    CTCTCTTCGATGGTCTCACA   TTTA || || ||| ||||| ||||| ||| || || |||
    AAAATATTAAACCTCTTTCT   AG   CT TTC TATTTT AAAATG GAG AG   CT CCA   A
    GATGGAGTCGTAAAAAAGTT   CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
    TTATCTCTTTCTCTCTTCGA
    TGGT
GAM322 ACCTCTTTCTGATGGAGTCG 308   TGATGGAGTC 657   TTTCT TG TC   AAG   CT TC
TCTTC T CTCACAA
    TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   TC   GA GAG GTAAAA TTTTAT CTT TC   GA
GGT   A
    CTCTCTTCGATGGTCTCACA   TTTA || || ||| ||||| ||||| ||| || || |||
    AAAATATTAAACCTCTTTCT   AG   CT TTC TATTTT AAAATG GAG AG   CT CCA   A
    GATGGAGTCGTAAAAAAGTT   CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
    TTATCTCTTTCTCTCTTCGA
    TGGT
GAM323 ACCTCTTTCTGATGGAGTCG 309   TGATGGAGTC 658   TTTCT TG TC   AAG   CT TC
TCTTC T CTCACAA
    TAAAAAAGTTTTATCTCTTT   GTAAAAAGT   TC   GA GAG GTAAAA TTTTAT CTT TC   GA
GGT   A
    CTCTCTTCGATGGTCTCACA   TTTA || || ||| ||||| ||||| ||| || || |||
    AAAATATTAAACCTCTTTCT   AG   CT TTC TATTTT AAAATG GAG AG   CT CCA   A
    GATGGAGTCGTAAAAAAGTT   CTTCT CT TC   GAA   CT GT TCTTT - AATTATA

```
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM324  ACCTCTTTCTGATGGAGTCG 310   TGATGGAGTC 659    TTTCT TG TC    AAG    CT TC
TCTTC T  CTCACAA
        TAAAAAAGTTTTATCTCTTT        GTAAAAAGT      TC  GA GAG GTAAAA TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA        TTTA           ||    || ||| ||||||  ||||||  ||| ||    || |||
        AAAATATTAAACCTCTTTCT               AG    CT TTC TATTTT AAAATG GAG AG    CT CCA      A
        GATGGAGTCGTAAAAAGTT                CTTCT CT TC    GAA    CT GT TCTTT - AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM325  ACCTCTTTCTGATGGAGTCG 311   TGATGGAGTC 660    TTTCT TG TC    AAG    CT TC
TCTTC T  CTCACAA
        TAAAAAAGTTTTATCTCTTT        GTAAAAAGT      TC  GA GAG GTAAAA TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA        TTTA           ||    || ||| ||||||  ||||||  ||| ||    || |||
        AAAATATTAAACCTCTTTCT               AG    CT TTC TATTTT AAAATG GAG AG    CT CCA      A
        GATGGAGTCGTAAAAAGTT                CTTCT CT TC    GAA    CT GT TCTTT - AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM326  ACCTCTTTCTGATGGAGTCG 312   TGATGGAGTC 661    TTTCT TG TC    AAG    CT TC
TCTTC T  CTCACAA
        TAAAAAAGTTTTATCTCTTT        GTAAAAAGT      TC  GA GAG GTAAAA TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA        TTTA           ||    || ||| ||||||  ||||||  ||| ||    || |||
        AAAATATTAAACCTCTTTCT               AG    CT TTC TATTTT AAAATG GAG AG    CT CCA      A
        GATGGAGTCGTAAAAAGTT                CTTCT CT TC    GAA    CT GT TCTTT - AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM327  ACCTCTTTCTGATGGAGTCG 313   TGATGGAGTC 662    TTTCT TG TC    AAG    CT TC
TCTTC T  CTCACAA
        TAAAAAAGTTTTATCTCTTT        GTAAAAAGT      TC  GA GAG GTAAAA TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA        TTTA           ||    || ||| ||||||  ||||||  ||| ||    || |||
        AAAATATTAAACCTCTTTCT               AG    CT TTC TATTTT AAAATG GAG AG    CT CCA      A
        GATGGAGTCGTAAAAAGTT                CTTCT CT TC    GAA    CT GT TCTTT - AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM328  ACCTCTTTCTGATGGAGTCG 314   TGATGGAGTC 663    TTTCT TG TC    AAG    CT TC
TCTTC T  CTCACAA
        TAAAAAAGTTTTATCTCTTT        GTAAAAAGT      TC  GA GAG GTAAAA TTTTAT CTT TC    GA
GGT    A
        CTCTCTTCGATGGTCTCACA        TTTA           ||    || ||| ||||||  ||||||  ||| ||    || |||
        AAAATATTAAACCTCTTTCT               AG    CT TTC TATTTT AAAATG GAG AG    CT CCA      A
        GATGGAGTCGTAAAAAGTT                CTTCT CT TC    GAA    CT GT TCTTT - AATTATA
        TTATCTCTTTCTCTCTTCGA
        TGGT
GAM329  ACCTCTTTCTGATGGAGTCG 315   TGATGGAGTC 664    TTTCT TG TC    AAG    CT TC
TCTTC T  CTCACAA
        TAAAAAAGTTTTATCTCTTT        GTAAAAAGT      TC  GA GAG GTAAAA TTTTAT CTT TC    GA
GGT    A
```

```
     CTCTCTTCGATGGTCTCACA      TTTA            ||  || ||| |||||| |||||| ||| ||   || |||
     AAAATATTAAACCTCTTTCT                  AG   CT TTC TATTTT AAAATG GAG AG   CT CCA     A
     GATGGAGTCGTAAAAAAGTT                     CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
     TTATCTCTTTCTCTCTTCGA
     TGGT
GAM330 ACCTCTTTCTGATGGAGTCG 316   TGATGGAGTC 665    TTTCT TG TC    AAG    CT TC
TCTTC T CTCACAA
     TAAAAAAGTTTTATCTCTTT       GTAAAAAAGT    TC  GA GAG GTAAAA TTTTAT CTT TC   GA
GGT    A
     CTCTCTTCGATGGTCTCACA      TTTA            ||  || ||| |||||| |||||| ||| ||   || |||
     AAAATATTAAACCTCTTTCT                  AG   CT TTC TATTTT AAAATG GAG AG   CT CCA     A
     GATGGAGTCGTAAAAAAGTT                     CTTCT CT TC   GAA   CT GT TCTTT - AATTATA
     TTATCTCTTTCTCTCTTCGA
     TGGT
GAM331 ACCTCTTTCTGATGGAGTCG 317   CGTAAAAAAG 666    TTTCT TG TC    AAG    CT  C TTC--
T CTCACAA
     TAAAAAAGTTTTATCTTTCT       TTTTATCTTT    TC  GA GAG GTAAAA TTTTAT TTCT TC   GA
GGT    A
     CTCTTCGATGGTCTCACAAA       CTCT            ||   || ||| |||||| |||||| |||| ||   || |||
     AATATTAAACCTCTTTCTGA               AG    CT TTC TATTTT AAAATG GAGG AG   CT CCA
A
     TGGAGTCGTAAAAAAGTTTT               CTTCT CT TC    GAA    CT T TCTTT - AATTATA
     ATCTCTTTCTCTCTTCGATG
     GT
GAM332 ATTAATTATAAAATTATGTA 318   TAAGTTAGTA 667      TA--    -  A--    - T
     TATGATTTACTAACTTTAGT       ATACATAAAT      ATTAAT   TAAAATT ATGTAT  TGATTTA CTAAC T
     TAGATAAGTTAGTAATACAT       TTTA            ||||||   |||||| |||||  |||||| |||||
     AAATTTTAGTATATTAAT                TAATTA   ATTTTAA TACATA   ATTGAAT GATTG T
                       TATG      A  ATG     A   A


GAM333 GATGGAGTCGTAAAAAAGTT 319   TGATGGAGTC 668    T  TC    AAG    --  T TCCTTC T
CTCACAA
     TTATCTCTTTCTCCTTCGAT       GTAAAAAAGT    GA GGAG GTAAAA TTTTAT CTCT TC    GA GGT
   A
     GGTCTCACAAAAATATTAAA       TTTA           || |||| |||||| |||||| |||| ||    || |||
     CCTCTTTCTGATGGAGTCGT               CT TCTC TATTTT AAAATG GAGG AG    CT CCA     A
     AAAAAAGTTTTATCTCTTTC               T  --    GAA    CT  T TCTTT- -  AATTATA


GAM334 GATGGAGTCGTAAAAAAGTT 320   TGATGGAGTC 669    T  TC    AAG    --  T TCCTTC T
CTCACAA
     TTATCTCTTTCTCCTTCGAT       GTAAAAAAGT    GA GGAG GTAAAA TTTTAT CTCT TC    GA GGT
   A
     GGTCTCACAAAAATATTAAA       TTTA           || |||| |||||| |||||| |||| ||    || |||
     CCTCTTTCTGATGGAGTCGT               CT TCTC TATTTT AAAATG GAGG AG    CT CCA     A
     AAAAAGTTTTATCTCTTTC               T  --    GAA    CT  T TCTTT- -  AATTATA


GAM335 GATGGAGTCGTAAAAAAGTT 321   TGATGGAGTC 670    T  TC    AAG    --  T TCCTTC T
CTCACAA
```

```
        TTATCTCTTTCTCCTTCGAT      GTAAAAAGT     GA GGAG GTAAAA TTTTAT CTCT TC    GA GGT
    A
        GGTCTCACAAAAATATTAAA      TTTA         || |||| ||||||  |||||| |||| ||    || |||
        CCTCTTTCTGATGGAGTCGT                  CT TCTC TATTTT AAAATG GAGG AG    CT CCA     A
        AAAAAAGTTTTATCTCTTTC                  T  --  GAA    CT  T TCTTT- - AATTATA


    GAM336  GATGGAGTCGTAAAAAAGTT 322    TGATGGAGTC 671     T  TC    AAG    CT  TC TCTTC T
    CTCACAA
        TTATCTCTTTCTCTCTTCGA      GTAAAAAGT     GA GGAG GTAAAA TTTTAT CTT TC    GA GGT
    A
        TGGTCTCACAAAAATATTAA      TTTA         || |||| ||||||  |||||| ||| ||    || |||
        ACCTCTTTCTGATGGAGTCG                  CT TCTC TATTTT AAAATG GAG AG    CT CCA     A
        TAAAAAAGTTTTATCTCTTT                  T  --  GAA    CT  GT TCTTT - AATTATA
        C


    GAM337  GATGGTCTCATAAAAAAGT 323    ATAAAAAAG 672     G  TCATAAAA  TTTTAC        ATTCT-
    CTCTCTT  TG
        TTTACAAAAATATTTTTATT      TTTTACAAAA    AT GTC    AAAG    AAAAATATTTTT    CTTT
    TGA  G
        CTCTTTCTCTCTTTGATGGT      ATAT         || |||     ||||   ||||||||||||   |||| |||
        CTCATAAAAAAGTTTTACA                  TG TAG    TTTC    TTTTTATAAAAA    GAAA    ACT /
        AAAATATTTTTATTCTCTTT                  G  TTTCTCTC  TCTTA-     CATTTT  AAAAT-- CT
        CTCTCTTTGATGGTC


    GAM338  GGAGTCATAAAATATTTTTA 324    TAAAATATTT 673     TC    A    T- T TCTCTTC T
    CTCACAA
        TTCTCTTTCTCTCTTCGATG      TTATTCTCTT    GGAG ATAAAAT TTTTTAT CTCT TC    GA GGT
    A
        GTCTCACAAAAATATTAAAC      TCTC         |||| ||||||| |||||| |||| ||    || |||
        CTCTTTCTGATGGAGTCGTA                  TCTC TATTTTG AAAAATG GAGG AG    CT CCA     A
        AAAAAGTTTTATCTCT                  --   A    CT  T TCTTT-- - AATTATA


    GAM339  TTAAACCTCTTTCTGATGGA 325    TGATGGAGTC 674     CTTTCT TG TC    AAG    -- T TCCTTC
    T CTCACAA
        GTCGTAAAAAAGTTTTATCT      GTAAAAAGT      GA GAG GTAAAA TTTTAT CTCT TC    GA
    GGT    A
        CTTTCTCCTTCGATGGTCTC      TTTA         || ||| ||||||  |||||| |||| ||    || |||
        ACAAAAATATTAAACCTCTT                  CT TTC TATTTT AAAATG GAGG AG    CT CCA     A
        TCTGATGGAGTCGTAAAAAA                  TCTTTC CT TC    GAA    CT  T TCTTT- - AATTATA
        GTTTTATCTCTTTCTCCTTT
        CTCACAAAAA
    GAM340  TTTTTCTTTGGTACAAAATT 326    TCTTTGGTAC 675     T    TT CACAA   ---- CA   A
        TCACACAAGTTTTTATACAG      AAAATTTCAC    TTTTTCTT GGTACAAAA TCA   GTTTT  TATA
    GACAA T
        ACAAATTCTTGTCCATATAT      ACAA         ||||||||| ||||||||| ||| ||||| |||| |||||
        TTTAAAACATTGACTTTTGT                  AAAAAGAA TCATGTTTT AGT    CAAAA  ATAT CTGTT T
        ACTAAGAAAAA                  -    C- TA---    TTTT  AC  C
```

GAM341   AGAGATAAAACTTTTTTACG 327   TGAGACCATC 676   --   AC ------ A A AAGA   A T
         ACTCCATCAGAAAGAGGTTT   GAAGGAGACT   AGAGATA AAACTTTTTT GA   CTCC TC GA
GGTTT ATA T
         AATATTTTTGTGAGACCATC   CCAT |||||| ||||||||| || |||| || || |||| |||
         GAAGGAGACTCCATCAGAAA   TTTTTAT TTTGGAGAAA CT   GAGG AG CT   CCAGA
TGT T
         GAGGTTTAATATTTTT   AA   GA ACCTCA A - A---   G T

GAM342   ATAAAAATATTTTTGTAAAA 328   AATATTTTTG 677   AAAA   A-- GA
         CTTTTTTTATGAGACCATCA   TAAAACTTTT   ATAAAAATATTTTTGT CTTTTTTT TGA C
         AAGAGAGAAAGAGAATAAAA   TTTA |||||||||||||| ||||||| |||
         ATATTTTTGT   TGTTTTTATAAAAATA GAAAGAGA ACT /
                                   AGA-   GAA AC

GAM343   ATAAAAATATTTTTGTAAAA 329   AATATTTTTG 678   AAAA   A-- GA
         CTTTTTTTATGAGACCATCA   TAAAACTTTT   ATAAAAATATTTTTGT CTTTTTTT TGA C
         AAGAGAGAAAGAGAATAAAA   TTTA |||||||||||||| ||||||| |||
         ATATTTTTGT   TGTTTTTATAAAAATA GAAAGAGA ACT /
                                   AGA-   GAA AC

GAM344   ATGGATTTTACTAGATCATT 330   TTATACGATC 679   - TTT -   ATTT- ACC
         TATATACCAAAAAATATTAT   TACGTTTTAT   ATG GAT AC TAGATC   ATAT A
         ACGATCTACGTTTTATTATA   TATA ||| ||| || |||||| ||||
         T   TAT TTA TG ATCTAG   TATA A
                                   A TTT C   CATAT AAA

GAM345   CTTTTTTACGACTCCATCAG 331   CATCAGAAAG 680   A CTCCA G   G T A   G GACCA -
         AAAGA
         AAAGAGGTTTAATATTTTTG   AGGTTTAATA   T CGA   TCA AAAGA GTT AAT TTTTT TGA   TCG
AAGAGAG   G
         TGAGACCATCGAAGAGAGAA   TTTT | ||| ||| ||||| ||| ||| ||||| ||| ||| |||||||
         AGAGATAAAACTTTTTTACG   A GCT   AGT TTTTT TAA TTG AGAAA ACT   AGC TTTTTTC
    A
         ACTCCATCAGAAAGAGGTTT   - ACCAG G   A T G   G ACCTC A   AAAAT
         AATATTTTTGTGAGACCATC
         GAAGAGAG
GAM346   CTTTTTTACGACTCCATCAG 332   CATCAGAAAG 681   A CTCCA G   G T A   G GACCA -
         AAAGA
         AAAGAGGTTTAATATTTTTG   AGGTTTAATA   T CGA   TCA AAAGA GTT AAT TTTTT TGA   TCG
AAGAGAG   G
         TGAGACCATCGAAGAGAGAA   TTTT | ||| ||| ||||| ||| ||| ||||| ||| ||| |||||||
         AGAGATAAAACTTTTTTACG   A GCT   AGT TTTTT TAA TTG AGAAA ACT   AGC TTTTTTC
    A
         ACTCCATCAGAAAGAGGTTT   - ACCAG G   A T G   G ACCTC A   AAAAT
         AATATTTTTGTGAGACCATC

GAAGAGAG

GAM347 CTTTTTTACGACTCCATCAG 333 CATCAGAAAG 682 A CTCCA G G T A G GACCA -
AAAGA

AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G

TGAGACCATCGAAGAGAGAA TTTT I III III IIIII III III IIIII III III IIIIIII
AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A

ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM348 CTTTTTTACGACTCCATCAG 334 CATCAGAAAG 683 A CTCCA G G T A G GACCA -
AAAGA

AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G

TGAGACCATCGAAGAGAGAA TTTT I III III IIIII III III IIIII III III IIIIIII
AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A

ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM349 CTTTTTTACGACTCCATCAG 335 CATCAGAAAG 684 A CTCCA G G T A G GACCA -
AAAGA

AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G

TGAGACCATCGAAGAGAGAA TTTT I III III IIIII III III IIIII III III IIIIIII
AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A

ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM350 CTTTTTTACGACTCCATCAG 336 CATCAGAAAG 685 A CTCCA G G T A G GACCA -
AAAGA

AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G

TGAGACCATCGAAGAGAGAA TTTT I III III IIIII III III IIIII III III IIIIIII
AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A

ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM351 CTTTTTTACGACTCCATCAG 337 CATCAGAAAG 686 A CTCCA G G T A G GACCA -
AAAGA

AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G

TGAGACCATCGAAGAGAGAA TTTT I III III IIIII III III IIIII III III IIIIIII
AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A

ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC

GAAGAGAG

GAM352 CTTTTTTACGACTCCATCAG 338   CATCAGAAAG 687   A CTCCA G G T A G GACCA -
    AAAG

    AAAGAGGTTTAATATTTTTG   AGGTTTAATA   TT CGA   TCA AAAGA GTT AAT TTTTT TGA   TCG
AAGAGAG   A

    TGAGACCATCGAAGAGAGAA   TTTT || ||| ||| ||||| ||| ||| ||||| ||| ||| |||||||
    AGATAAAACTTTTTTACGAC   AA GCT   AGT TTTTT TAA TTG AGAAA ACT   AGC
TTTTTTC   T

    TCCATCAGAAAGAGGTTTAA   - ACCAG G   A T G   G ACCTC A   AAAA
    TATTTTTGTGAGACCATCGA
    AGAGAG

GAM353 GTGTGCCTGAATCGTTCGAT 339   TGAATAGAGT 688   C   TTCGAT C C   CAA
    TAACCCTACTCATCCAATTT   TATCGATTCA   GTGTG CTGAATCG   TAAC CTA TCATC T
    CAGATGAATAGAGTTATCGA   GACA |||||| |||||||| |||| ||| |||||
    TTCAGACACAC   CACAC GACTTAGC   ATTG GAT AGTAG T
                    A   T----- A A   ACT

GAM354 TCAGAAAGAGGTTTAATATT 340   AGAGGTTTAA 689   AAA GTTT--   GAGACCA- GA
    TTTGTGAGACCATCGAAGAG   TATTTTTGTG   TCAG GAG   AATATTTTGT   TC A
    AGAAAGAGAATAAAATATT   AGAC |||| ||| |||||||||||| ||
    TTATGACTCCATTGA   AGTT CTC   TTATAAAAATA   AG /
                    AC- AGTATT   AGAGAAAG AG

GAM355 TGAGACCATCAAAGAGAGAA 341   AGAGAGAAAG 690   ACCA AAG   AGA-   AAAA
A-- GA
    AGAGAATAAAAATATTTTTG   AGAATAAAAA   TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTT TGA C
    TAAAACTTTTTTTATGAGAC   TATT ||| ||||||| |||||||||||||||| |||||||| |||
    CATCAAAGAGAGAAAGAGAA   AGT TTTTTTTC TGTTTTTATAAAAATA GAAAGAGA
ACT /
    TAAAAATATTTTTGTAAAAC   CCAG A--   AAAA   AGA-   GAA AC
    TTTTTTTATGAGACCATCA

GAM356 TTTTATGAGACCATCAAAGA 342   GAAGAGAGAA 691   ACCA AAG   AGA-   AAAA---
 - A
    GAGAAAGAGAATAAAAATAT   AGAGAATAAA   TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTTTG TG G
    TTTTGTAAAACTTTTTTTGT   AATA ||| |||||||| |||||||||||||||| |||||||||| ||
    GAGACCATCGAAGAGAGAAA   AGT TTTTTTTC TGTTTTTATAAAAATA
GAGAGAAGC AC A
    GAGAATAAAAATATTTTTGT   CCAG A--   AAAA   AGAGAAA   T C
    AAAACTTTTTTTATGAGACC
    ATCAAAGAGAG

GAM357 TTTTTCTTAGTACAAAAGTC 343   TCAATGTTTT 692   A-   G- AT---   AAAA   G
    AATGTTTTAAAATATATGGA   AAAATATATG   TTTTTCTT GTACAAAA TCA   GTTTT
TATATGGACAA A
    CAAGAATTTGTCTGTATAAA   GACA ||||||||| |||||||| ||| ||||| ||||||||||
    AACTTGTGTGAAATTTTGTA   AAAAAGAA CATGTTTT AGT   CAAAA ATATGTCTGTT A

CCAAAGAAAAA   AC   AA GTGTT   ----   T

GAM358 TCACCTTATCAAAGTCGTTT 344   TTGGTTGTGG 693   CCTT A   TT CACAT TATA   T-
     TT
     ATATCACATTGTATATAGTT   ATCTTCTACA   TCA ATCA AGTCGT ATAT   TGTA
GTTTATAACC TAACT C
     TATAACCTTAACTTTCGAGG   ATAT ||| |||||||||| |||| |||| |||||||||| |||||
     TTATTGGTTGTGGATCTTCT   AGT   TAGT TCAGTA TATA   ACAT   TAGGTGTTGG
ATTGG /
     ACAATATCTATGACTCTGAT   TCTT C   TC ----- CTTC   TT   AG
     TTCTTGA

GAM359 TCGGCCATACGTTTACTTTT 345   TATCATAAAG 694   AC T   C- - GT
     TGCGTATACATGTCCTGGTG   GGTATGCTCA   TCGGCCAT GT TACTTTTG GTATA CAT C
     ATATATCATAAAGGGTATGC   TGGC ||||||| || |||||||| ||||| |||
     TCATGGCCGA   AGCCGGTA CG ATGGGAAAT TATAT GTG C
                            CT T   AC   A GT

GAM360 TCGATGATACATGTATTAAA 346   TGATACATGT 695   A---   TGTA   T TCC
     ATACTTTCCGAATAAGTCTT   ATTAAAATAC   TCG TGATACA TTAAAA ACTT G
     TTAAATATTGTATTAATTAT   TTTC ||| ||||||| |||||| ||||
     GA   AGT   ATTATGT AATTTT TGAA /
                            ATTA   TATA   C   TAA

GAM361 AAAATCGATTCCGTCCAAGA 347   TCGATTCCGT 696   C   CCAAG   AAAAACA
     TGATAAAAACATTTACCGGC   CCAAGATGAT   AAAAT GATTCCGT ATGAT   T
     ATCATAAACACGGAGTTTAT   AAAA ||||| |||||||| |||||
     TTT   TTTTA TTGAGGCA   TACTA   T
                            T   CAAA-   CGGCCAT

GAM362 CATGGAGATACTTTATTACT 348   TAATGTCCTG 697   ------------ T   TAAATA
     CCATTAAATAATTTATCATG   TTTCATTTGT   CATGGAGAT   AC TTATTACTCCAT   A
     GAGTGATAATGTCCTGTTTC   TTCC ||||||||| || |||||||||||
     ATTTGTTTCCATG   GTACCTTG   TG AATAGTGAGGTA   /
                            TTTACTTTGTCC T   CTATTT

GAM363 AGTATGTTGTACGGAAAGAA 349   TGATTGGAGA 698   --   A GAAAGAACCA-- AAATATTA
TG---   AAGA
     CCATTACAAATATTATCCAT   AGTAGGAAAC   AGTA TGTTGT CG   TTAC   TCCA
ATAGA   A
     GATAGAAAGAAAATATCTAT   AGGA |||| ||||||| || |||| |||| |||||
     ATGATTGGAGAAGTAGGAAA   TCAT GCAACA GC   GATG   AGGT   TATCT /
     CAGGAACACGACAACGATTA   TA - ACAAGGACAAAG   AAG----- TAGTA ATAA
     CT

```
GENE    TARGET   UTR SEQUENCE              SEQID   BINDING-SITE
========  ==========  ===  =====================  ========  ===========================
GAM15    CAPN2    3' AAAACTTTATGAACTTCACCA 855    A    _   AAA
                            TG TGGAGT CGTAA  AGTTTT
                            || |||||| |||||  ||||||
                            AC ACTTCA GTATT  TCAAAA
                               C     A      ___
GAM15    DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG A
                   A            TGATGGAGT TA AAAAGTTTT
                                ||||||||| || |||||||||
                                ACTACCTCA AT TTTTTAAAA
                                  AA C
GAM15    SELE     3' AAAACTCTCCTACACTTCCATT 747       _ C AAAA
                   A            TGATGGA GT GTA   AGTTTT
                                ||||||| || |||   ||||||
                                ATTACCT CA CAT   TCAAAA
                                  T _  CCTC
GAM15    KIAA0475 3' AAAACCTTGCATTCCATCA    1570       C   AAAA
                                TGATGGAGT GTAA   GTTTT
                                ||||||||| ||||   |||||
                                ACTACCTTA CGTT   CAAAA
                                     _  C___
GAM15    LOC222671 5' GCTTCTACGACTCCGCCA    3582    A      AAA
                            TG TGGAGTCGTA   AAGT
                            || ||||||||||   ||||
                            AC GCCTCAGCAT   TTCG
                               C      C__
GAM15    LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                            TG TGGAGTC GT AA AAGTT
                            || ||||||| || || |||||
                            AC ACCTCAG CA TT TTTAA
                               C     T C C
GAM15    LOC257615 5' GCTTCTACGACTCCGCCA    3749    A      AAA
                            TG TGGAGTCGTA   AAGT
                            || ||||||||||   ||||
                            AC GCCTCAGCAT   TTCG
                               C        C__
GAM16    CAPN2    3' AAAACTTTATGAACTTCACCA 855    A    _   AAA
                            TG TGGAGT CGTAA  AGTTTT
                            || |||||| |||||  ||||||
                            AC ACTTCA GTATT  TCAAAA
                               C     A      ___
GAM16    DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG A
                   A            TGATGGAGT TA AAAAGTTTT
                                ||||||||| || |||||||||
                                ACTACCTCA AT TTTTTAAAA
                                  AA C
GAM16    SELE     3' AAAACTCTCCTACACTTCCATT 747       _ C AAAA
                   A            TGATGGA GT GTA   AGTTTT
                                ||||||| || |||   ||||||
```

```
                      ATTACCT CA CAT   TCAAAA
                        T _  CCTC
GAM16   KIAA0475 3' AAAACCTTGCATTCCATCA   1570       C   AAAA
                     TGATGGAGT GTAA   GTTTT
                     ||||||||| ||||   |||||
                     ACTACCTTA CGTT   CAAAA
                              _  C___
GAM16   LOC222671 5' GCTTCTACGACTCCGCCA    3582    A      AAA
                     TG TGGAGTCGTA   AAGT
                     || |||||||||   ||||
                     AC GCCTCAGCAT   TTCG
                        C      C__
GAM16   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                     TG TGGAGTC GT AA AAGTT
                     || ||||||| || || |||||
                     AC ACCTCAG CA TT TTTAA
                        C      T C C
GAM16   LOC257615 5' GCTTCTACGACTCCGCCA    3749    A      AAA
                     TG TGGAGTCGTA   AAGT
                     || |||||||||   ||||
                     AC GCCTCAGCAT   TTCG
                        C      C__
GAM17   CAPN2    3' AAAACTTTATGAACTTCACCA 855    A   _  AAA
                     TG TGGAGT CGTAA   AGTTTT
                     || |||||| |||||   |||||
                     AC ACTTCA GTATT   TCAAAA
                        C   A      ___
GAM17   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559     CG A
             A           TGATGGAGT TA AAAAGTTTT
                     ||||||||| || |||||||||
                     ACTACCTCA  AT TTTTTAAAA
                          AA C
GAM17   SELE     3' AAAACTCTCCTACACTTCCATT 747      _ C AAAA
             A           TGATGGA GT GTA   AGTTTT
                     ||||||| || ||| ||||||
                     ATTACCT CA CAT   TCAAAA
                        T _  CCTC
GAM17   KIAA0475 3' AAAACCTTGCATTCCATCA   1570       C   AAAA
                     TGATGGAGT GTAA   GTTTT
                     ||||||||| ||||   |||||
                     ACTACCTTA CGTT   CAAAA
                              _  C___
GAM17   LOC222671 5' GCTTCTACGACTCCGCCA    3582    A      AAA
                     TG TGGAGTCGTA   AAGT
                     || |||||||||   ||||
                     AC GCCTCAGCAT   TTCG
                        C      C__
GAM17   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                     TG TGGAGTC GT AA AAGTT
                     || ||||||| || || |||||
```

```
                            AC ACCTCAG CA TT TTTAA
                             C     T C C
GAM17   LOC257615 5' GCTTCTACGACTCCGCCA    3749    A      AAA
                         TG TGGAGTCGTA  AAGT
                         || |||||||||| ||||
                         AC GCCTCAGCAT  TTCG
                          C       C__
GAM18   CAPN2   3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| ||||| |||||
                         AC ACTTCA GTATT  TCAAAA
                          C    A     ___
GAM18   DAAM2   3' AAAATTTTTCTAAAACTCCATC 3559      CG  A
          A              TGATGGAGT TA AAAAGTTTT
                         ||||||||| || |||||||||
                         ACTACCTCA AT TTTTTAAAA
                            AA  C
GAM18   SELE   3' AAAACTCTCCTACACTTCCATT 747       _ C AAAA
          A              TGATGGA GT GTA   AGTTTT
                         ||||||| || |||   ||||||
                         ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM18   KIAA0475 3' AAAACCTTGCATTCCATCA   1570        C  AAAA
                         TGATGGAGT GTAA   GTTTT
                         ||||||||| ||||   |||||
                         ACTACCTTA CGTT   CAAAA
                            _  C___
GAM18   LOC222671 5' GCTTCTACGACTCCGCCA    3582    A      AAA
                         TG TGGAGTCGTA  AAGT
                         || |||||||||| ||||
                         AC GCCTCAGCAT  TTCG
                          C       C__
GAM18   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                         TG TGGAGTC GT AA AAGTT
                         || |||||||| || || |||||
                         AC ACCTCAG CA TT TTTAA
                          C     T C C
GAM18   LOC257615 5' GCTTCTACGACTCCGCCA    3749    A      AAA
                         TG TGGAGTCGTA  AAGT
                         || |||||||||| ||||
                         AC GCCTCAGCAT  TTCG
                          C       C__
GAM19   CAPN2   3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| ||||| |||||
                         AC ACTTCA GTATT  TCAAAA
                          C    A     ___
GAM19   DAAM2   3' AAAATTTTTCTAAAACTCCATC 3559      CG  A
          A              TGATGGAGT TA AAAAGTTTT
                         ||||||||| || |||||||||
```

```
                          ACTACCTCA  AT TTTTTAAAA
                            AA  C
GAM19    SELE     3' AAAACTCTCCTACACTTCCATT 747        _ C  AAAA
         A                    TGATGGA GT GTA   AGTTTT
                     IIIIIII II III   IIIIII
                     ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM19    KIAA0475 3' AAAACCTTGCATTCCATCA  1570        C  AAAA
                        TGATGGAGT GTAA   GTTTT
                     IIIIIIIII IIII   IIIII
                     ACTACCTTA CGTT   CAAAA
                            _  C___
GAM19    LOC222671 5' GCTTCTACGACTCCGCCA   3582     A      AAA
                        TG TGGAGTCGTA  AAGT
                     II IIIIIIIIII  IIII
                     AC GCCTCAGCAT  TTCG
                        C       C__
GAM19    LOC254901 5' AATTTCTTCACTGACTCCACCA 3699     A    _ A A
                        TG TGGAGTC GT AA AAGTT
                     II IIIIIII II II IIIII
                     AC ACCTCAG CA TT TTTAA
                        C    T C  C
GAM19    LOC257615 5' GCTTCTACGACTCCGCCA   3749     A      AAA
                        TG TGGAGTCGTA  AAGT
                     II IIIIIIIIII  IIII
                     AC GCCTCAGCAT  TTCG
                        C       C__
GAM20    CAPN2    3' AAAACTTTATGAACTTCACCA 855     A   _  AAA
                        TG TGGAGT CGTAA  AGTTTT
                     II IIIIII IIIII   IIIIII
                     AC ACTTCA GTATT   TCAAAA
                        C   A   ___
GAM20    DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559       CG A
         A                    TGATGGAGT TA AAAAGTTTT
                     IIIIIIIII II IIIIIIIII
                     ACTACCTCA  AT TTTTTAAAA
                            AA  C
GAM20    SELE     3' AAAACTCTCCTACACTTCCATT 747        _ C  AAAA
         A                    TGATGGA GT GTA   AGTTTT
                     IIIIIII II III   IIIIII
                     ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM20    KIAA0475 3' AAAACCTTGCATTCCATCA  1570        C  AAAA
                        TGATGGAGT GTAA   GTTTT
                     IIIIIIIII IIII   IIIII
                     ACTACCTTA CGTT   CAAAA
                            _  C___
GAM20    LOC222671 5' GCTTCTACGACTCCGCCA   3582     A      AAA
                        TG TGGAGTCGTA  AAGT
                     II IIIIIIIIII  IIII
```

```
                            AC GCCTCAGCAT  TTCG
                            C       C__
GAM20   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A      _ A A
                          TG TGGAGTC GT AA AAGTT
                          || ||||||| || || |||||
                          AC ACCTCAG CA TT TTTAA
                          C        T C  C
GAM20   LOC257615 5' GCTTCTACGACTCCGCCA   3749    A      AAA
                        TG TGGAGTCGTA  AAGT
                        || |||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C       C__
GAM21   CAPN2    3' AAAACTTTATGAACTTCACCA 855    A    _   AAA
                      TG TGGAGT CGTAA  AGTTTT
                      || |||||| |||||  ||||||
                      AC ACTTCA GTATT  TCAAAA
                      C      A    ___
GAM21   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559      CG A
             A              TGATGGAGT TA AAAAGTTTT
                        ||||||||| || |||||||||
                        ACTACCTCA AT TTTTTAAAA
                         AA  C
GAM21   SELE    3' AAAACTCTCCTACACTTCCATT 747      _ C AAAA
             A              TGATGGA GT GTA  AGTTTT
                        ||||||| || |||  |||||
                        ATTACCT CA CAT  TCAAAA
                        T _  CCTC
GAM21   KIAA0475 3' AAAACCTTGCATTCCATCA  1570      C  AAAA
                        TGATGGAGT GTAA  GTTTT
                        ||||||||| ||||  |||||
                        ACTACCTTA CGTT  CAAAA
                         _  C___
GAM21   LOC222671 5' GCTTCTACGACTCCGCCA   3582    A      AAA
                        TG TGGAGTCGTA  AAGT
                        || |||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C       C__
GAM21   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A      _ A A
                          TG TGGAGTC GT AA AAGTT
                          || ||||||| || || |||||
                          AC ACCTCAG CA TT TTTAA
                          C        T C  C
GAM21   LOC257615 5' GCTTCTACGACTCCGCCA   3749    A      AAA
                        TG TGGAGTCGTA  AAGT
                        || |||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C       C__
GAM22   CAPN2    3' AAAACTTTATGAACTTCACCA 855    A    _   AAA
                      TG TGGAGT CGTAA  AGTTTT
                      || |||||| |||||  ||||||
```

```
                        AC ACTTCA GTATT  TCAAAA
                        C   A     ___
GAM22  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
         A                TGATGGAGT  TA AAAAGTTTT
                        |||||||| || |||||||||
                        ACTACCTCA  AT TTTTTAAAA
                           AA  C
GAM22  SELE    3' AAAACTCTCCTACACTTCCATT 747       _  C  AAAA
         A                TGATGGA GT GTA   AGTTTT
                        ||||||| || |||   ||||||
                        ATTACCT CA CAT   TCAAAA
                           T _  CCTC
GAM22  KIAA0475 3' AAAACCTTGCATTCCATCA  1570       C   AAAA
                          TGATGGAGT GTAA   GTTTT
                        ||||||||| |||| |||||
                        ACTACCTTA CGTT   CAAAA
                          _   C___
GAM22  LOC222671 5' GCTTCTACGACTCCGCCA  3582   A      AAA
                        TG TGGAGTCGTA  AAGT
                        || ||||||||| ||||
                        AC GCCTCAGCAT  TTCG
                        C      C__
GAM22  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699   A    _ A A
                        TG TGGAGTC GT AA AAGTT
                        || ||||||| || || |||||
                        AC ACCTCAG CA TT TTTAA
                        C    T C C
GAM22  LOC257615 5' GCTTCTACGACTCCGCCA   3749   A      AAA
                        TG TGGAGTCGTA  AAGT
                        || ||||||||| ||||
                        AC GCCTCAGCAT  TTCG
                        C      C__
GAM23  CAPN2    3' AAAACTTTATGAACTTCACCA 855    A    _   AAA
                        TG TGGAGT CGTAA  AGTTTT
                        || |||||| ||||| ||||||
                        AC ACTTCA GTATT  TCAAAA
                        C   A     ___
GAM23  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
         A                TGATGGAGT  TA AAAAGTTTT
                        ||||||||| || |||||||||
                        ACTACCTCA  AT TTTTTAAAA
                           AA  C
GAM23  SELE    3' AAAACTCTCCTACACTTCCATT 747       _  C  AAAA
         A                TGATGGA GT GTA   AGTTTT
                        ||||||| || |||   ||||||
                        ATTACCT CA CAT   TCAAAA
                           T _  CCTC
GAM23  KIAA0475 3' AAAACCTTGCATTCCATCA  1570       C   AAAA
                          TGATGGAGT GTAA   GTTTT
                        ||||||||| |||| |||||
```

```
                              ACTACCTTA CGTT   CAAAA
                              _    C___
GAM23   LOC222671 5'  GCTTCTACGACTCCGCCA    3582    A       AAA
                      TG TGGAGTCGTA   AAGT
                      || |||||||||| ||||
                      AC GCCTCAGCAT  TTCG
                         C        C__
GAM23   LOC254901 5'  AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                      TG TGGAGTC GT AA AAGTT
                      || |||||||| || || |||||
                      AC ACCTCAG CA TT TTTAA
                         C     T C  C
GAM23   LOC257615 5'  GCTTCTACGACTCCGCCA     3749    A       AAA
                      TG TGGAGTCGTA   AAGT
                      || |||||||||| ||||
                      AC GCCTCAGCAT  TTCG
                         C        C__
GAM24   CAPN2     3'  AAAACTTTATGAACTTCACCA  855     A    _   AAA
                      TG TGGAGT CGTAA  AGTTTT
                      || |||||| ||||| ||||||
                      AC ACTTCA GTATT  TCAAAA
                         C     A    ___
GAM24   DAAM2     3'  AAAATTTTTCTAAAACTCCATC 3559       CG A
              A              TGATGGAGT  TA AAAAGTTTT
                             ||||||||| || |||||||||
                             ACTACCTCA  AT TTTTTAAAA
                               AA  C
GAM24   SELE      3'  AAAACTCTCCTACACTTCCATT 747       _ C AAAA
              A              TGATGGA GT GTA   AGTTTT
                             |||||||| || ||| ||||||
                             ATTACCT CA CAT   TCAAAA
                               T _  CCTC
GAM24   KIAA0475 3'  AAAACCTTGCATTCCATCA   1570       C   AAAA
                     TGATGGAGT GTAA   GTTTT
                     ||||||||| ||||  |||||
                     ACTACCTTA CGTT   CAAAA
                       _    C___
GAM24   LOC222671 5'  GCTTCTACGACTCCGCCA    3582    A       AAA
                      TG TGGAGTCGTA   AAGT
                      || |||||||||| ||||
                      AC GCCTCAGCAT  TTCG
                         C        C__
GAM24   LOC254901 5'  AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                      TG TGGAGTC GT AA AAGTT
                      || |||||||| || || |||||
                      AC ACCTCAG CA TT TTTAA
                         C     T C  C
GAM24   LOC257615 5'  GCTTCTACGACTCCGCCA     3749    A       AAA
                      TG TGGAGTCGTA   AAGT
                      || |||||||||| ||||
```

```
                              AC GCCTCAGCAT  TTCG
                              C        C__
GAM25   CAPN2    3' AAAACTTTATGAACTTCACCA 855    A    _   AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| ||||   ||||||
                         AC ACTTCA GTATT  TCAAAA
                         C        A     ___
GAM25   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559      CG A
         A                   TGATGGAGT  TA AAAAGTTTT
                             ||||||||| || |||||||||
                             ACTACCTCA  AT TTTTTAAAA
                               AA  C
GAM25   SELE     3' AAAACTCTCCTACACTTCCATT 747       _  C AAAA
         A                   TGATGGA GT GTA   AGTTTT
                             |||||||| || |||   ||||||
                             ATTACCT CA CAT   TCAAAA
                             T  _  CCTC
GAM25   KIAA0475 3' AAAACCTTGCATTCCATCA 1570      C   AAAA
                         TGATGGAGT GTAA   GTTTT
                         ||||||||| ||||   |||||
                         ACTACCTTA CGTT   CAAAA
                                 _  C___
GAM25   LOC222671 5' GCTTCTACGACTCCGCCA  3582    A    AAA
                         TG TGGAGTCGTA   AAGT
                         || ||||||||||   ||||
                         AC GCCTCAGCAT   TTCG
                         C        C__
GAM25   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699   A    _  A A
                         TG TGGAGTC GT AA AAGTT
                         || ||||||| || || |||||
                         AC ACCTCAG CA TT TTTAA
                         C       T C C
GAM25   LOC257615 5' GCTTCTACGACTCCGCCA  3749    A     AAA
                         TG TGGAGTCGTA  AAGT
                         || ||||||||||  ||||
                         AC GCCTCAGCAT  TTCG
                         C        C__
GAM26   ITGB7    5' AGAGAAAGTCTGACTTGCCCCA 783      AAAA_   TTAT
         C                   GT   AAGTT  CTTTCTCT
                             ||   |||||  |||||||||
                             CA   TTCAG   GAAAGAGA
                             CCCCG    TCT_
GAM26   RPP30    3' AGAGAAAGACAACTGTTCTGCG 1297     A A  TTA
                         CGTA AA AGTT  TCTTTCTCT
                         |||| || ||||  |||||||||
                         GCGT TT TCAA  AGAAAGAGA
                             C  G  C__
GAM26   FLJ13263 3' AGAGAAAGATTTTAGCTTTT 2139        TT_
                         AAAAGTT ATCTTTCTCT
                         ||||||| |||||||||
```

```
                              TTTTCGA   TAGAAAGAGA
                                TTT
GAM26   FLJ23074 5' AGAGAAAGACAAGGGTTT   2133      G    A
                              AAA TTTT TCTTTCTCT
                              ||| |||| |||||||||
                              TTT GGAA AGAAAGAGA
                                G    C
GAM26   GTF2A2   3' AGAAAAAATATGACTTTTTTAC 1119          T   C_
                              GTAAAAAAGTT TAT  TTTCT
                              |||||||||| ||| |||||
                              CATTTTTTCAG ATA  AAAGA
                                 T   AA
GAM26   IMP-2    3' AGAGAAAGCAGGCTTTTCTA 1308     A      TAT
                              TA AAAAGTTT  CTTTCTCT
                              || ||||||||  ||||||||
                              AT TTTTCGGA   GAAAGAGA
                                C     C__
GAM26   KIAA0212 3' AGAAAGGTAAATCTTTTTAC 1518       A T
                              GTAAAAA G TTTATCTTTCT
                              ||||||| | |||||||||||
                              CATTTTT C AAATGGAAAGA
                                 _ T
GAM26   OSBPL2   5' AGAGAAAGTTTGTAAAATTCCT 1566       AAA       ___
            TAC               GTAA  AGTTTTAT  CTTTCTCT
                              |||| |||||||| ||||||||
                              CATT  TTAAAATG  GAAAGAGA
                                CC_       TTT
GAM26   OSBPL2   5' AGAGAAAGTTTGTAAAATTCCT 2482       AAA       ___
            TAC               GTAA  AGTTTTAT  CTTTCTCT
                              |||| |||||||| ||||||||
                              CATT  TTAAAATG  GAAAGAGA
                                CC_       TTT
GAM26   RBM9     3' AGAAAGAATACTTTTTTAT 1489          TTTA
                              GTAAAAAAGT   TCTTTCT
                              ||||||||||   |||||||
                              TATTTTTTCA   AGAAAGA
                                TA__
GAM26   LOC254826 3' AGAGAAAGTCTTGCTTTTT 3732          TTTAT
                              AAAAAGT   CTTTCTCT
                              |||||||   ||||||||
                              TTTTTCG   GAAAGAGA
                                TTCT_
GAM27   CAPN2    3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                              TG TGGAGT CGTAA  AGTTTT
                              || |||||| ||||  ||||||
                              AC ACTTCA GTATT  TCAAAA
                                 C  A  ___
GAM27   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
            A                 TGATGGAGT TA AAAAGTTTT
                              ||||||||| || |||||||||
```

```
                          ACTACCTCA  AT TTTTTAAAA
                            AA  C
GAM27    SELE      3' AAAACTCTCCTACACTTCCATT 747          _  C  AAAA
           A                    TGATGGA GT GTA    AGTTTT
                          ||||||| || |||   ||||||
                          ATTACCT CA CAT   TCAAAA
                            T  _  CCTC
GAM27    KIAA0475 3' AAAACCTTGCATTCCATCA   1570          C  AAAA
                          TGATGGAGT GTAA   GTTTT
                          ||||||||| ||||   |||||
                          ACTACCTTA CGTT   CAAAA
                            _  C___
GAM27    LOC222671 5' GCTTCTACGACTCCGCCA    3582      A      AAA
                          TG TGGAGTCGTA  AAGT
                          || |||||||||  ||||
                          AC GCCTCAGCAT  TTCG
                          C       C__
GAM27    LOC254901 5' AATTTCTTCACTGACTCCACCA 3699     A     _  A A
                          TG TGGAGTC GT AA AAGTT
                          || |||||||| || || |||||
                          AC ACCTCAG CA TT TTTAA
                          C       T C  C
GAM27    LOC257615 5' GCTTCTACGACTCCGCCA    3749      A      AAA
                          TG TGGAGTCGTA  AAGT
                          || |||||||||  ||||
                          AC GCCTCAGCAT  TTCG
                          C       C__
GAM28    CAPN2     3' AAAACTTTATGAACTTCACCA 855       A   _  AAA
                          TG TGGAGT CGTAA  AGTTTT
                          || |||||| |||||  ||||||
                          AC ACTTCA GTATT  TCAAAA
                          C     A    ___
GAM28    DAAM2     3' AAAATTTTTCTAAAACTCCATC 3559         CG A
           A                    TGATGGAGT TA AAAAGTTTT
                          ||||||||| || |||||||||
                          ACTACCTCA AT TTTTTAAAA
                            AA  C
GAM28    SELE      3' AAAACTCTCCTACACTTCCATT 747          _  C  AAAA
           A                    TGATGGA GT GTA    AGTTTT
                          ||||||| || |||   ||||||
                          ATTACCT CA CAT   TCAAAA
                            T  _  CCTC
GAM28    KIAA0475 3' AAAACCTTGCATTCCATCA   1570          C  AAAA
                          TGATGGAGT GTAA   GTTTT
                          ||||||||| ||||   |||||
                          ACTACCTTA CGTT   CAAAA
                            _  C___
GAM28    LOC222671 5' GCTTCTACGACTCCGCCA    3582      A      AAA
                          TG TGGAGTCGTA  AAGT
                          || |||||||||  ||||
```

```
                              AC GCCTCAGCAT  TTCG
                                 C         C__
GAM28   LOC254901 5'  AATTTCTTCACTGACTCCACCA 3699      A      _  A A
                              TG TGGAGTC GT AA AAGTT
                              || ||||||| || || |||||
                              AC ACCTCAG CA TT TTTAA
                                 C        T  C  C
GAM28   LOC257615 5'  GCTTCTACGACTCCGCCA   3749    A       AAA
                              TG TGGAGTCGTA  AAGT
                              || ||||||||||  ||||
                              AC GCCTCAGCAT  TTCG
                                 C         C__
GAM29   CAPN2    3'  AAAACTTTATGAACTTCACCA 855     A    _   AAA
                              TG TGGAGT CGTAA  AGTTTT
                              || |||||| ||||| ||||||
                              AC ACTTCA GTATT  TCAAAA
                                 C       A    ___
GAM29   DAAM2    3'  AAAATTTTTCTAAAACTCCATC 3559        CG A
            A                 TGATGGAGT TA AAAAGTTTT
                              ||||||||| || |||||||||
                              ACTACCTCA  AT TTTTTAAAA
                                 AA  C
GAM29   SELE    3'  AAAACTCTCCTACACTTCCATT 747       _ C  AAAA
            A                 TGATGGA GT GTA   AGTTTT
                              ||||||| || ||| ||||||
                              ATTACCT CA CAT   TCAAAA
                                 T _  CCTC
GAM29   KIAA0475 3'  AAAACCTTGCATTCCATCA   1570      C  AAAA
                              TGATGGAGT GTAA   GTTTT
                              ||||||||| ||||  |||||
                              ACTACCTTA CGTT   CAAAA
                                 _  C___
GAM29   LOC222671 5'  GCTTCTACGACTCCGCCA   3582    A      AAA
                              TG TGGAGTCGTA  AAGT
                              || ||||||||||  ||||
                              AC GCCTCAGCAT  TTCG
                                 C         C__
GAM29   LOC254901 5'  AATTTCTTCACTGACTCCACCA 3699      A      _  A A
                              TG TGGAGTC GT AA AAGTT
                              || ||||||| || || |||||
                              AC ACCTCAG CA TT TTTAA
                                 C        T  C  C
GAM29   LOC257615 5'  GCTTCTACGACTCCGCCA   3749    A       AAA
                              TG TGGAGTCGTA  AAGT
                              || ||||||||||  ||||
                              AC GCCTCAGCAT  TTCG
                                 C         C__
GAM30   FGF2    3'  ATATTTTTGTGGCTGCTTTTT 884          T_
                              AAAAAGT TTACAAAAATAT
                              ||||||| |||||||||||
```

```
                              TTTTTCG GGTGTTTTTATA
                                TC
GAM30   MPHOSPH1 3' ATATTTTTATAAGGCTTTTTT 1670          C
                       AAAAAAGTTTTA AAAAATAT
                       |||||||||||| ||||||||
                       TTTTTTCGGAAT TTTTTATA
                                 A
GAM30   FLJ11274 3' ATATCTTTGTAGTAGCTTTTTT 1820          _     A
             TA              TAAAAAAAGTT TTACAAA ATAT
                       |||||||||| |||||| ||||
                       ATTTTTTTCGA GATGTTT TATA
                                 T     C
GAM30   FLJ31101 3' ATATTTTTGTAAAATGTATTTG 1771       AAAA
             T               ATAAA  GTTTTACAAAAATAT
                       |||||  |||||||||||||
                       TGTTT  TAAAATGTTTTTATA
                            ATG_
GAM30   GPT2     3' ATATTTTTGTAACAATTGCTTT 2417       T____
             TTT              AAAAAAGT  TTACAAAAATAT
                       ||||||||  |||||||||||
                       TTTTTTCG  AATGTTTTTATA
                            TTAAC
GAM30   RMP      3' TTTTGTAAAACTTTTTTTTC 2430    T
                            A AAAAAAAGTTTTACAAAA
                            | |||||||||||||||||
                            C TTTTTTTCAAAATGTTTT
                              T
GAM30   RMP      3' TTTTGTAAAACTTTTTTTTC 1059    T
                            A AAAAAAAGTTTTACAAAA
                            | |||||||||||||||||
                            C TTTTTTTCAAAATGTTTT
                              T
GAM30   SOX6     3' ATATTTTTGTCTTACTTTTTTT 2328        TTT
                       AAAAAAAGT  ACAAAAATAT
                       ||||||||| ||||||||||
                       TTTTTTTCA  TGTTTTTATA
                            TTC
GAM30   LOC136288 3' ATATTCTGAGGCTTTTTTTGT 3018          CAA
                       ATAAAAAAAGTTTTA AAATAT
                       ||||||||||||||| ||||||
                       TGTTTTTTTCGGAGT TTTATA
                              C__
GAM31   AICDA    3' AGAAAGAGAACAATATTT 1922       TTTA
                       AAATATT  TTCTCTTTCT
                       |||||||  ||||||||||
                       TTTATAA  AAGAGAAAGA
                             C___
GAM31   AS3      3' AGAAAGATTTAAAGTATTTTA 1652       TATTC
                       TAAAATATTTT  TCTTCT
                       ||||||||||| |||||||
```

```
                        ATTTTATGAAA   AGAAAGA
                        TTT__
GAM31   EPM2A    3' AGAAAGAGAAGTGTTTT   1234        TTTTA
                        AAAATAT   TTCTCTTTCT
                        ||||||| |||||||||||
                        TTTTGTG   AAGAGAAAGA
                        _____
GAM31   HRH1     3' AGAAAGAGAAATGAAATATTTT 780          TA
                        AAAATATTTT TTCTCTTTCT
                        |||||||||| ||||||||||
                        TTTTATAAAG AAGAGAAAGA
                            TA
GAM31   MAPK14   3' GAGAAAGGGCAAATTATTTTA 818        T  TATT
                        TAAAATA TTT  CTCTTTCTC
                        ||||||| |||  |||||||||
                        ATTTTAT AAA   GGGAAAGAG
                            T  C___
GAM31   MAPK14   3' GAGAAAGGGCAAATTATTTTA 2465       T  TATT
                        TAAAATA TTT  CTCTTTCTC
                        ||||||| |||  |||||||||
                        ATTTTAT AAA   GGGAAAGAG
                            T  C___
GAM31   MAPK14   3' GAGAAAGGGCAAATTATTTTA 2466       T  TATT
                        TAAAATA TTT  CTCTTTCTC
                        ||||||| |||  |||||||||
                        ATTTTAT AAA   GGGAAAGAG
                            T  C___
GAM31   NOTCH2   3' GAGAATTAAAAATATTTTA   2058          T
                        TAAAATATTTT ATTCTC
                        ||||||||||| ||||||
                        ATTTTATAAAA TAAGAG
                            T
GAM31   SIM1     3' GAGAAAGAGAGAGATA     1181      TAT
                        TATTTT TCTCTTTCTC
                        |||||| ||||||||||
                        ATAGAG  AGAGAAAGAG
                            ___
GAM31   C11orf25 3' AAAGAGAAAAATATTTTA   2193          TAT
                        TAAAATATTTT TCTCTTT
                        ||||||||||| |||||||
                        ATTTTATAAAA  AGAGAAA
                            ___
GAM31   DKFZP564D116 3' GAAAAGCAATAAAAATATTTTA 2938              _ C
                        TAAAATATTTTTATT CT TTTC
                        ||||||||||||||| || ||||
                        ATTTTATAAAAATAA GA AAAG
                            C _
GAM31   DSCR6    3' GAGAAAGAGAAGGTCTATGTCA 1866    A  TTTTA
                        A ATAT   TTCTCTTTCTC
                        | |||   |||||||||||
```

```
                        A TGTA    AAGAGAAAGAG
                        C    TCTGG
GAM31   FLJ10006  3' GAGAAAGAAGATATTTTA  3152         A
                        TAAAATATTTTT TTCTC
                        |||||||||| |||||
                        ATTTTATAGAAG AAGAG
                             A
GAM31   HTPAP    3' GAGAATAAAAAGATTTTA   2255      A
                        TAAAAT TTTTTATTCTC
                        |||||| ||||||||||
                        ATTTTA AAAAATAAGAG
                          G
GAM31   KIAA0979 3' AGAAAGATTTAAAGTATTTTA 1601          TATTC
                        TAAAATATTTT   TCTTTCT
                        ||||||||||   |||||||
                        ATTTTATGAAA   AGAAAGA
                            TTT__
GAM31   KIAA1634 3' GAGAATAAAACTATTTTA   2657       T
                        TAAAATA TTTTATTCTC
                        ||||||| ||||||||||
                        ATTTTAT AAAATAAGAG
                           C
GAM31   PTD012   3' GAGATTGGGAACAAAAATAT 1465        A    TT
                        ATATTTTT TTCTC  TCTC
                        |||||||| |||||  ||||
                        TATAAAAA AAGGG  AGAG
                          C    TT
GAM31   SAMHD1   3' AGAAAGAGAAAGAAATAT   2593       A
                        ATATTTTT TTCTCTTTCT
                        |||||||| ||||||||||
                        TATAAAGA AAGAGAAAGA

                          _
GAM31   LOC196758 3' GAGAAAGAGCAGGTGAAATATT 3410         TATT_
        TT                 AAAATATTTT   CTCTTTCTC
                        ||||||||||   |||||||||
                        TTTTATAAAG   GAGAAAGAG
                          TGGAC
GAM31   LOC219790 3' GAGAATAAAAATAATTTA   3520      A
                        TAAA TATTTTTATTCTC
                        |||| |||||||||||||
                        ATTT ATAAAAATAAGAG
                          A
GAM32   CAPN2    3' AAAACTTTATGAACTTCACCA  855     A    _  AAA
                        TG TGGAGT CGTAA  AGTTTT
                        || |||||| |||||  ||||||
                        AC ACTTCA GTATT  TCAAAA
                          C    A   ___
GAM32   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
        A                  TGATGGAGT TA AAAAGTTTT
                        |||||||| || |||||||||
```

```
                              ACTACCTCA  AT TTTTTAAAA
                                AA  C
GAM32    SELE     3' AAAACTCTCCTACACTTCCATT 747         _  C  AAAA
         A                      TGATGGA GT GTA    AGTTTT
                  ||||||| || |||    ||||||
                  ATTACCT CA CAT   TCAAAA
                         T _  CCTC
GAM32    KIAA0475 3' AAAACCTTGCATTCCATCA  1570          C  AAAA
                    TGATGGAGT GTAA   GTTTT
                  ||||||||| |||| |||||
                  ACTACCTTA CGTT   CAAAA
                            _  C___
GAM32    LOC222671 5' GCTTCTACGACTCCGCCA   3582     A      AAA
                    TG TGGAGTCGTA  AAGT
                  || |||||||||| ||||
                  AC GCCTCAGCAT  TTCG
                     C       C__
GAM32    LOC254901 5' AATTCTTCACTGACTCCACCA 3699    A     _ A A
                    TG TGGAGTC GT AA AAGTT
                  || ||||||| || || |||||
                  AC ACCTCAG CA TT TTTAA
                     C       T C  C
GAM32    LOC257615 5' GCTTCTACGACTCCGCCA   3749    A      AAA
                    TG TGGAGTCGTA  AAGT
                  || |||||||||| ||||
                  AC GCCTCAGCAT  TTCG
                     C       C__
GAM33    CAPN2    3' AAAACTTTATGAACTTCACCA 855     A    _  AAA
                    TG TGGAGT CGTAA  AGTTTT
                  || ||||||| |||||  ||||||
                  AC ACTTCA GTATT  TCAAAA
                     C    A    ___
GAM33    DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559       CG A
         A                  TGATGGAGT TA AAAAGTTTT
                  ||||||||| || |||||||||
                  ACTACCTCA  AT TTTTTAAAA
                    AA  C
GAM33    SELE     3' AAAACTCTCCTACACTTCCATT 747         _  C  AAAA
         A                      TGATGGA GT GTA    AGTTTT
                  ||||||| || |||    ||||||
                  ATTACCT CA CAT   TCAAAA
                         T _  CCTC
GAM33    KIAA0475 3' AAAACCTTGCATTCCATCA  1570          C  AAAA
                    TGATGGAGT GTAA   GTTTT
                  ||||||||| |||| |||||
                  ACTACCTTA CGTT   CAAAA
                            _  C___
GAM33    LOC222671 5' GCTTCTACGACTCCGCCA   3582     A      AAA
                    TG TGGAGTCGTA  AAGT
                  || |||||||||| ||||
```

```
                              AC GCCTCAGCAT  TTCG
                               C       C__
GAM33   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                        TG TGGAGTC GT AA AAGTT
                        || ||||||| || || |||||
                        AC ACCTCAG CA TT TTTAA
                         C    T C C
GAM33   LOC257615 5' GCTTCTACGACTCCGCCA   3749    A      AAA
                        TG TGGAGTCGTA  AAGT
                        || |||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                         C       C__
GAM34   ADCY6    3' TTGTACAATATTTTGTACAAAG 1617       G    TTCAC
            A            TCTTTG TACAAAAT   ACAA
                         |||||| |||||||    ||||
                         AGAAAC ATGTTTTA   TGTT
                          _      TAACA
GAM34   ADCY6    3' TTGTACAATATTTTGTACAAAG 1933       G    TTCAC
            A            TCTTTG TACAAAAT   ACAA
                         |||||| |||||||    ||||
                         AGAAAC ATGTTTTA   TGTT
                          _      TAACA
GAM34   APBB2    5' TGAGCTTTGTACCAAAGA    2946         AT
                         TCTTTGGTACAAA TTCA
                         ||||||||||| ||||
                         AGAAACCATGTTT GAGT
                                C_
GAM34   ATP8B2   3' TGATTTTTATACCAAAGA    2716      C TT
                         TCTTTGGTA AAAA TCA
                         ||||||||| |||| |||
                         AGAAACCAT TTTT AGT
                           A  T_
GAM34   CEACAM1  3' TGTGTGAACTAGCAAAGA    848     G CAAAAT
                         TCTTTG TA    TTCACACA
                         |||||| ||    ||||||||
                         AGAAAC AT    AAGTGTGT
                           G C_____
GAM34   CHST1    3' TGTGATATTTCTTTGTGCCAAA 1046       ___ T
                         TTTGGTACAAA  AT TCACA
                         |||||||||||  || |||||
                         AAACCGTGTTT  TA AGTGT
                           CTT  T
GAM34   FBXL7    3' TGCGTGTTTTCCACCAAAGA  1425      AC  TTT A
                         TCTTTGGT AAAA  CAC CA
                         |||||||| |||| ||| ||
                         AGAAACCA TTTT  GTG GT
                           CC   ___  C
GAM34   HOXC9    3' TGCGTGCAGATTTTGTAC    2592        _ A
                         GTACAAAATTT CAC CA
                         ||||||||||| ||| ||
```

```
                          CATGTTTTAGA GTG GT
                             C   C
GAM34   IGF1    3' TGTGGCATTTGTACCAAA   763         ATT
                          TTTGGTACAAA  TCACA
                          ||||||||||| |||||
                          AAACCATGTTT  GGTGT
                             AC_
GAM34   ITGAL   3' TGTGAAATTCTGTCCAAA   907      T A
                          TTTGG ACA AATTTCACA
                          ||||| ||| |||||||||
                          AAACC TGT TTAAAGTGT
                             _    C
GAM34   LBR     3' TGTACTGGATTGCACCAAGGA 2522      A  AAT  C_
                          TCTTTGGT CAA  TTCA ACA
                          |||||||| |||  |||| |||
                          AGGAACCA GTT  AGGT TGT
                             C  ___   CA
GAM34   MIP     3' TGTGTGAAATCTTTCAAG   1399      TACAAA
                          TTTGG   ATTTCACACA
                          |||||   ||||||||||
                          GAACT   TAAAGTGTGT
                             TTC___
GAM34   RLN2    3' TGTTGGTTGTACCAAA     1175      AATT  C
                          TTTGGTACAA  TCA ACA
                          ||||||||||  ||| |||
                          AAACCATGTT   GGT TGT
                             ____  _
GAM34   SART2   3' TGATTTTCATACCAAAGA   1444       CA TT
                          TCTTTGGTA AAA TCA
                          ||||||||| ||| |||
                          AGAAACCAT TTT AGT
                             AC  T_
GAM34   TPK1    3' AAATTTTGCTACCAAAGA   1987        _
                          TCTTTGGTA CAAAATTT
                          ||||||||| ||||||||
                          AGAAACCAT GTTTTAAA
                             C
GAM34   TRIP12  3' TGTGTGAAATTTAAAAAAGG 1094      GGTACA
                          TCTTT   AAATTTCACACA
                          |||||   |||||||||||
                          GGAAA   TTTAAAGTGTGT
                             AAA___
GAM34   BRD3    3' GTGTGAGATTCGTACCGAAGA 1398        AA
                          TCTTTGGTAC AATTTCACAC
                          |||||||||| ||||||||||
                          AGAAGCCATG TTAGAGTGTG
                             C_
GAM34   FLJ13397 3' GTGTGAAATTTACTAGCAAA 2116      G CA
                          TTTG TA AAATTTCACAC
                          |||| || |||||||||||
```

```
                                AAAC AT  TTTAAAGTGTG
                                  G  CA
GAM34   FLJ22202 3' TGTATCATTTTGTACCAAA   2103              TTC
                        TTTGGTACAAAAT  ACA
                        ||||||||||| |||
                        AAACCATGTTTTA  TGT
                                  CTA
GAM34   GROS1    3' TGTGTAGACAACCAAAGA     1986       ACAAAATT _
                        TCTTTGGT    TC ACACA
                        ||||||||    || |||||
                        AGAAACCA    AG TGTGT
                           AC_____  A
GAM34   KIAA0981 3' TGTGTAAAACTGCCAAGGA    2598          CAAAA  C
                        TCTTTGGTA  TTT ACACA
                        ||||||||| ||| |||||
                        AGGAACCGT  AAA TGTGT
                             C____  A
GAM34   KIAA1243 3' TGTGACATGACCAAAGA      2978       A AAATT
                        TCTTTGGT CA   TCACA
                        |||||||| ||    |||||
                        AGAAACCA GT    AGTGT
                           _ AC___
GAM34   KIAA1462 3' TTGTGTGAGAGGAACCCAAAGA 3524          TACAAAA
                        TCTTTGG    TTTCACACAA
                        |||||||    ||||||||||
                        AGAAACC    AGAGTGTGTT
                           CAAGG__
GAM34   MGC1136  3' TTGTGTGAAACCCCTAGCATAG 2041      T G CAAAA
            A                TCT TG TA    TTTCACACAA
                        ||| || ||    ||||||||||
                        AGA AC AT    AAAGTGTGTT
                         T G CCCC_
GAM34   MSTP043  3' TGTCTTTATTTTTACCAAAGA  2223          C   TTC_
                        TCTTTGGTA AAAAT  ACA
                        ||||||||| ||||| |||
                        AGAAACCAT TTTTA  TGT
                            _  TTTC
GAM34   Nup43    3' TGTGCAAAATTTTAGTATCAGA 2075          _     CA
                        TTTGGTAC AAAATTT CACA
                        |||||||| ||||||| ||||
                        AGACTATG TTTTAAA GTGT
                            A   AC
GAM34   RPS6KA4  3' TGTGCAATTACGTCCACCAAAG 1072          __ AA  T
            A               TCTTTGGT AC AATT CACA
                        |||||||| || |||| ||||
                        AGAAACCA TG TTAA GTGT
                          CC CA  C
GAM34   SLC17A6  3' TGAAACTTGTGCCACAGA     1911      T    AA
                        TCT TGGTACAA TTTCA
                        ||| ||||||| |||||
```

```
                        AGA ACCGTGTT  AAAGT
                        C       C_
GAM34   TERA      3' TGTATGAATAGTACCAAAG 1949        AAAAT   C
                        CTTTGGTAC   TTCA ACA
                        ||||||||    |||| |||
                        GAAACCATG   AAGT TGT
                        AT___    A
GAM34   VAV3      3' TTGTGTAGAGTTCTAATACCAA 1273      CAA_  TC
          AGA                 TCTTTGGTA  AATT ACACAA
                        ||||||||   |||| ||||||
                        AGAAACCAT  TTGA TGTGTT
                        AATC   GA
GAM34   LOC120892 3' TGCAATTTTTTTTACCAAAGA 2987       C__   T
                        TCTTTGGTA  AAAATT CA
                        |||||||||  |||||| ||
                        AGAAACCAT  TTTTAA GT
                        TTT    C
GAM34   LOC155434 3' TTGTGTGATTTCGTACCAAA 3376      A  TT
                        TTTGGTAC AAA  TCACACAA
                        ||||||||| |||  |||||||||
                        AAACCATG TTT  AGTGTGTT
                        C   __
GAM34   LOC169966 3' ATTTTGCCTTTACCAAAGA 3252          ____
                        TCTTTGGTA  CAAAAT
                        |||||||||  ||||||
                        AGAAACCAT  GTTTTA
                        TTCC
GAM34   LOC221272 3' TGTCTGCTCTGTACCAGAGA 3616          AAATTT  C
                        TCTTTGGTACA   CA ACA
                        |||||||||||   || |||
                        AGAGACCATGT   GT TGT
                        CTC___  C
GAM34   LOC221968 3' TTGTGTGAAATTTTGTCGAA 3569       GT
                        TTTG ACAAAATTTCACACAA
                        |||| ||||||||||||||||
                        AAGC TGTTTTAAAGTGTGTT
                        __
GAM34   LOC86651  5' TTGTGTGAAAGATGTTTCATAC 2830       CA   ____
          CAAGGA              CTTTGGTA AAAT  TTCACACAA
                        ||||||||| ||||  |||||||||
                        GGAACCAT TTTG   AAGTGTGTT
                        AC   TAGA
GAM34   LOC90322 3' GAGATTCCATACTAAAGA  2632      CAA
                        TCTTTGGTA  AATTTC
                        |||||||||  ||||||
                        AGAAATCAT  TTAGAG
                        ACC
GAM35   MYO1E    5' ATGGAGTCCCCTCTAGGGTT 1168     ATC A A
                        GACC  GA GG GACTCCAT
                        ||||  || || ||||||||
```

```
                              TTGG  CT CC CTGAGGTA
                              GAT  C _
GAM35  ROCK2    3' ATGAAGTCTTTTAACAGTCTC 2737      CATCGA     C
                              GAGAC   AGGAGACT CAT
                              |||||    ||||||||| |||
                              CTCTG   TTTTCTGA GTA
                              ACAA__      A
GAM35  MGC15937 5' GAGTTTCTTCTTCAAGGTCTCA 2383       ATC      __
                              TGAGACC  GAAGGAGA CTC
                              |||||||| ||||||||| |||
                              ACTCTGG  CTTCTTCT GAG
                              AA_   TT
GAM35  STK16    5' GAGCTCTTCGGTAGCCTCA 2937      ACC    G A
                              TGAG  ATCGAAG AG CTC
                              ||||  ||||||| || |||
                              ACTC  TGGCTTC TC GAG
                              CGA       _ _
GAM35  LOC148029 5' GGAGTCTCCATCCTCA    3116      ACCATC A
                              TGAG   GA GGAGACTCC
                              ||||   || |||||||||
                              ACTC   CT CCTCTGAGG
                              _____    A
GAM35  LOC169436 5' TGGAGTTCAATGAGCTCA  3261     AC  C AGGAG
                              TGAG  CAT GA   ACTCCA
                              ||||  ||| ||    ||||||
                              ACTC  GTA CT   TGAGGT
                              GA  A _____
GAM35  LOC256267 3' ATGGAGTCTCCCTCTGTC   3713     CATC A
                              GAC   GA GGAGACTCCAT
                              |||   || ||||||||||
                              CTG   CT CCTCTGAGGTA
                              T___  C
GAM35  LOC257426 3' GAGTCCTTCGGTGGCCTCA  2755      A      GA
                              TGAG CCATCGAAGGA CTC
                              |||| ||||||||||| |||
                              ACTC GGTGGCTTCCT GAG
                              C         __
GAM35  LOC92466  3' ATGGAGTCTCCCTCTGTC  2858     CATC A
                              GAC   GA GGAGACTCCAT
                              |||   || |||||||||||
                              CTG   CT CCTCTGAGGTA
                              T___  C
GAM36  MME      3' AAAAAAAGTTACAGAAATA 785          AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                              __
GAM36  MME      3' AAAAAAAGTTACAGAAATA 1377         AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
```

```
                        ATAAAGACAT TGAAAAAAA
                                 __
GAM36   MME        3' AAAAAAAGTTACAGAAATA  1378        AA
                        TATTTTTGTA ACTTTTTT
                        |||||||||| ||||||||
                        ATAAAGACAT TGAAAAAAA
                                 __
GAM36   MME        3' AAAAAAAGTTACAGAAATA  1379        AA
                        TATTTTTGTA ACTTTTTT
                        |||||||||| ||||||||
                        ATAAAGACAT TGAAAAAAA
                                 __
GAM36   DKFZP434C212 3' AAAAAGTACACAGAAATATT 2832         AAA
                        AATATTTTTGT ACTTTT
                        ||||||||||| ||||||
                        TTATAAAGACA TGAAAAA
                                  CA_
GAM36   FLJ11275 3' TAAAATGGGATTTATAAAAATA 1821           A TT
            TT              AATATTTTTGTAAA CT TTTTA
                        ||||||||||||| || |||||
                        TTATAAAAATATTT GG AAAAT
                          A GT
GAM36   GOLPH3   3' TAAAAAAAGTTTTACTGCCATA 1981      TTTT
            TT              AATAT  GTAAAACTTTTTTTA
                        |||||  |||||||||||||
                        TTATA  CATTTTGAAAAAAAT
                          CCGT
GAM36   KIAA0563 5' TAAAAAAAGGAGCAAAAGTAT 1565          AAAA
                        ATATTTTTGT CTTTTTTTA
                        |||||||||| |||||||||
                        TATGAAAACG GAAAAAAAT
                          AG__
GAM36   TAF2      3' AGAAAGTTTGACAAAAATA 997          A
                        TATTTTTGT AAACTTTTT
                        ||||||||| |||||||||
                        ATAAAAACA TTTGAAAGA
                          G
GAM36   LOC147071 5' TAAAAAAAGGAGCAAAAGTAT 2965         AAAA
                        ATATTTTTGT CTTTTTTTA
                        |||||||||| |||||||||
                        TATGAAAACG GAAAAAAAT
                          AG__
GAM36   LOC147639 5' AAAAGTGCTGCAAAAATATT 3110         AA
                        AATATTTTTGTA ACTTTT
                        |||||||||||| ||||||
                        TTATAAAACGT TGAAAA
                          CG
GAM36   LOC201173 5' TAAAAAAAGGAGCAAAAGTAT 3405         AAAA
                        ATATTTTTGT CTTTTTTTA
                        |||||||||| |||||||||
```

```
                        TATGAAAACG  GAAAAAAAT
                          AG__
GAM36   LOC201220 5'  TAAAAAAAGGAGCAAAAGTAT 3406          AAAA
                        ATATTTTTGT  CTTTTTTTA
                        |||||||||  |||||||||
                        TATGAAAACG  GAAAAAAAT
                          AG__
GAM37   MME       3'  AAAAAAAGTTACAGAAATA 785          AA
                        TATTTTTGTA ACTTTTTTT
                        |||||||||| |||||||||
                        ATAAAGACAT TGAAAAAAA
                             __
GAM37   MME       3'  AAAAAAAGTTACAGAAATA 1377         AA
                        TATTTTTGTA ACTTTTTTT
                        |||||||||| |||||||||
                        ATAAAGACAT TGAAAAAAA
                             __
GAM37   MME       3'  AAAAAAAGTTACAGAAATA 1378         AA
                        TATTTTTGTA ACTTTTTTT
                        |||||||||| |||||||||
                        ATAAAGACAT TGAAAAAAA
                             __
GAM37   MME       3'  AAAAAAAGTTACAGAAATA 1379         AA
                        TATTTTTGTA ACTTTTTTT
                        |||||||||| |||||||||
                        ATAAAGACAT TGAAAAAAA
                             __
GAM37   DKFZP434C212 3'  AAAAAGTACACAGAAATATT 2832           AAA
                        AATATTTTTGT ACTTTTT
                        ||||||||||| |||||||
                        TTATAAAGACA TGAAAAA
                          CA_
GAM37   FLJ11275 3'  TAAAATGGGATTTATAAAAATA 1821           A TT
          TT              AATATTTTTGTAAA CT TTTTA
                        ||||||||||||| || |||||
                        TTATAAAAATATTT GG AAAAT
                          A GT
GAM37   GOLPH3   3'  TAAAAAAAGTTTTACTGCCATA 1981       TTTT
          TT              AATAT  GTAAAACTTTTTTTA
                        |||||  |||||||||||||||
                        TTATA  CATTTTGAAAAAAAT
                          CCGT
GAM37   KIAA0563 5'  TAAAAAAAGGAGCAAAAGTAT 1565           AAAA
                        ATATTTTTGT  CTTTTTTTA
                        |||||||||  |||||||||
                        TATGAAAACG  GAAAAAAAT
                          AG__
GAM37   TAF2      3'  AGAAAGTTTGACAAAAATA 997          A
                        TATTTTTGT AAACTTTTT
                        ||||||||| |||||||||
```

```
                    ATAAAAACA TTTGAAAGA
                       G
GAM37   LOC147071 5' TAAAAAAAGGAGCAAAAGTAT 2965        AAAA
                    ATATTTTGT   CTTTTTTTA
                    |||||||||   |||||||||
                    TATGAAAACG  GAAAAAAAT
                       AG__
GAM37   LOC147639 5' AAAAGTGCTGCAAAAATATT 3110         AA
                    AATATTTTGTA ACTTTT
                    |||||||||||  |||||
                    TTATAAAACGT TGAAAA
                       CG
GAM37   LOC201173 5' TAAAAAAAGGAGCAAAAGTAT 3405        AAAA
                    ATATTTTGT   CTTTTTTTA
                    |||||||||   |||||||||
                    TATGAAAACG  GAAAAAAAT
                       AG__
GAM37   LOC201220 5' TAAAAAAAGGAGCAAAAGTAT 3406        AAAA
                    ATATTTTGT   CTTTTTTTA
                    |||||||||   |||||||||
                    TATGAAAACG  GAAAAAAAT
                       AG__
GAM38   MARK1    3' TATAATAAAACATGATTGCTTA 1857    TA   TAC
          A            TTA CGATC  GTTTTATTATA
                       ||| |||||  ||||||||||
                    AAT GTTAG  CAAAATAATAT
                    TC    TA_
GAM39   DKK1     3' AAAATACTAGCTTATTTTCTGA 1417        _    TAA
                    TCAGAAAG AGGTT  TATTTT
                    |||||||| |||||  ||||||
                    AGTCTTTT TTCGA  ATAAAA
                       A    TC_
GAM39   KERA     3' AAAATATTGAATGCTTTCT 1349      AG
                    AGAAAG GTTTAATATTTT
                    |||||| |||||||||||
                    TCTTTC TAAGTTATAAAA
                       G_
GAM39   PPP1R12A 3' AAAATACTACATCTTTCTGG 931         G TTAA
                    TCAGAAAGA GT   TATTTT
                    ||||||||| ||   ||||||
                    GGTCTTTCT CA   ATAAAA
                       A TC__
GAM39   S100B    3' AAAATTGAAAACCTCTTTC 1284         AAT
                    GAAAGAGGTTT ATTTT
                    |||||||||||  |||||
                    CTTTCTCCAAA  TAAAA
                       AGT
GAM39   DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A GTT
                    ATCAGAA GAG   TAATATTTT
                    ||||||| |||   |||||||||
```

```
                                  TAGTCTT CTT  GTTATAAAA
                                  _   AC_
GAM39    EML4      3' AAAATGTTTCCTCTTTCT  1876          TTT
                        AGAAAGAGG  AATATTTT
                        |||||||||  ||||||||
                        TCTTTCTCC  TTGTAAAA
                               T__
GAM39    FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990      AA   GTTT
                        ATCAG  AGAG   AATATTTT
                        |||||  ||||   ||||||||
                        TAGTC  TCTC   TTATAAAA
                         CG    ATT_
GAM39    KIAA1054 3' AAAATGGTACCTCTTTC      2820          TTAA
                        GAAAGAGGT   TATTTT
                        |||||||||   |||||
                        CTTTCTCCA   GTAAAA
                              TG__
GAM39    SEMA3E   5' AAAATACAGCTTCTTCCTGA  1431      A     TAA
                        TCAG AAGAGGTT  TATTTT
                        |||| ||||||||  ||||||
                        AGTC TTCTTCGA  ATAAAA
                          C        C__
GAM39    LOC130507 3' AAAATATTAAGATAACTTTCTG 3011        AGG_
                        CAGAAAG   TTTAATATTTT
                        |||||||   |||||||||||
                        GTCTTTC   GAATTATAAAA
                               AATA
GAM39    LOC148145 5' AAAATATTAAACCTGGACCTGA 3296        AAAG
            T                ATCAG  AGGTTTAATATTTT
                        |||||  ||||||||||||||
                        TAGTC   TCCAAATTATAAAA
                          CAGG
GAM40    DKK1      3' AAAATACTAGCTTATTTTCTGA 1417        _   TAA
                        TCAGAAAG AGGTT  TATTTT
                        |||||||| |||||  ||||||
                        AGTCTTTT TTCGA  ATAAAA
                          A    TC_
GAM40    KERA      3' AAAATATTGAATGCTTTCT  1349      AG
                        AGAAAG  GTTTAATATTTT
                        ||||||  ||||||||||||
                        TCTTTC  TAAGTTATAAAA
                              G_
GAM40    PPP1R12A 3' AAAATACTACATCTTTCTGG  931          G TTAA
                        TCAGAAAGA GT   TATTTT
                        ||||||||| ||   ||||||
                        GGTCTTTCT CA   ATAAAA
                          A TC__
GAM40    S100B     3' AAAATTGAAAACCTCTTTC  1284          AAT
                        GAAAGAGGTTT  ATTTT
                        |||||||||||  |||||
```

```
                    CTTTCTCCAAA  TAAAA
                           AGT
GAM40   DKFZP564I0422 3'  AAAATATTGCATTCTTCTGAT 2196       A  GTT
                    ATCAGAA GAG   TAATATTTT
                    ||||||| |||  |||||||||
                    TAGTCTT CTT  GTTATAAAA
                          _  AC_
GAM40   EML4    3' AAAATGTTTCCTCTTTCT   1876       TTT
                    AGAAAGAGG  AATATTTT
                    ||||||||| ||||||||
                    TCTTTCTCC  TTGTAAAA
                            T__
GAM40   FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990     AA  GTTT
                    ATCAG AGAG   AATATTTT
                    ||||| ||||   ||||||||
                    TAGTC TCTC   TTATAAAA
                       CG  ATT_
GAM40   KIAA1054 3' AAAATGGTACCTCTTTC    2820       TTAA
                    GAAAGAGGT  TATTTT
                    ||||||||| ||||||
                    CTTTCTCCA  GTAAAA
                          TG__
GAM40   SEMA3E  5' AAAATACAGCTTCTTCCTGA 1431     A    TAA
                    TCAG AAGAGGTT  TATTTT
                    |||| ||||||||  ||||||
                    AGTC TTCTTCGA  ATAAAA
                       C   C__
GAM40   LOC130507 3' AAAATATTAAGATAACTTTCTG 3011       AGG_
                    CAGAAAG  TTTAATATTTT
                    ||||||| |||||||||||
                    GTCTTTC  GAATTATAAAA
                          AATA
GAM40   LOC148145 5' AAAATATTAAACCTGGACCTGA 3296      AAAG
           T              ATCAG  AGGTTTAATATTTT
                    ||||| |||||||||||||
                    TAGTC  TCCAAATTATAAAA
                       CAGG
GAM41   DKK1    3' AAAATACTAGCTTATTTTCTGA 1417         _  TAA
                    TCAGAAAG AGGTT  TATTTT
                    |||||||| ||||| ||||||
                    AGTCTTTT TTCGA  ATAAAA
                       A  TC_
GAM41   KERA   3' AAAATATTGAATGCTTTCT  1349      AG
                    AGAAAG GTTTAATATTTT
                    |||||| |||||||||||
                    TCTTTC TAAGTTATAAAA
                         G_
GAM41   PPP1R12A 3' AAAATACTACATCTTTCTGG 931         G TTAA
                    TCAGAAAGA GT   TATTTT
                    ||||||||| ||   ||||||
```

```
                      GGTCTTTCT CA   ATAAAA
                       A  TC__
GAM41   S100B    3' AAAATTGAAAACCTCTTTC  1284          AAT
                      GAAAGAGGTTT ATTTT
                      ||||||||||  |||||
                      CTTTCTCCAAA TAAAA
                          AGT
GAM41   DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196       A  GTT
                      ATCAGAA GAG  TAATATTTT
                      |||||| |||  |||||||||
                      TAGTCTT CTT  GTTATAAAA
                         _  AC_
GAM41   EML4     3' AAAATGTTTCCTCTTTCT   1876          TTT
                      AGAAAGAGG  AATATTTT
                      |||||||||  ||||||||
                      TCTTTCTCC  TTGTAAAA
                            T__
GAM41   FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990      AA   GTTT
                      ATCAG AGAG   AATATTTT
                      ||||| ||||   ||||||||
                      TAGTC TCTC   TTATAAAA
                       CG   ATT_
GAM41   KIAA1054 3' AAAATGGTACCTCTTTC    2820          TTAA
                      GAAAGAGGT   TATTTT
                      |||||||||   ||||||
                      CTTTCTCCA   GTAAAA
                          TG__
GAM41   SEMA3E   5' AAAATACAGCTTCTTCCTGA 1431       A     TAA
                      TCAG AAGAGGTT  TATTTT
                      |||| |||||||||  ||||||
                      AGTC TTCTTCGA  ATAAAA
                        C     C__
GAM41   LOC130507 3' AAAATATTAAGATAACTTTCTG 3011          AGG_
                      CAGAAAG  TTTAATATTTT
                      |||||||  |||||||||||
                      GTCTTTC  GAATTATAAAA
                          AATA
GAM41   LOC148145 5' AAAATATTAAACCTGGACCTGA 3296         AAAG
          T               ATCAG  AGGTTTAATATTTT
                      |||||  |||||||||||||||
                      TAGTC  TCCAAATTATAAAA
                          CAGG
GAM42   DKK1     3' AAAATACTAGCTTATTTTCTGA 1417            _  TAA
                      TCAGAAAG AGGTT  TATTTT
                      |||||||| |||||  ||||||
                      AGTCTTTT TTCGA  ATAAAA
                          A    TC_
GAM42   KERA     3' AAAATATTGAATGCTTTCT   1349          AG
                      AGAAAG GTTTAATATTTT
                      |||||| |||||||||||
```

```
                        TCTTTC TAAGTTATAAAA
                          G_
GAM42   PPP1R12A 3' AAAATACTACATCTTTCTGG 931        G TTAA
                        TCAGAAAGA GT   TATTTT
                        |||||||| ||   ||||||
                        GGTCTTTCT CA   ATAAAA
                          A TC__
GAM42   S100B    3' AAAATTGAAAACCTCTTTC   1284        AAT
                        GAAAGAGGTTT ATTTT
                        |||||||||| |||||
                        CTTTCTCCAAA TAAAA
                          AGT
GAM42   DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A GTT
                        ATCAGAA GAG   TAATATTTT
                        |||||| ||| |||||||||
                        TAGTCTT CTT  GTTATAAAA
                          _   AC_
GAM42   EML4    3' AAAATGTTTCCTCTTTCT  1876       TTT
                        AGAAAGAGG AATATTTT
                        ||||||||| ||||||||
                        TCTTTCTCC TTGTAAAA
                          T__
GAM42   FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990     AA  GTTT
                        ATCAG AGAG   AATATTTT
                        ||||| |||| ||||||||
                        TAGTC TCTC   TTATAAAA
                          CG   ATT_
GAM42   KIAA1054 3' AAAATGGTACCTCTTTC    2820       TTAA
                        GAAAGAGGT  TATTTT
                        ||||||||| ||||||
                        CTTTCTCCA  GTAAAA
                          TG__
GAM42   SEMA3E  5' AAAATACAGCTTCTTCCTGA  1431     A     TAA
                        TCAG AAGAGGTT  TATTTT
                        |||| |||||||| ||||||
                        AGTC TTCTTCGA  ATAAAA
                          C     C__
GAM42   LOC130507 3' AAAATATTAAGATAACTTTCTG 3011        AGG_
                        CAGAAAG  TTTAATATTTT
                        ||||||| |||||||||||
                        GTCTTTC  GAATTATAAAA
                          AATA
GAM42   LOC148145 5' AAAATATTAAACCTGGACCTGA 3296        AAAG
            T                ATCAG  AGGTTTAATATTTT
                        ||||| ||||||||||||
                        TAGTC   TCCAAATTATAAAA
                          CAGG
GAM43   DKK1    3' AAAATACTAGCTTATTTTCTGA 1417       _ TAA
                        TCAGAAAG AGGTT  TATTTT
                        ||||||| ||||| ||||||
```

```
                            AGTCTTTT TTCGA  ATAAAA
                              A    TC_
GAM43   KERA      3' AAAATATTGAATGCTTTCT  1349       AG

                            AGAAAG GTTTAATATTTT
                            ||||| |||||||||||
                            TCTTTC TAAGTTATAAAA
                              G_
GAM43   PPP1R12A 3' AAAATACTACATCTTTCTGG  931         G TTAA

                            TCAGAAAGA GT   TATTTT
                            ||||||||| ||   ||||||
                            GGTCTTTCT CA   ATAAAA
                              A TC__
GAM43   S100B    3' AAAATTGAAAACCTCTTTC  1284         AAT

                            GAAAGAGGTTT  ATTTT
                            |||||||||||  |||||
                            CTTTCTCCAAA  TAAAA
                              AGT
GAM43   DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A GTT

                            ATCAGAA GAG  TAATATTTT
                            ||||||| ||| |||||||||
                            TAGTCTT CTT  GTTATAAAA
                              _  AC_
GAM43   EML4     3' AAAATGTTTCCTCTTTCT  1876        TTT

                            AGAAAGAGG  AATATTTT
                            ||||||||| ||||||||
                            TCTTTCTCC  TTGTAAAA
                              T__
GAM43   FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990     AA  GTTT

                            ATCAG AGAG  AATATTTT
                            ||||| |||| |||||||||
                            TAGTC TCTC  TTATAAAA
                              CG  ATT_
GAM43   KIAA1054 3' AAAATGGTACCTCTTTC  2820        TTAA

                            GAAAGAGGT  TATTTT
                            ||||||||| ||||||
                            CTTTCTCCA  GTAAAA
                              TG__
GAM43   SEMA3E   5' AAAATACAGCTTCTTCCTGA  1431     A   TAA

                            TCAG AAGAGGTT  TATTTT
                            |||| |||||||| ||||||
                            AGTC TTCTTCGA  ATAAAA
                              C     C__
GAM43   LOC130507 3' AAAATATTAAGATAACTTTCTG 3011        AGG_

                            CAGAAAG  TTTAATATTTT
                            ||||||| |||||||||||
                            GTCTTTC  GAATTATAAAA
                              AATA
GAM43   LOC148145 5' AAAATATTAAACCTGGACCTGA 3296        AAAG
          T                 ATCAG  AGGTTTAATATTTT
                            ||||| |||||||||||||
```

```
                              TAGTC  TCCAAATTATAAAA
                                CAGG
GAM44    DKK1      3' AAAATACTAGCTTATTTTCTGA 1417         _      TAA
                         TCAGAAAG AGGTT  TATTTT
                         ||||||||| |||||   ||||||
                         AGTCTTTT TTCGA  ATAAAA
                            A     TC_
GAM44    KERA      3' AAAATATTGAATGCTTTCT  1349       AG
                         AGAAAG GTTTAATATTTT
                         |||||| |||||||||||
                         TCTTTC TAAGTTATAAAA
                              G_
GAM44    PPP1R12A 3' AAAATACTACATCTTTCTGG  931          G TTAA
                         TCAGAAAGA GT   TATTTT
                         ||||||||| ||   ||||||
                         GGTCTTTCT CA   ATAAAA
                              A TC__
GAM44    S100B    3' AAAATTGAAAACCTCTTTC  1284          AAT
                         GAAAGAGGTTT ATTTT
                         ||||||||||| |||||
                         CTTTCTCCAAA TAAAA
                              AGT
GAM44    DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A  GTT
                         ATCAGAA GAG   TAATATTTT
                         |||||| |||  |||||||||
                         TAGTCTT CTT  GTTATAAAA
                              _  AC_
GAM44    EML4     3' AAAATGTTTCCTCTTTCT  1876         TTT
                         AGAAAGAGG  AATATTTT
                         |||||||||  ||||||||
                         TCTTTCTCC  TTGTAAAA
                              T__
GAM44    FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990      AA  GTTT
                         ATCAG AGAG   AATATTTT
                         ||||| ||||  ||||||||
                         TAGTC TCTC   TTATAAAA
                            CG  ATT_
GAM44    KIAA1054 3' AAAATGGTACCTCTTTC  2820         TTAA
                         GAAAGAGGT  TATTTT
                         |||||||||  ||||||
                         CTTTCTCCA  GTAAAA
                              TG__
GAM44    SEMA3E   5' AAAATACAGCTTCTTCCTGA  1431      A    TAA
                         TCAG AAGAGGTT  TATTTT
                         |||| ||||||||  ||||||
                         AGTC TTCTTCGA  ATAAAA
                            C    C__
GAM44    LOC130507 3' AAAATATTAAGATAACTTTCTG 3011          AGG_
                         CAGAAAG  TTTAATATTTT
                         |||||||  |||||||||||
```

```
                        GTCTTTC  GAATTATAAAA
                        AATA
GAM44   LOC148145 5' AAAATATTAAACCTGGACCTGA 3296      AAAG
          T               ATCAG  AGGTTTAATATTTT
                        IIIII  IIIIIIIIIIII
                        TAGTC  TCCAAATTATAAAA
                        CAGG
GAM45   DKK1    3' AAAATACTAGCTTATTTCTGA 1417       _   TAA
                        TCAGAAAG AGGTT  TATTTT
                        IIIIIIII IIIII  IIIIII
                        AGTCTTTT TTCGA  ATAAAA
                        A    TC_
GAM45   KERA    3' AAAATATTGAATGCTTTCT 1349      AG
                        AGAAAG GTTTAATATTTT
                        IIIIII IIIIIIIIIII
                        TCTTTC TAAGTTATAAAA
                        G_
GAM45   PPP1R12A 3' AAAATACTACATCTTTCTGG 931       G TTAA
                        TCAGAAAGA GT   TATTTT
                        IIIIIIIII II   IIIIII
                        GGTCTTTCT CA   ATAAAA
                        A TC__
GAM45   S100B   3' AAAATTGAAAACCTCTTTC 1284       AAT
                        GAAAGAGGTTT ATTTT
                        IIIIIIIIIII IIIII
                        CTTTCTCCAAA TAAAA
                        AGT
GAM45   DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A  GTT
                        ATCAGAA GAG  TAATATTTT
                        IIIIIII III  IIIIIIIII
                        TAGTCTT CTT  GTTATAAAA
                        _  AC_
GAM45   EML4    3' AAAATGTTTCCTCTTTCT 1876       TTT
                        AGAAAGAGG AATATTT
                        IIIIIIIII IIIIIIII
                        TCTTTCTCC TTGTAAAA
                        T__
GAM45   FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990      AA  GTTT
                        ATCAG AGAG  AATATTTT
                        IIIII IIII  IIIIIIII
                        TAGTC TCTC  TTATAAAA
                        CG  ATT_
GAM45   KIAA1054 3' AAAATGGTACCTCTTTC 2820        TTAA
                        GAAAGAGGT  TATTTT
                        IIIIIIIII  IIIIII
                        CTTTCTCCA  GTAAAA
                        TG__
GAM45   SEMA3E  5' AAAATACAGCTTCTTCCTGA 1431      A    TAA
                        TCAG AAGAGGTT  TATTTT
                        IIII IIIIIIIII  IIIIII
```

```
                        AGTC TTCTTCGA  ATAAAA
                           C        C__
GAM45   LOC130507 3' AAAATATTAAGATAACTTTCTG 3011      AGG_
                        CAGAAAG  TTTAATATTTT
                        ||||||  |||||||||||
                        GTCTTTC  GAATTATAAAA
                           AATA
GAM45   LOC148145 5' AAAATATTAAACCTGGACCTGA 3296      AAAG
            T            ATCAG  AGGTTTAATATTTT
                        |||||  ||||||||||||
                        TAGTC  TCCAAATTATAAAA
                           CAGG
GAM46   EFG1     3' TGTCTATCTCAACTCTATT 3661        ATC TC
                        AATAGAGTT  GAT AGACA
                        ||||||||| ||| |||||
                        TTATCTCAA  CTA TCTGT
                           CT_  __
GAM46   PHYH     3' TCTGCTATAACTCTTTCA 1281     T    CGATT
                        TGAA AGAGTTAT   CAGA
                        |||| |||||||    ||||
                        ACTT TCTCAATA   GTCT
                         _      TC___
GAM46   SLC6A3   3' TGTCTGTTGACCAATCTCTATT 795       TTA__  TT
            CA              TGAATAGAG  TCGA CAGACA
                        ||||||||| |||| |||||
                        ACTTATCTC  AGTT GTCTGT
                           TAACC  __
GAM46   H2AV     3' TGCCTGACAATTAGCTCTATTC 2447        TCGAT  A
            A              TGAATAGAGTTA  TCAG CA
                        ||||||||||| |||| ||
                        ACTTATCTCGAT  AGTC GT
                           TAAC_  C
GAM46   HMP19    3' GTCTGAACCGATATTTCT 3408     T    A
                        AGAG TATCG TTCAGAC
                        |||| ||||| |||||||
                        TCTT ATAGC AAGTCTG
                          T      C
GAM46   KIAA1726 3' TGTCTGAAAGCAACCCTACTC 2786   A  A  ATCGA
                        GA TAG GTT   TTCAGACA
                        || ||| |||   ||||||||
                        CT ATC CAA   AAGTCTGT
                          C  C  CGA__
GAM47   SOX11    3' GTCTCACTGTTTGATCAAACTT 992       A ATTTTT
            CT              AGAGGTTT AT   GTGAGAC
                        |||||||| ||   |||||||
                        TCTTCAAA TA   CACTCTG
                           C GTTGT
GAM47   CAP350   3' TCTTGTAATAGTTAAACCTC 1554       ATTT  TG
                        GAGGTTTAAT  TTG AGA
                        |||||||||  ||| |||
```

```
                              CTCCAAATTG  AAT TCT
                              AT__   GT
GAM47   DKFZP564A022 3' TCTCACAAATATAAAACC  2174     A   TT
                              GGTTT ATATT TGTGAGA
                              ||||| ||||| |||||||
                              CCAAA TATAA ACACTCT
                                A      __
GAM47   FLJ11730 3' CTCACAAAGATAAACATC   2005    G  TAA
                              GA GTT  TATTTTTGTGAG
                              || |||  ||||||||||||
                              CT CAA  ATAGAAACACTC
                                A    ___
GAM47   FLJ20686 5' CTCACAGTCCTACTGAACCTC 1765      A TTT
                              GAGGTTTA TA  TTGTGAG
                              |||||||| ||  |||||||
                              CTCCAAGT AT  GACACTC
                                C CCT
GAM47   FRSB    3' GTCCCAGGGAGATATTAGACCT 1236          G  A
           CT              AGAGGTTTAATATTTTT TG GAC
                              |||||||||||||||| || |||
                              TCTCCAGATTATAGAGG AC CTG
                                G  C
GAM47   KIAA1600 3' ACAAAAAGACTAAACCTCT  2919      ATA
                              AGAGGTTTA TTTTTGT
                              ||||||||| |||||||
                              TCTCCAAAT AAAAACA
                                CAG
GAM47   LOC124801 3' GTCTCACATTTGGCCCAAACCT 2996        AATATTT
           C              GAGGTTT    TGTGAGAC
                              |||||||    ||||||||
                              CTCCAAA    ACACTCTG
                                CCCGGTTT
GAM47   LOC221035 3' TCCCAGTATTAAACCT     3593       TTTTG A
                              AGGTTTAATAT   TG GA
                              |||||||||||   || ||
                              TCCAAATTATG   AC CT
                                _____  C
GAM47   LOC51611 3' CGAAAATTAAACCTCT     1653        AT
                              AGAGGTTTAAT TTTTG
                              ||||||||||| |||||
                              TCTCCAAATTA AAAGC
                                __
GAM48   AXUD1   3' TTTATTCCATTTCTCTCT    2309       GA
                              AGAGAGAAA GAATAAA
                              ||||||||| |||||||
                              TCTCTCTTT CTTATTT
                                AC
GAM48   BSN    3' ATTTTTCTTTTGTTTCTCTCT 1024      G  T
                              AGAGAGAAA AGAA AAAAAT
                              ||||||||| |||| ||||||
```

```
                        TCTCTCTTT TTTT TTTTTA
                            G    C
GAM48   DPYSL2  3' AATATTTTCGTGTCTGTCTCTC 822        A   GA TA
          T                 AGAGAGA AGA  A  AAAATATT
                            ||||||| ||| |  ||||||||
                            TCTCTCT TCT  T  TTTTATAA
                                G    G_ GC
GAM48   EVA1    3' AATGTGTTTACTCTCTTTCCTT 1250     A      A   A
          C                   GAG GAAAGAGA TAAA ATATT
                              ||| |||||||| |||| |||||
                              CTT CTTTCTCT ATTT TGTAA
                                C      C   G
GAM48   PTMS    3' TTTGCTCTCTTTCTCCCT   959      A      A
                              AG GAGAAAGAGA TAAA
                              || |||||||||| ||||
                              TC CTCTTTCTCT GTTT
                                C      C
GAM48   SELE    3' TTTTGTGGCTTTCTTTCT   748        AGA
                              AGAGAGAAAG  ATAAAA
                              ||||||||||  ||||||
                              TCTTTCTTTC  TGTTTT
                                  GG_
GAM48   SLC7A6  3' AATATTTTTGTACCTTTCTCCT 1076    A    AGA
                              AG GAGAAAG  ATAAAAATATT
                              || |||||||  |||||||||||
                              TC CTCTTTC  TGTTTTTATAA
                              _      CA_
GAM48   TGFBR2  5' TTTCTTCTAGTTCTTTCT   1003        AG  T
                              AGAGAGAA AGAA AAA
                              |||||||| |||| |||
                              TCTTTCTT TCTT TTT
                                  GA   C
GAM48   DKFZP586N0721 5' TTTTATTCCCTTTCCTCT   1627     A   A
                              AGAG GAAAG GAATAAAA
                              |||| ||||| ||||||||
                              TCTC CTTTC CTTATTTT
                                  _    C
GAM48   DKFZp761J139 5' TTTATTCTCTCTGTCTCT   2242      GAA
                              AGAGA AGAGAATAAA
                              ||||| ||||||||||
                              TCTCT TCTCTTATTT
                                GTC
GAM48   FLJ10468 3' TTTTATTCTCCTTTC      1779     AAA
                              GAGAG GAGAATAAAA
                              ||||| ||||||||||
                              CTTTC CTCTTATTTT
                                   ___
GAM48   FLJ20485 3' AATATTTTTAAAATCTCCTTTC 1874       AAA  A__
          T                 AGAGAG GAGA TAAAAATATT
                            |||||| |||| ||||||||||
```

```
                        TCTTTC  CTCT  ATTTTTATAA
                         ___     AAA
GAM48  H2BFQ   3' ATATTTACTCTTTCTGTC    2523    G      AATAA
                  GA AGAAAGAG    AAATAT
                  || ||||||||    ||||||
                  CT TCTTTCTC    TTTATA
                   G      A____
GAM48  KIAA0077 3' TTTTATTCTCTCTCCCTTT   2774     A A
                  AGAG GA AGAGAATAAAA
                  |||| || ||||||||||
                  TTTC CT TCTCTTATTTT
                    C C
GAM48  KIAA0295 3' TTTTTTCCCTTTCTCTCT    2807        A  T
                  AGAGAGAAAG GAA AAA
                  |||||||||| ||| |||
                  TCTCTCTTTC CTT TTT
                     C  T
GAM48  KIAA0828 3' AATATTTTGCCTTCTTTCTTTC 3195         AATA
            T             AGAGAGAAAGAG   AAAATATT
                          |||||||||||   ||||||||
                          TCTTTCTTTCTT   TTTTATAA
                             CCG_
GAM48  KIAA1203 3' AATATTTTTATTCTTGAGTTAT 2921    GAGAAA
            CT              AGA    GAGAATAAAAATATT
                           |||    ||||||||||||||
                           TCT    TTCTTATTTTTATAA
                           ATTGAG
GAM48  OSBPL8  3' TTTTTATTATCCTCCTCTCT    1928     AAA  G
                  AGAGAG  GA AATAAAAA
                  ||||||  || ||||||||
                  TCTCTC  CT TTATTTTT
                    CTC  A
GAM48  PAK6    3' AATATTTTTAGATTCTTCTGCT 1897    _   A  AA
            C              GAG AGAA GAG  TAAAAATATT
                           ||| |||| |||  ||||||||||
                           CTC TCTT CTT  ATTTTTATAA
                            G   _   AG
GAM48  POLR3F  3' AATATTTTCACTGTTCCTTCTT 2547        A A  ___
            TCT             AGAGAGAA G GAATA  AAAATATT
                           ||||||||| | ||||| ||||||||
                           TCTTTCTT C CTTGT  TTTTATAA
                              _ _    CAC
GAM48  RNF11   3' TTTATTCTCTTTCTTCT    1495    G
                  AGA AGAAAGAGAATAAA
                  ||| ||||||||||||||
                  TCT TCTTTCTCTTATTT
                     _
GAM48  SLC16A6 5' TTTATTCTCTTCCCTTCT    1143      AGA
                  AGAG  AAGAGAATAAA
                  ||||  |||||||||||
```

```
                          TCTT  TTCTCTTATTT
                              CCC
GAM48    LOC144321 3' TTTTATTCCCTTCTCTC    3267       A A
                          GAGAGAA G GAATAAAA
                          ||||||| | ||||||||
                          CTCTCTT C CTTATTTT
                              _ C
GAM48    LOC150951 5' ATATTTTATTTTCTTCCT   3336     A
                          AG AAGAGAATAAAAATAT
                          || ||||||||||||||||
                          TC TTCTTTTATTTTTATA
                              C
GAM48    LOC199920 5' AATATTTTTATTCTTTGATTCT 3435       AA
              T            GAGAG AGAGAATAAAAATATT
                          ||||| |||||||||||||||
                          TTCTT TTTCTTATTTTTATAA
                              AG
GAM48    LOC256435 3' AATATTTTTAAATGTTGTCTCT 3675       AAGAGAA
              CT            AGAGAGA   TAAAAATATT
                          |||||||   |||||||||
                          TCTCTCT   ATTTTTATAA
                              GTTGTAA
GAM49    ADAMTS5  3' TATTTTCACAACTACTTTCTCT 1352       _ AATA_
              CT            AGAGAGAAAG AG   AAAAATA
                          |||||||||| ||   |||||
                          TCTCTCTTTC TC   TTTTAT
                              A AACAC
GAM49    ADAT1    3' TATTCCCAGCCTTTCTTTCTTC 1404          A____
                          GAAGAGAGAAAG   GAATA
                          |||||||||||   |||||
                          CTTCTTTCTTC   CTTAT
                              CGACC
GAM49    ADCY2    3' TTTTATTTTCCTGTCTTC    2711     G AAA
                          GAAGA AG  GAGAATAAAA
                          ||||| ||  ||||||||||
                          CTTCT TC  CTTTTATTTT
                              G ___
GAM49    AHR      3' ATTTTTGTTACTCTCTTC    840        _ A
                          GAAGAGAG AA GAGAAT
                          |||||||| || ||||||
                          CTTCTCTC TT TTTTTA
                              A G
GAM49    BSN      3' ATTTTTCTTTTGTTCTCTCT 1025       G  T
                          AGAGAGAAA AGAA AAAAAT
                          ||||||||| |||| ||||||
                          TCTCTCTTT TTTT TTTTTA
                              G  C
GAM49    BSN      3' TCTCCCCCTTTCTCTCTTC 1026         ____
                          GAAGAGAGAAA  GAGA
                          ||||||||||  ||||
```

CTTCTCTCTTT CTCT
                                CCCC
GAM49   C7   3' TATTCCTTATTTCTCTTT   756   _   A
                       GAAGAGAGA AAG GAATA
                       |||||||||| ||| |||||
                       TTTCTCTTT TTC CTTAT
                            A _
GAM49   CFTR   3' TATTCCTTTTTCTCTCCTC   753   A   _
                       GA GAGAGAAAGAG AATA
                       || ||||||||||| ||||
                       CT CTCTCTTTTTC TTAT
                          C   C
GAM49   CHD2   3' ATATTTTTTCTGATCCCCCACT 813   AA_____ GAAT_ |||
                CTCTCTTC   AGA   GA   AAAAATA T
                       ||| || ||||||| |
                       TCT   CT   TTTTTAT A
                          CACCCC AGTCT |||
GAM49   CKN1   3' TATTTTATTCTTTCTTC   703   AG
                       GAAGAGAGAA AGAATA
                       |||||||||| ||||||
                       CTTCTTTCTT TTTTAT
                            A_
GAM49   CTH   5' TGTTCTTTTCCTCTCTTC   867   A
                       GAAGAGAG AAGAGAATA
                       |||||||| |||||||||
                       CTTCTCTC TTTTCTTGT
                            C
GAM49   EVA1   3' ATTTTTATTTTTATGTCTCTC 1251   AA_
                       GAGAGA GAGAATAAAAAT
                       |||||| ||||||||||||
                       CTCTCT TTTTTATTTTTA
                            GTA
GAM49   FBXL11 3' TTGTTCCCCCTCTCTCTTT   1426   AAGA
                       GAAGAGAGA GAATAA
                       ||||||||| |||||||
                       TTTCTCTCT CTTGTT
                            CCCC
GAM49   GATA3 3' TATTTTCCTTCTCTCTC   893   A   A
                       GA GAGAGAA GAGAATA
                       || |||||||| ||||||||
                       CT CTCTCTT CTTTTAT
                          _   C
GAM49   GDI2   5' TTTTCCTCTCTTTCTCTT   832   AT
                       GAGAGAAAGAGA AAAA
                       |||||||||||| ||||
                       TTCTCTTTCTCT TTTT
                            CC
GAM49   HD   3' ATTCTCCCTTCTCTCTTT   899   A_
                       GAAGAGAGAA GAGAAT
                       |||||||||| ||||||

```
                              TTTCTCTCTT CTCTTA
                                CC
GAM49    HTR2C    3' TATTTTGCTCTCCCTCCCTTC 781      A   AAA   A
                              GAAG GAG   GAGA TAAAAATA
                              |||| |||   |||| ||||||||
                              CTTC CTC   CTCT GTTTTTAT
                                C   C__   C
GAM49    LGR6     3' TTCTCTTCCCCTCTCTTC   3302      A__
                              GAAGAGAG  AAGAGAA
                              ||||||||  |||||||
                              CTTCTCTC  TTCTCTT
                                CCC
GAM49    LRP8     3' TCTCTTATTTCTCTTTTC   2326      ___
                              GAAGAGAGAA  AGAGA
                              ||||||||||  |||||
                              CTTTTCTCTT  TCTCT
                                TAT
GAM49    LRP8     3' TCTCTTATTTCTCTTTTC   1139      ___
                              GAAGAGAGAA  AGAGA
                              ||||||||||  |||||
                              CTTTTCTCTT  TCTCT
                                TAT
GAM49    MEF2C    5' TTTTTTTTCTCTCTCTCTCT 926     _      A   T
             C               GA AGAGAGA AGAGAA AAAAA
                             || ||||||| |||||| |||||
                             CT TCTCTCT TCTCTT TTTTT
                                C      C      T
GAM49    MSR1     3' TATTTTGGTTTCTCTCT    929       __
                             AGAGAGAAA GAGAATA
                             ||||||||| |||||||
                             TCTCTCTTT TTTTTAT
                                GG
GAM49    PCDH11X  3' TATTTTCACATTTTCTCTCT 2299        ____
                             AGAGAGAAA  GAGAATA
                             |||||||||  |||||||
                             TCTCTCTTT  CTTTTAT
                                TACA
GAM49    PCDH11X  3' TATTTTCACATTTTCTCTCT 2301        ____
                             AGAGAGAAA  GAGAATA
                             |||||||||  |||||||
                             TCTCTCTTT  CTTTTAT
                                TACA
GAM49    PCDH11Y  3' TATTTTCACATTTTCTCTCT 2303        ____
                             AGAGAGAAA  GAGAATA
                             |||||||||  |||||||
                             TCTCTCTTT  CTTTTAT
                                TACA
GAM49    PCMT1    3' TATCTTCTGCTCTTTCTTC  1205      A_ GA
                             GAAGAGAGA AGA ATA
                             ||||||||| ||| |||
```

```
                              CTTCTTTCT TCT TAT
                              CG   TC
GAM49    PCNA      3' TATTTTTTTTCTCTATTC   939      G
                         GAA AGAGAAAGAGAATA
                         ||| |||||||||||||
                         CTT TCTCTTTTTTTAT
                              A
GAM49    PRELP     3' ATTCGTTTTCTCTCTCTC   950      _      A
                         GA AGAGAGAAAG GAAT
                         || |||||||||| ||||
                         CT TCTCTCTTTT CTTA
                              C      G
GAM49    PTMS      3' TTTGCTCTCTTTCTCCCT   958      A      A
                         AG GAGAAAGAGA TAAA
                         || |||||||||| ||||
                         TC CTCTTTCTCT GTTT
                              C        C
GAM49    SLC4A4    3' TATTTTTATTCTCTTAAGTCTT 1054       GAGA
              T              GAAGA  AAGAGAATAAAAATA
                         |||||  |||||||||||||||
                         TTTCT  TTCTCTTATTTTTAT
                              GAA_
GAM49    TRPS1     5' TATTTCCTTTCTCTTTCTCTCT 1471              TAA
                         AGAGAGAAAGAGAA  AAATA
                         ||||||||||||||  |||||
                         TCTCTCTTTCTCTT  TTTAT
                                   TCC
GAM49    ARS2      5' TTTTGTTCGCCTCTCTTC   1650       AAAGA
                         GAAGAGAG   GAATAAAA
                         ||||||||   ||||||||
                         CTTCTCTC   CTTGTTTT
                              CG___
GAM49    BRD4      3' TATTTTTAATTCTCTCTTC   2368       A_
                         GAAGAGAGAA GAGAATA
                         |||||||||| |||||||
                         CTTCTCTCTT TTTTTAT
                              AA
GAM49    CAPN13    3' TATTTTACCTGCCTCTCTTC   2485       AA __
                         GAAGAGAG AG AGAATA
                         |||||||| || ||||||
                         CTTCTCTC TC TTTTAT
                              CG CA
GAM49    CECR6     3' TTACCCTCTCCTCTCTTC   2218       AA AA
                         GAAGAGAG AGAG TAA
                         |||||||| |||| |||
                         CTTCTCTC TCTC ATT
                              C_ CC
GAM49    DKFZP434I0714 5' TTTTTGTTTTTCCCCCTCTTC 3362       AGAAA
                         GAAGAG  GAGAATAAAAA
                         ||||||  |||||||||||
```

```
                        CTTCTC    TTTTTGTTTTT
                          CCCC_
GAM49   DKFZP564G092 5'  TATTCCTCTTTCTTTTC    1639         A A

                        GAAGAGAGA AG GAATA
                        |||||||||| || |||||
                        CTTTTCTTT TC CTTAT
                           C    _
GAM49   DKFZp564K142 3'  TATCCTCTTAACCTTCTCTTC 2231          A___    A

                        GAAGAGAG   AAGAG ATA
                        ||||||||   ||||| |||
                        CTTCTCTT   TTCTC TAT
                          CCAA    C
GAM49   DKFZp566D234 3'  TATTTTTTTTCTCTGTC    2612    AG

                        GA  AGAGAAAGAGAATA
                        ||  |||||||||||||
                        CT  TCTCTTTTTTTTAT
                          G_
GAM49   DKFZP566I1024 3'  TTTTAAAATCTATTCTCTC  2878        _  GAA

                        GAGAGAA AGA  TAAAA
                        ||||||| ||| |||||
                        CTCTCTT TCT  ATTTT
                           A  AAA
GAM49   EPI64    3'  TATTTTGACATCTCTCTCTT 3681        A   GAATA
          C                 GAAGAGAGA AGA   AAAATA
                        ||||||||| |||   ||||||
                        CTTCTCTCT TCT    TTTTAT
                         C  ACAG_
GAM49   FLJ00012 3'  TATTTTTATCTCTATCTCCT 2985    A   A   A

                        AG GAGA AGAGA TAAAAATA
                        || |||| ||||| ||||||||
                        TC CTCT TCTCT ATTTTTAT
                          _   A    _
GAM49   FLJ10460 3'  ATTTTTATTCTACCTTTC    1778        AAAG

                        GAGAG   AGAATAAAAAT
                        |||||   ||||||||||
                        CTTTC   TCTTATTTTTA
                          CA__
GAM49   FLJ10687 3'  TTTATTCATTTCTCTCCTC  1793    A     GA

                        GA GAGAGAAA  GAATAAA
                        || ||||||||  |||||||
                        CT CTCTCTTT  CTTATTT
                          C   A_
GAM49   FLJ10738 3'  TATTTTTACTCTCCCTCTTC  1799        AGAAA   A

                        GAAGAG   GAGA TAAAAATA
                        ||||||   |||| |||||||||
                        CTTCTC   CTCT ATTTTTAT
                          C____   C
GAM49   FLJ13158 3'  TTCTCTCCCTTTCTCTTC    2109         A__

                        GAAGAGAGA  AGAGAA
                        |||||||||  ||||||
```

```
                           CTTCTCTTT  TCTCTT
                             CCC
GAM49   FLJ20294  5' TATTCCTGTCTCCTCTTT   1747      _   A  A
                        GAAGAG AGA AG GAATA
                        |||||| ||| || |||||
                        TTTCTC TCT TC CTTAT
                             C   G  _
GAM49   FLJ21657  3' TATTCTACTTCTCTCTTC   1991         AG
                        GAAGAGAGAA  AGAATA
                        ||||||||||  ||||||
                        CTTCTCTCTT  TCTTAT
                             CA
GAM49   GT650    3' TATTTCTGATTCTCCCTCTCTT 2341       AAA    AA_
          C                 GAAGAGAG  GAGAAT  AAATA
                            |||||||| |||||| |||||
                            CTTCTCTC  CTCTTA  TTTAT
                             C__      GTC
GAM49   HEY2     3' TATTCTCTTTTTTTTCTC   1420    AG
                        GA AGAGAAAGAGAATA
                        || |||||||||||||
                        CT TTTTTTCTCTTAT
                             CT
GAM49   HIC2     3' ATTTTTTTTTCTCTCTCTTTTC 2717        A     T
                        GAAGAGAGA AGAGAA AAAAAT
                        ||||||||| |||||| ||||||
                        CTTTTCTCT TCTTTT TTTTTA
                             C    _
GAM49   HOOK3    3' ATTTTGAGGACTTTTTCTCTCT 2249          AATA_
                        AGAGAGAAAGAG   AAAAT
                        ||||||||||||   |||||
                        TCTCTCTTTTTC   TTTTA
                             AGGAG
GAM49   IL1RAPL1 5' TATTCTTATTTTCCCCTCTCTT 1488       AAA    A
          T                 GAAGAGAG  GAGAATAA AATA
                            |||||||| |||||||| ||||
                            TTTCTCTC  CTTTTATT TTAT
                             CC_      C
GAM49   KALI     3' TTTTGTTCTTGTCCCTCTC   2347      AAA_
                        GAGAG   GAGAATAAAA
                        |||||   ||||||||||
                        CTCTC   TTCTTGTTTT
                             CCTG
GAM49   KIAA0077 3' TTTTATTCTCTCTCCCTTT   2773    A  AA
                        GAAG GAGA  GAGAATAAAA
                        |||| |||| ||||||||||
                        TTTC CTCT  CTCTTATTTT
                             C    __
GAM49   KIAA0089 3' ATTTTTAGCCTCTTTTCTCTTC 2873        A  AA
                        GAAGAGAGAA GAG  TAAAAAT
                        |||||||||| ||| |||||||
```

```
                    CTTCTCTTTT CTC ATTTTTA
                    _          CG
GAM49  KIAA0286 3'  TATTTTCACCCTCTTTTC  2814      AAA
                    GAAGAGAG  GAGAATA
                    ||||||||  |||||||
                    CTTTTCTC  CTTTTAT
                            CCA
GAM49  KIAA0295 3'  TTTTTTCCCTTTCTCTCT   2808      A  T
                    AGAGAGAAAG GAA AAA
                    |||||||||| ||| |||
                    TCTCTCTTTC CTT TTT
                            C  T
GAM49  KIAA0342 3'  TATTCTCATTACTTCTCTTT 2890        _ _  A
                    GAAGAGA G AA GAGAATA
                    |||||||| | || |||||||
                    TTTCTCT C TT CTCTTAT
                          T A  A
GAM49  KIAA0564 3'  TATTTTTATTTTCTCCCTGCTC 2743    _  AA
                    GAG AG  AGAGAATAAAAATA
                    ||| ||  ||||||||||||||
                    CTC TC  TCTTTTATTTTTAT
                    G  CC
GAM49  KIAA0630 3'  TATTTTTTAAAAGTCTTTCTCT 3465         GAAT__
            CT              AGAGAGAAAGA    AAAAATA
                            |||||||||||    |||||||
                            TCTCTCTTTCT    TTTTTAT
                                GAAAAT
GAM49  KIAA0662 3'  TGTTCTCTCTCTCTCTTT   3215       A
                    GAAGAGAGA AGAGAATA
                    ||||||||| ||||||||
                    TTTCTCTCT TCTCTTGT
                            C
GAM49  KIAA0830 3'  TTTGCTTCTCTTTCTCCT   2866    A       _
                    AG GAGAAAGAGAA TAAA
                    || ||||||||||| ||||
                    TC CTCTTTCTCTT GTTT
                    _          C
GAM49  KIAA0964 3'  ATTCTTATGTTTTTCTCTTTTC 1579        GA  A
                    GAAGAGAGAAAGA ATAA AAT
                    ||||||||||||| |||| |||
                    CTTTTCTCTTTTT TATT TTA
                        G_   C
GAM49  KIAA1076 3'  TATTTTTTGCTTTCTCTC   2723       AGAAT
                    GAGAGAAAG    AAAAATA
                    |||||||||    |||||||
                    CTCTCTTTC    TTTTTAT
                        GT___
GAM49  KIAA1181 3'  ATTCCTCTTCCTCTCTTC   2817     A   _
                    GAAGAGAG AAGAG AAT
                    |||||||| ||||| |||
```

```
                              CTTCTCTC TTCTC TTA
                              C     C
GAM49   KIAA1319  3' TATTTTTGTCTTCTTCCTTTC 1925      A   GA
                        GAGAG AAGA  ATAAAAATA
                        ||||| |||| |||||||||
                        CTTTC TTCT  TGTTTTTAT
                        C     TC
GAM49   KIAA1522  3' ATTCTCTGACCTTTCTCTCT 2708           _____
                        AGAGAGAA   AGAGAAT
                        ||||||||   |||||||
                        TCTCTCTT   TCTCTTA
                          TCCAG
GAM49   KIAA1906  3' ATTTTTATTCTCTGCTT    2971      AA
                        GAG AGAGAATAAAAAT
                        ||| ||||||||||||
                        TTC TCTCTTATTTTTA
                          G_
GAM49   MAPK6     5' TATTTTTCTTCTCCCTTT    952     A   AG
                        GAAG GAGAA  AGAATA
                        |||| ||||| ||||||
                        TTTC CTCTT  TTTTAT
                        C     CT
GAM49   MGC13138  3' TATTTTTATTCTTGTGACCCTC 2332     AGAAA_
                        GAG    GAGAATAAAAATA
                        |||    |||||||||||||
                        CTC    TTCTTATTTTTAT
                          CCAGTG
GAM49   MGC2742   5' TATTTCTTTTCTCTCTTC    2040           AG
                        GAAGAGAGAAAG AATA
                        ||||||||||| ||||
                        CTTCTCTCTTTT TTAT
                          CT
GAM49   MGC32043  3' TATTCCTGTTTTCTCTTT    2486        _ A
                        GAAGAGAGAA AG GAATA
                        |||||||||| || |||||
                        TTTCTCTTTT TC CTTAT
                          G _
GAM49   NFAT5     3' TATTCCCTTTTTCTCTTC    2452           A
                        GAAGAGAGAAAG GAATA
                        ||||||||||| |||||
                        CTTCTCTTTTTC CTTAT
                          C
GAM49   OSBPL8    3' TTTTTATTATCCTCCTCTCTTC 1929       AAA G
                        GAAGAGAG  GA AATAAAAA
                        |||||||  || ||||||||
                        CTTCTCTC  CT TTATTTTT
                          CTC A
GAM49   RAB10     3' TGTTCTGCTTTTCCTCCTC   3337      A  AG  _
                        GA GAG  AAAG AGAATA
                        || ||| |||| ||||||
```

```
                          CT CTC  TTTC TCTTGT
                          C  CT   G
GAM49   RANBP1   3' TATTTTCTTTTCCTCTCTTT 969          __
                   GAAGAGAG  AAAGAGAATA
                   ||||||||  ||||||||||
                   TTTCTCTC  TTTCTTTTAT
                          CT
GAM49   RASSF2   3' TATTTTCACAATCCTCTCTTC 1537        AAA___
                   GAAGAGAG   GAGAATA
                   ||||||||   |||||||
                   CTTCTCTC   CTTTTAT
                           CTAACA
GAM49   STK22D   3' TATTTTCATCAGCTTCTTCTCT 2226       AG AATA__
            CT             AGAGAGAA AG   AAAATA
                           |||||||| ||   ||||||
                           TCTCTCTT TC   TTTTAT
                           CT GACTAC
GAM49   SYNJ2   3' ATTTTAGGTTTTCTCTTC 2606        AGAGAA
                   GAAGAGAGAA   TAAAAAT
                   ||||||||||   |||||||
                   CTTCTCTTTT   ATTTTTA
                           GG___
GAM49   TBLR1   3' TATTCTTTTTTTCCCTTC 2079     A
                   GAAG GAGAAAGAGAATA
                   |||| |||||||||||||
                   CTTC CTTTTTTTCTTAT
                        C
GAM49   TM9SF1   3' TATTGCTGTTCTCTCCCTTTCT 1296      AA     AA
             TC            GAAGAGAG AGAGAATA AATA
                           |||||||| |||||||| ||||
                           CTTCTTTC TCTCTTGT TTAT
                           CC       CG
GAM49   ULK2    3' TATTCTATCCTCTCCTCTTC 1523      _  AAG_
                   GAAGAG AGA   AGAATA
                   |||||| |||   ||||||
                   CTTCTC TCT   TCTTAT
                        C  CCTA
GAM49   UNC5D   3' TTATTCTTTCTTCCTCTTC 2393     A  _
                   GAAGAG GAA AGAGAATAA
                   |||||| ||| |||||||||
                   CTTCTC CTT TTTCTTATT
                        _  C
GAM49   LOC121219 5' TTATTAACTCCTTCTCTCTTT 2988       A  __
                   GAAGAGAGAA GAG  AATAA
                   |||||||||| ||| |||||
                   TTTCTCTCTT CTC  TTATT
                           C  AA
GAM49   LOC128077 3' ATTTGTTTTCTCTTTCTTTCCT 3006   A        TAA
             C            GA GAGAGAAAGAGAA  AAAT
                          || |||||||||||||  ||||
```

```
                          CT CTTTCTTTCTCTT  TTTA
                          C            TTG
GAM49   LOC143451 3'  TTCTCTCCTTCTCTCTTC   3058            __
                          GAAGAGAGAA AGAGAA
                          |||||||||| ||||||
                          CTTCTCTCTT TCTCTT
                                  CC
GAM49   LOC145125 3'  TTCTCTCCTTCTCTCTTC   3075            __
                          GAAGAGAGAA AGAGAA
                          |||||||||| ||||||
                          CTTCTCTCTT TCTCTT
                                  CC
GAM49   LOC149351 3'  ATTTTTCAGATCTTTCTCTTT 3131            GAAT
                          AGAGAGAAAGA   AAAAAT
                          ||||||||||   ||||||
                          TTTCTCTTTCT   TTTTTA
                                  AGAC
GAM49   LOC149722 5'  TATTCTTTCTTTCTCTTC   3312          A
                          GAAGAGAGA AGAGAATA
                          ||||||||| ||||||||
                          CTTCTCTTT TTTCTTAT
                                  C
GAM49   LOC149837 5'  TATTCCTGTCTTTCTCTCT  3318            ___
                          AGAGAGAAAGA  GAATA
                          ||||||||||  |||||
                          TCTCTCTTTCT  CTTAT
                                  GTC
GAM49   LOC150054 3'  TATTCTGTCTTTCTCCTC   3323      _   __
                          GAG AGAAAGA  GAATA
                          ||| ||||||| |||||
                          CTC TCTTTCT  CTTAT
                              C       GT
GAM49   LOC150150 5'  TTTTGTGCCTCTCTTTCTTC 3324          AA  A_
                          GAAGAGAGA GAG ATAAAA
                          ||||||||| ||| ||||||
                          CTTCTTTCT CTC TGTTTT
                              __  CG
GAM49   LOC150225 3'  TATTTTGTTTCCCTCTTC   3327        A  G
                          GAAGAG GAAA AGAATA
                          |||||| |||| ||||||
                          CTTCTC CTTT TTTTAT
                                  C  G
GAM49   LOC152816 3'  TATTTTTATCCTCAACCTCTT 3364        AAA  A
                          GAGAG  GAG ATAAAAATA
                          |||||  ||| |||||||||
                          TTCTC  CTC TATTTTAT
                                  CAA  C
GAM49   LOC155038 3'  ATTGCGTTTCTCTTTCTCCTTC 3198      A        TAAA
                          GAAG GAGAAAGAGAA   AAT
                          |||| ||||||||||   |||
```

```
                         CTTC CTCTTTCTCTT   TTA
                         _                 TGCG
GAM49   LOC158629 3' TATTTTCTTTCCCTCTC     3394    A   A
                         GA GAG GAAAGAGAATA
                         || ||| ||||||||||
                         CT CTC CTTTCTTTTAT
                         _      C
GAM49   LOC158943 3' TATTTTCTTTCCTCTCTTT  2572          __
                         GAAGAGAG AAAGAGAATA
                         |||||||| ||||||||||
                         TTTCTCTC TTTCTTTTAT
                              CT
GAM49   LOC170082 3' ATTCTTTTCCCCTCTCTTTC 3254          ____
                         GAAGAGAGA  AAGAGAAT
                         ||||||||| ||||||||
                         CTTTTCTCT  TTTTCTTA
                              CCCC
GAM49   LOC199920 5' TATTTTTATTCTTTGATTCTTC 3436      AGAA
                         GAAGAG  AGAGAATAAAAATA
                         ||||||  |||||||||||||
                         CTTCTT  TTTCTTATTTTAT
                              AG__
GAM49   LOC219667 3' ATTTTTGTTATCTCTCTTC   3516      AAGAG
                         GAAGAGAGA   AATAAAAAT
                         |||||||||  |||||||||
                         CTTCTCTCT   TTGTTTTTA
                              A____
GAM49   LOC220279 5' TATTTTCTTCCCCTACCTCTCT 3653          A_____
          TC               GAAGAGAG   AAGAGAATA
                         ||||||||  |||||||||
                         CTTCTCTC   TTCTTTTAT
                              CATCCCC
GAM49   LOC221830 3' TATTTTCTTTTCTTTCTTC   3567       _
                         GAAGAGAGAAA GAGAATA
                         ||||||||||| ||||||
                         CTTCTTTCTTT CTTTTAT
                              T
GAM49   LOC222166 3' ATTTTACCTTCTCTCTTT   3635         AG_
                         GAAGAGAGAA  AGAAT
                         |||||||||| |||||
                         TTTCTCTCTT  TTTTA
                              CCA
GAM49   LOC254440 3' TTCTCTCCTTCTCTCTTC   3729       __
                         GAAGAGAGAA AGAGAA
                         |||||||||| ||||||
                         CTTCTCTCTT TCTCTT
                              CC
GAM49   LOC51123 3' ATTTTTATGCTGTTCCCTCTT 2571    A  AG  A
                         AAGAG GAA  AG ATAAAAAT
                         ||||| |||  || ||||||||
```

```
                         TTCTC CTT  TC TATTTTTA
                           C  G_ G
GAM49   LOC51596 5' TATTTTCCAAGTTTCTCTCTC 1651      A       ____
                         GA GAGAGAAA   GAGAATA
                         II IIIIIIII   IIIIIII
                         CT CTCTCTTT   CTTTTAT
                          _      GAAC
GAM49   LOC84570 5' TTTCGTTTTCCTCTCTCTTC 2257        AA   TA
                         GAAGAGAGA GAGAA AAA
                         IIIIIIIII IIIII III
                         CTTCTCTCT CTTTT TTT
                           C_   GC
GAM49   LOC92710 5' TATTTTTATGCCTCTGTCTC 2885      A  A_
                         GAGA AGAG ATAAAAATA
                         IIII IIII IIIIIIIII
                         CTCT TCTC TATTTTTAT
                          G   CG
GAM50   FANCF    3' GTCCCTTTAAAGCATTGA  1997            ATATAT
                         TCAATGTTTTAAA   GGAC
                         IIIIIIIIIIII    IIII
                         AGTTACGAAATTT   CCTG
                              C_____
GAM50   GPR65    5' TCCACCCTTTAAAAGCATTGA 2544        A  TATA
                         TCAATGTTTT AAA   TGGA
                         IIIIIIIIII III   IIII
                         AGTTACGAAA TTT   ACCT
                          A  CCC_
GAM50   LMNB1    3' TGTCCATACACTTTGTTGCA  1226     TT   ATA
                         TGT TAAA  TATGGACA
                         III IIII  IIIIIIII
                         ACG GTTT  ATACCTGT
                          TT    CAC
GAM50   MEN1     5' CATAATATTTTAAAACATT  3600         _
                         AATGTTTTAAAATAT ATG
                         IIIIIIIIIIIIII III
                         TTACAAAATTTTATA TAC
                              A
GAM50   PLAG1    3' TGTCCATATACCAGATTTAAAAA 944       A____
         TATT                AATGTTTTAAA   TATATGGACA
                         IIIIIIIIIII   IIIIIIIIII
                         TTATAAAATTT   ATATACCTGT
                            AGACC
GAM50   S100A11  3' TGTCACTTTTTTAAAACATGA  1231   A        TATATG
                         TCA TGTTTTAAAA   GACA
                         III IIIIIIIIII   IIII
                         AGT ACAAAATTTT   CTGT
                          _    TTCA__
GAM50   SLC9A6   3' TCCAGTTAGAACATTGA  1290          AATATA
                         TCAATGTTTTAA   TGGA
                         IIIIIIIIIII    IIII
```

```
                          AGTTACAAGATT    ACCT
                             G_____
GAM50    SOD2    3' TCCATATACTTTGGGGACTTG 766      T    TA  _
                          CAA GTTT  AAA TATATGGA
                          ||| |||| ||| ||||||||
                          GTT CAGG  TTT ATATACCT
                           _    GG   C
GAM50    BIRC2   5' TATATTTTTAAAACATTGA 2784              T
                          TCAATGTTTTAAAA ATATG
                          |||||||||||| |||||
                          AGTTACAAAATTTT TATAT
                             _
GAM50    CXorf1  5' TGTCCATAGAAAAAATATT 1145        AAAATA
                          AATGTTTT    TATGGACA
                          ||||||||    ||||||||
                          TTATAAAA    ATACCTGT
                             AAG___
GAM50    KIAA0367 3' TGTCCCACAATGCCTAAAACAT 2787           AAATATAT_
          TGA             TCAATGTTTTA    GGACA
                          ||||||||||    |||||
                          AGTTACAAAAT    CCTGT
                             CCGTAACAC
GAM50    KIAA1321 3' TCCTTGAGCTTTAAAGCATTGA 2627           ATATAT
                          TCAATGTTTTAAA    GGA
                          ||||||||||||    |||
                          AGTTACGAAATTT    CCT
                             CGAGTT
GAM50    KIAA1718 3' TGTATTTTAAAATATTGA    2686
                          TCAATGTTTTAAAATATA
                          ||||||||||||||||
                          AGTTATAAAATTTTATGT

GAM50    KIAA1789 5' TGTCCCTGCCCTAGAAACATTG 2781          AAAATATAT
          A               TCAATGTTTT    GGACA
                          ||||||||||    |||||
                          AGTTACAAAG    CCTGT
                             ATCCCGTC_
GAM50    PRO2964  3' CAAGTATTTTAAAACACTG 1842     A        A
                          CA TGTTTTAAAATAT TG
                          || |||||||||||| ||
                          GT ACAAAATTTTATG AC
                             C        A
GAM50    SLC17A6  3' TGTCCATACACAGAAACAT 1912      AAAATA
                          ATGTTTT    TATGGACA
                          |||||||    ||||||||
                          TACAAAG    ATACCTGT
                             ACAC__
GAM50    TRAF3   5' CATTTTATTTTAAAACGTTGA 2542              T_
                          TCAATGTTTTAAAATA ATG
                          |||||||||||||| |||
```

```
                        AGTTGCAAAATTTTAT TAC
                        TT
GAM50   LOC151361 3' TGTCTGTGTTTTTAAAAC   3344          T
                     GTTTTAAAA ATATGGACA
                     ||||||||| |||||||||
                     CAAAATTTT TGTGTCTGT
                             _
GAM50   LOC158714 3' TCCACACATTTAAAACATTGA 3224          ATATA
                     TCAATGTTTTAAA   TGGA
                     ||||||||||||   ||||
                     AGTTACAAAATTT   ACCT
                           ACAC_
GAM50   LOC219667 3' TATACCTTAGAACATTGA   3518           AA
                     TCAATGTTTTAA TATA
                     |||||||||||| ||||
                     AGTTACAAGATT ATAT
                           CC
GAM50   LOC91565 3' TCCATTTTAAAACATT     2749          ATAT
                    AATGTTTTAAA  ATGGA
                    |||||||||||  |||||
                    TTACAAAATTT  TACCT
                          ____
GAM51   C1orf1  5' TATGCTGACAGAAGAACCA   809          CC A A
                   TGGTTCTTT GT CA CATA
                   ||||||||| || || ||||
                   ACCAAGAAG CA GT GTAT
                     A_ _ C
GAM51   LRAT   3' AGTATGCATACATAAAAGCAAC 2556      _  CC_  CAA
             CA            TGGTT CTTT GTA  CATACT
                   |||||| |||| ||| ||||||
                   ACCAA GAAA CAT  GTATGA
                     C   ATA AC_
GAM51   MYBL1  3' AGTATGTTATACAAATGCCA   2679      TCTTTCC  C
                   TGGT    GTA AACATACT
                   ||||    ||| ||||||||
                   ACCG    CAT TTGTATGA
                     TAAA___  A
GAM51   KIAA1028 3' TATGTCTGCATTGAAAAGAACC 3547          C TA_ _
             A             TGGTTCTTT CG  CA ACATA
                   |||||||||| || || |||||
                   ACCAAGAAA GT  GT TGTAT
                     A TAC C
GAM51   MGC2488 3' TGTAGTGGAAAGAAGCAT   2045       G        _
                   ATG TTCTTTCCG TACA
                   ||| ||||||||| ||||
                   TAC AAGAAAGGT ATGT
                      G     G
GAM52   CX3CR1 3' ACTGCCTACTGCATCGAGTCA 2891          TCCCTTAA
                  TGACTCG   TAGGCAGT
                  |||||||   |||||||||
```

```
                       ACTGAGC     ATCCGTCA
                      TACGTC__
GAM52  WNT14    3' CTGCAAGGGACGAGTC     1014          AATAG
                      GACTCGTCCCTT  GCAG
                      ||||||||||| ||||
                      CTGAGCAGGGAA  CGTC
                         _____
GAM52  FLJ20275 3' TACTGCCTTCATAAGATCAAGT 1745      CGTCC  AT_
         CA              TGACT  CTTA AGGCAGTA
                      ||||| |||| ||||||||
                      ACTGA  GAAT TCCGTCAT
                       ACTA_  ACT
GAM52  FLJ22390 5' TACTGCCTATCAAACG      2002      CCC A
                      CGT  TT ATAGGCAGTA
                      ||| || ||||||||||
                      GCA  AA TATCCGTCAT
                        ___  C
GAM53  LOC120864 5' CAAGGTCCAAACTGATATAA 2986          CGTAG
                      TTGTATCAGTTT  TCTTG
                      |||||||||||| |||||
                      AATATAGTCAAA  GGAAC
                         CCT__
GAM54  KIAA0626 3' AACATCAGGGTGCAGAATTGAT 1954      C_ A_
                      ATCGATTC CAT TGATGTT
                      |||||||| ||| |||||||
                      TAGTTAAG GTG ACTACAA
                        AC  GG
GAM54  KIAA1239 3' AACATCATGATTATTGATG   2914          TCCCA
                      CATCGAT  TATGATGTT
                      ||||||| |||||||||
                      GTAGTTA  GTACTACAA
                        TTA__
GAM54  LOC201475 5' AACATCATATATTTTGATGTTA 3428         TTCCC
                      TAACATCGA  ATATGATGTT
                      |||||||||  |||||||||
                      ATTGTAGTT  TATACTACAA
                        TTA__
GAM55  ARCN1    3' CCCATTTCCTTCCAGTCA    844          GAAGT   CA
                      TGATTGGA  AGGAAA GG
                      ||||||||  |||||| ||
                      ACTGACCT  TCCTTT CC
                         _____       AC
GAM55  CTSK     3' TCCTACTTTGCTTCTCTCCACC 736      AT      _____
         CA              TG TGGAGA  AGTAGGA
                      || |||||| |||||||
                      AC ACCTCT  TCATCCT
                        CC  CTTCGTT
GAM55  HMG20A   3' TCCTATTTCCCTGCCATCA   1800      T___ A
                      TGAT  GG GAAGTAGGA
                      ||||  || |||||||||
```

```
                         ACTA   CC CTTTATCCT
                           CCGT _
GAM55   PRDM2    3' TCCTGTTTCCCACCCAG   1415     AGAA A
                         TTGG   GT GGAAACAGGA
                         |||| || ||||||||||
                         GACC   CA CCTTTGTCCT
                           ____  C
GAM55   RNMT     3' CCTGCCTATCCTCTCCGATCA 1060      A_  AAA
                         TGATTGGAGA GTAGG  CAGG
                         |||||||||| ||||| ||||
                         ACTAGCCTCT TATCC  GTCC
                           CC   ___
GAM55   SCAP1    3' TCCCACTCCCTACTTCTGCCA 1052    _     AAACA
                         TGG AGAAGTAGG   GGA
                         ||| |||||||||   |||
                         ACC TCTTCATCC   CCT
                           G    CTCAC
GAM55   USH3A    5' CCTATTTTATTTCTCCATCA 2355     T     AAC
                         TGAT GGAGAAGTAGGA  AGG
                         |||| |||||||||||| |||
                         ACTA CCTCTTTATTTT  TCC
                           _        A__
GAM55   VAT1     3' TCCTGTTTCCCACCTCCTTCTC 1292     TA____
                   C              GGAGAAG    GGAAACAGGA
                                  |||||||    ||||||||||
                                  CCTCTTC    CCTTTGTCCT
                           CTCCAC
GAM55   AIF1     5' CCTGCTGAAAACCCTCCAGTCA 2297        A_____
                         TGATTGGAG     AGTAGG
                         |||||||||     ||||||
                         ACTGACCTC     TCGTCC
                           CCAAAAG
GAM55   CPLX1    3' CCTGTTTCTCCTCCATTCA   1317    T   AAGTA
                         TGA TGGAG   GGAAACAGG
                         ||| |||||   |||||||||
                         ACT ACCTC   TCTTTGTCC
                           T   C____
GAM55   CXYorf1  3' CCTGTTCCCCACCTCCCGGCTC 3228    _  A A A A
                         GA TTGG GA GT GG AACAGG
                         || |||| || || || ||||||
                         CT GGCC CT CA CC TTGTCC
                           C   _  C  C
GAM55   FLJ12221 3' CCCACCCTTGCTCTCCAATTA 2637        A   AAACA
                         TGATTGGAGA GTAGG   GG
                         |||||||||| |||||   ||
                         ATTAACCTCT CGTTC    CC
                           _   CCAC_
GAM55   FLJ20207 3' CCTGCCCTGCTTCCCCACCCA 1741    AT A     AAA
                         TG TGG GAAGTAGG  CAGG
                         || ||| |||||||||  ||||
```

```
                          AC  ACC CTTCGTCC  GTCC
                          CC  C        C__
GAM55   FLJ22215  3' CCTGCCCCCTACCCTGTTCTCC 3715          ____      AAA
                          GGAGAA  GTAGG  CAGG
                          ||||||  |||||  ||||
                          CCTCTT  CATCC  GTCC
                          GTCC   CCC
GAM55   FLJ31547  3' TCCCATAATTTCTCCCGCAATC 2511          ___       A___
                    A            TGATT  GGAGAAGT  GGA
                          |||||  ||||||||  |||
                          ACTAA  CCTCTTTA  CCT
                          CGC     ATAC
GAM55   HSCBCIP1  3' TCCTACCTATGTCTTCTCCAAT 3449          ___   AAAC
                          ATTGGAGAAG  TAGG  AGGA
                          ||||||||||  ||||  ||||
                          TAACCTCTTC  ATCC  TCCT
                          TGT  A___
GAM55   KIAA0515  5' TCCTACCAGAACTCCTCCGATC 2670       A  A__  AAAC
                    A            TGATTGGAG AGT  GG  AGGA
                          ||||||||| |||  ||  ||||
                          ACTAGCCTC TCA  CC  TCCT
                          C  AGA  A___
GAM55   KIAA1514  3' CCTGCTCAACTTCTCCA    1877       A AAA
                          TGGAGAAGT GG  CAGG
                          ||||||||| ||  ||||
                          ACCTCTTCA CT  GTCC
                          A  C__
GAM55   KIAA1553  3' TCCTCACTTCTCCATCCA   3544     AT       _
                          TG  TGGAGAAGT AGGA
                          ||  ||||||||| ||||
                          AC  ACCTCTTCA TCCT
                          CT       C
GAM55   KIAA1656  3' CCCACTTCCTTCCAGTCA   2730       __   A
                          TGATTGGA GAAGT GG
                          |||||||| ||||| ||
                          ACTGACCT CTTCA CC
                          TC    C
GAM55   KIAA1877  3' CCTACCTTATTTCTCCAGCCA 2741    AT       AAAC
                          TG TGGAGAAGTAGG  AGG
                          || |||||||||||  |||
                          AC ACCTCTTTATTC  TCC
                          CG       CA__
GAM55   MTCH1     3' CCCGTCTACCCCTCCAGTCA 1493       AA   AAACA
                          TGATTGGAG GTAGG   GG
                          ||||||||| |||||   ||
                          ACTGACCTC CATCT   CC
                          CC  GC___
GAM55   N-PAC     3' CCGCCCTCACCCCTCCAATC 2902       AA _ AAACA
                          GATTGGAG GT AGG   GG
                          |||||||| || |||   ||
```

```
                              CTAACCTC  CA TCC    CC
                                CC  C  CG___
GAM55    SEMA4B   5'  CCTGTTTCCCACCTCC      2839      AA  A
                              GGAG  GT GGAAACAGG
                              |||| || |||||||||
                              CCTC  CA CCTTTGTCC
                                __  C
GAM55    SPRY1    3'  CCTGTTTCCCACCTTCTCT  2709        TA_
                              GGAGAAG  GGAAACAGG
                              |||||||  |||||||||
                              TCTCTTC  CCTTTGTCC
                                     CAC
GAM55    WS-3     5'  CCTGCCAGGCTCTCCAATC  1312        A  A_  AAA
                              GATTGGAGA GT GG  CAGG
                              ||||||||| || ||  ||||
                              CTAACCTCT CG CC  GTCC
                                   _  GA ___
GAM55    LOC123242 5' TCTGTACCTTCTCCATCCA  3030     AT     TAGGAA
                              TG TGGAGAAG    ACAGG
                              || |||||||||    |||||
                              AC ACCTCTTC    TGTCT
                                   CT      CA____
GAM55    LOC127702 3' CCTGCCCACAACTTCTCCAAAC 3024    A      A__ AAA
                A             TG TTGGAGAAGT GG  CAGG
                              || |||||||||| || ||||
                              AC AACCTCTTCA CC  GTCC
                                 A      ACA C__
GAM55    LOC146745 5' TCCTGCCACCATTTCTCCAACC 3099    A      A AAA
                A             TG TTGGAGAAGT GG  CAGGA
                              || |||||||||| ||  |||||
                              AC AACCTCTTTA CC  GTCCT
                                 C      _  ACC
GAM55    LOC147791 3' CCCATTCCCTAACCTCCAATC  3294        AAG  A CA
                              GATTGGAG  TAGG AA  GG
                              ||||||||  |||| || ||
                              CTAACCTC  ATCC TT CC
                                   CA_  C AC
GAM55    LOC196892 3' TCCTGGTGATTCTTCTCCAATC 3417              TAGGAAA
                A             TGATTGGAGAAG    CAGGA
                              |||||||||||    |||||
                              ACTAACCTCTTC     GTCCT
                                     TTAGTG_
GAM55    LOC200093 3' CCTGTTCCCCACCTCCCGGCTC 2648    _  A A A A
                              GA TTGG GA GT GG AACAGG
                              || |||| || || || ||||||
                              CT GGCC CT CA CC TTGTCC
                                 C  _  C C C
GAM55    LOC201243 5' TCCTGCCACCATTTCTCCAACC 3426    A      A AAA
                A             TG TTGGAGAAGT GG  CAGGA
                              || |||||||||| ||  |||||
```

```
                          AC AACCTCTTTA CC  GTCCT
                          C       _  ACC
GAM55  LOC219404 3' CCTGCTCCCTACTTCCTGGCA 3606    A TG A     AAA
                          TG T  G GAAGTAGG  CAGG
                          || |  | |||||||| ||||
                          AC G  C CTTCATCC  GTCC
                          _ GT _       CTC
GAM55  LOC222066 3' TCCTGCAAACCACCTTCTCCAA 3574            TA AAA_
           TCA              TGATTGGAGAAG GG  CAGGA
                          |||||||||||| ||  |||||
                          ACTAACCTCTTC CC  GTCCT
                             CA  AAAC
GAM55  LOC253001 5' TCTGTACCTTCTCCATCCA  3698    AT     TAGGAA
                          TG TGGAGAAG    ACAGG
                          || |||||||    |||||
                          AC ACCTCTTC    TGTCT
                          CT     CA____
GAM55  LOC91040 3' CCTGTTCCCCACCTCCCGGCTC 2700   _  A  A  A  A
                          GA TTGG GA GT GG AACAGG
                          || |||| || || || ||||||
                          CT GGCC CT CA CC TTGTCC
                          C  _  C  C
GAM56  GCNT2    5' TCTCGGGATGAAACGGAATCGA 831            _____  A
                          TCGATTCCGT    CC AGA
                          ||||||||||    || |||
                          AGCTAAGGCA    GG TCT
                             AAGTAG  C
GAM56  BLP1     3' TTACCTTGCAGACGGAATGA 2222     G     __    A
                          TC ATTCCGTC  CAAG TGA
                          || |||||||| |||| |||
                          AG TAAGGCAG  GTTC ATT
                          _      AC   C
GAM56  BLP1     3' TTACCTTGCAGACGGAATGA 2371     G     __    A
                          TC ATTCCGTC  CAAG TGA
                          || |||||||| |||| |||
                          AG TAAGGCAG  GTTC ATT
                          _      AC   C
GAM56  LOC143914 5' TCACTCAAACGGAATCGA    3062        CCA A
                          TCGATTCCGT  AG TGA
                          ||||||||||  || |||
                          AGCTAAGGCA  TC ACT
                             AAC  _
GAM56  LOC253891 5' CACTGGGACGGAATCGG    3654        A A
                          TCGATTCCGTCC AG TG
                          |||||||||||| || ||
                          GGCTAAGGCAGG TC AC
                             G  _
GAM57  ADSS     3' GAAACAAATGATGAAAACAT 2925        CCTGTT
                          ATGT   TCATTTGTTTC
                          ||||   |||||||||||
```

```
                              TACA    AGTAAACAAAG
                             AAAGT_
GAM57   CASP6    3' GAAACAAAATCCTCAGGAAATT 2305      G    TTTCA
           A              TAAT TCCTG    TTTGTTTC
                          |||| |||||    ||||||||
                          ATTA AGGAC    AAACAAAG
                          A    TCCTA
GAM57   CASP6    3' GAAACAAAATCCTCAGGAAATT 810       G    TTTCA
           A              TAAT TCCTG    TTTGTTTC
                          |||| |||||    ||||||||
                          ATTA AGGAC    AAACAAAG
                          A    TCCTA
GAM57   CKTSF1B1 3' AAGTGGATAAACAGAACATT 1445       C    C TG
                          AATGT CTGTTT ATT  TTT
                          ||||| |||||| |||  |||
                          TTACA GACAAA TAG  GAA
                          A     _ GT
GAM57   F2R      3' AAACAATGCAGTACAGGACAT 879        TTCAT_
                          ATGTCCTGT    TTGTTT
                          |||||||||    ||||||
                          TACAGGACA    AACAAA
                              TGACGT
GAM57   GPRK7    3' GGAAACAAATGTTTCTGACATT 2476      CTGTTT
                          AATGTC    CATTGTTTCC
                          ||||||    ||||||||||
                          TTACAG    GTAAACAAAGG
                              TCTTT_
GAM57   NLGN1    3' AAACAAATGAGATGGAC    1591      T
                          GTCC GTTTCATTTGTTT
                          |||| ||||||||||||
                          CAGG TAGAGTAAACAAA
                              _
GAM57   APC10    5' GGAAACTGTAACAGGACATT 1574        T TTT
                          AATGTCCTGTT CA  GTTTCC
                          |||||||||||| ||  ||||||
                          TTACAGGACAA GT  CAAAGG
                              T ___
GAM57   C20orf139 3' GGAACAAAAACAGGACATTA 3319       CAT
                          TAATGTCCTGTTT TTGTTTC
                          ||||||||||||| |||||||
                          ATTACAGGACAAA AACAAGG
                              ___
GAM57   FLJ11186 3' GAAGCCCGAAACAAGACATTA 1818     C    ATTT
                          TAATGTC TGTTTC  GTTTC
                          ||||||| ||||||  |||||
                          ATTACAG ACAAAG  CGAAG
                              A   CC__
GAM57   FLJ22116 5' GGAATTGCGGAAAACAGGAC 2073        CA   __
                          GTCCTGTTT TTTGT TTCC
                          ||||||||| ||||| ||||
```

```
                        CAGGACAAA AGGCG AAGG
                          __      TT
GAM57  FLJ32978  3' AAACAAATGAAATCAACA   2487     CCT
                        TGT  GTTTCATTTGTTT
                        |||  |||||||||||
                        ACA  TAAAGTAAACAAA
                          AC_
GAM57  KIAA1164  3' GGAAACAAACAAAACAAAC 2862    CC   CA_
                        GT TGTTT  TTTGTTTCC
                        || |||||  |||||||||
                        CA ACAAA  AAACAAAGG
                          AA   ACA
GAM57  KIAA1762  3' AAAGAGAGAAACGGACA    2668      T   A  G
                        TGTCC GTTTC TTT TTT
                        ||||| ||||| ||| |||
                        ACAGG CAAAG AGA AAA
                          _   _  G
GAM57  KIAA1918  5' GAAAGGAGACAGAACATTA  2969     C    ATTTG
                        TAATGT CTGTTTC   TTTC
                        |||||| |||||||   ||||
                        ATTACA GACAGAG   AAAG
                          A   G____
GAM57  POPX1     3' GGAAACAAACTTCAGGTCA  1583    T TTTCA
                        TG CCTG   TTTGTTTCC
                        || ||||   |||||||||
                        AC GGAC   AAACAAAGG
                          T  TTC__
GAM57  PRO0800   3' AAACAAAGAGACAGGAATTA 1852     G    A
                        TAAT TCCTGTTTC TTTGTTT
                        |||| |||||||||| |||||||
                        ATTA AGGACAGAG AAACAAA
                          _    _
GAM57  LOC142779 3' GGAGTAACAAAATAGGACATTA 3050          CATT   __
                        TAATGTCCTGTTT  TGTT TCC
                        |||||||||||||  |||| |||
                        ATTACAGGATAAA  ACAA AGG
                          ____    TG
GAM57  LOC143274 5' GGAAACAAACAAAAGGA    3053     G  CA
                        TCCT TTT  TTTGTTTCC
                        |||| |||  |||||||||
                        AGGA AAA  AAACAAAGG
                          _   AC
GAM57  LOC154089 3' AAACAAATACTGAGACAG    3186         ___
                        CTGTTTCA TTTGTTT
                        |||||||| |||||||
                        GACAGAGT AAACAAA
                          CAT
GAM57  LOC169679 3' AGCATATGAAGACAGGACAT  3404       _ T
                        ATGTCCTGTTT CAT TGTT
                        |||||||||| ||| ||||
```

```
                       TACAGGACAGA GTA ACGA
                          A   T
GAM57   LOC202052 5' GAAACAAATACCCAGAAGACA 3484      __  TTTC
                        TGTC CTG   ATTTGTTTC
                        |||| |||   |||||||||
                        ACAG GAC   TAAACAAAG
                          AA  CCA_
GAM57   LOC256021 3' GAAACGAGAACAATGACATTA 3708      C_   CAT
                        TAATGTC TGTTT TTGTTTC
                        ||||||| ||||| |||||||
                        ATTACAG ACAAG AGCAAAG
                           TA  ___
GAM57   LOC91650 5' AAACAAAACATCTCAGGACAT 2765       TTTCA_
                       ATGTCCTG   TTTGTTT
                       ||||||||   |||||||
                       TACAGGAC   AAACAAA
                         TCTACA
GAM57   LOC91752 5' AAGTCAAATAAAACAGGACA 2777        C   _
                       TGTCCTGTTT ATTTG TTT
                       |||||||||| ||||| |||
                       ACAGGACAAA TAAAC GAA
                          A        T
GAM58   DRD1    3' ATTAACTCCGTTTCCAAATACA 774       GCTCCT
                      TGTAT   AGCGGAGTTAAT
                      |||||   ||||||||||||
                      ACATA   TTGCCTCAATTA
                        AACCT_
GAM58   KIAA0182 3' AAGTCCTAGGAGCACACA 2931     A    GC  G
                       TGT TGCTCCTA GGA TT
                       ||| |||||||| ||| ||
                       ACA ACGAGGAT CCT AA
                         C      __  G
GAM58   SSH2    3' AGCCCCAGGAGCATACA   2626        AGC  A
                      TGTATGCTCCT GG GTT
                      |||||||||||  || |||
                      ACATACGAGGA  CC CGA
                          C__  _
GAM58   LOC90918 5' ATTAAATCCAGGAACATATA 2687     C  AGC  G
                       TGTATG TCCT  GGA TTAAT
                       |||||| ||||  ||| |||||
                       ATATAC AGGA  CCT AATTA
                          A    ___   A
GAM59   EHHADH  3' TATGAATCATACATACACTC 877         TCTC_
                      GGGTGTAT   ATTCATA
                      ||||||||   |||||||
                      CTCACATA   TAAGTAT
                        CATAC
GAM59   ADAM9   3' TATGAATGAAAACAAAACACC 1063      A  C___
                      GGTGT TT  TCATTCATA
                      ||||| ||  |||||||||
```

```
                          CCACA AA   AGTAAGTAT
                          A CAAA
GAM59   BCAR3    3' ATGAATGAAAATACATCT   1036         C
                          GGGTGTATT TCATTCAT
                          ||||||||| |||||||
                          TCTACATAA AGTAAGTA
                                  A
GAM59   XAP135   5' AATGGCCACCTGATGA       1809          TATTC
                          TCATCGGGTG   TCATT
                          ||||||||||   |||||
                          AGTAGTCCAC   GGTAA
                                  C____
GAM59   XAP135   5' AATGGCCACCTGATGA        2408         TATTC
                          TCATCGGGTG   TCATT
                          ||||||||||   |||||
                          AGTAGTCCAC   GGTAA
                                  C____
GAM59   LOC252983 5' ATGAATAAAAATACATCTACTG 3668    TC      CTC
                          CA GGGTGTATT  ATTCAT
                          || |||||||||  ||||||
                          GT TCTACATAA  TAAGTA
                          CA        AAA
GAM60   MGC5242  5' CCTTACAATCCGAGACTA    2042             ___
                          TGGTCTCGGATT  AGG
                          ||||||||||||  |||
                          ATCAGAGCCTAA  TCC
                                    CAT
GAM60   LOC197259 3' GCCAATCAAGACCAGAA      3422        CG   A
                          TTCTGGTCT GATT GGC
                          ||||||||| |||| |||
                          AAGACCAGA CTAA CCG
                          A_   _
GAM61   DKFZP564I052 3' ATGGATGAAGATGATGACCGAT 2759     A  _   ATA
                          ATCG TCAT ATCT  TCATCCAT
                          |||| |||| ||||  ||||||||
                          TAGC AGTA TAGA  AGTAGGTA
                          C   G   ___
GAM61   KIAA0825 3' ATGGACAATACTATTGGTCGAT 2588         TATCTA  CA
                          ATCGATCA   TAT TCCAT
                          ||||||||   ||| |||||
                          TAGCTGGT   ATA AGGTA
                          TATC__  AC
GAM61   KIAA0976 3' ATGATGTATATTATCGAT    1588      C  TC
                          ATCGAT ATA  TATATCAT
                          |||||| |||  ||||||||
                          TAGCTA TAT  ATGTAGTA
                          T  __
GAM61   PLAC3    3' ATGGAAGGGGAAATATGATAGA 2853      G    CTATA  A
        T                   ATC ATCATAT   TC TCCAT
                          ||| |||||||    || |||||
```

```
                          TAG TAGTATA   GG AGGTA
                           A      AAGG_ A
GAM61   LOC147991 5' ATGTATATAGATATGATC    3115              _
                      GATCATATCTATAT CAT
                      |||||||||||||| |||
                      CTAGTATAGATATA GTA
                                    T
GAM62   HDAC7A    3' CTCTGGCAAAGTCTTCAA    1628         CTT
                      TTGAAGACT  CCAGAG
                      ||||||||| ||||||
                      AACTTCTGA GGTCTC
                                 AAC
GAM62   HDAC7A    3' CTCTGGCAAAGTCTTCAA    1700         CTT
                      TTGAAGACT  CCAGAG
                      ||||||||| ||||||
                      AACTTCTGA GGTCTC
                                 AAC
GAM62   LTBP1     3' TCTCAAATGAAAAAGTCTTCGA 764        C C ___
                      TTGAAGACT TT CA  GAGA
                      ||||||||| || ||  ||||
                      AGCTTCTGA AA GT  CTCT
                                A A AAA
GAM62   PDGFB     3' CTGGGAGAAGGTCTCCAA    941      A  __
                      TTG AGAC  TCTTCCAG
                      ||| ||||  ||||||||
                      AAC TCTG  AGAGGGTC
                        C   GA
GAM62   PRDM4     3' CTTACAGAAGAGTCTCTAA   1427      A     CA_
                      TTG AGACTCTTC  GAG
                      ||| |||||||||  |||
                      AAT TCTGAGAAG  TTC
                        C        ACA
GAM62   SIRT6     3' TTCTGGAAAAGTCCTCAA    1695      A  C
                      TTGA GACT TTCCAGAG
                      |||| |||| ||||||||
                      AACT CTGA AAGGTCTT
                         C   A
GAM62   XYLB      3' TCTCTGGAAGAATTTCCAA   1187      A  C
                      TTG AGA TCTTCCAGAGA
                      ||| ||| |||||||||||
                      AAC TTT AGAAGGTCTCT
                         C   A
GAM62   DKFZP434N093 3' TGTAAACAGAAGGTCTTCAA 3147        T  CAGAG
                      TTGAAGAC CTTC   ACG
                      |||||||| ||||   |||
                      AACTTCTG GAAG    TGT
                         _  ACAAA
GAM62   DKFZP547E1010 5' TTTCCAGAAGGGTCTCCAA 2768    A     CA
                      TTG AGACTCTTC  GAGA
                      ||| ||||||||| ||||
```

```
                      AAC TCTGGGAAG CTTT
                       C        AC
GAM62   DKFZP547E1010 5' TTTCCAGAAGGGTCTCCAA  1640     A      CA
                      TTG AGACTCTTC GAGA
                      ||| ||||||||| ||||
                      AAC TCTGGGAAG CTTT
                       C        AC
GAM62   FLJ13942 3' TTGAGATGGAAGAGTCTTTAA 2067              GAGA
                    TTGAAGACTCTTCCA  CGA
                    ||||||||||||||  |||
                    AATTTCTGAGAAGGT  GTT
                        AGA_
GAM62   FLJ14596 3' TCATCTGGGAGTCCCCAA   2282     AA   TT    _
                    TTG GACTC CCAGA GA
                    ||| ||||| ||||| ||
                    AAC CTGAG GGTCT CT
                      CC    __    A
GAM62   HRLP5    3' TTCTGGAAGAATCTACAA   2364     A  C
                    TTG AGA TCTTCCAGAG
                    ||| ||| |||||||||
                    AAC TCT AGAAGGTCTT
                      A  A
GAM62   KCNS1    3' CGTTGGAAGAGTCTT    917          GAG
                    AAGACTCTTCCA  ACG
                    ||||||||||||  |||
                    TTCTGAGAAGGT  TGC
                        ___
GAM62   KIAA0992 5' TCTCTGGAGTCTTCAA    1662        TCT
                    TTGAAGAC  TCCAGAGA
                    ||||||||  ||||||||
                    AACTTCTG  AGGTCTCT
                        ___
GAM62   KIAA1975 5' TATCATCTCTGGAAGTTGAGAG 2982   A  _____     C  |||
           CCTCCAA            G CTCT   TCCAGAGA GAT  A
                    | ||||   ||||||||| |||  |
                    C GAGA   AGGTCTCT CTA  T
                      C  GTTGA    A  |||
GAM62   MGC5590  3' TCTCAGAAAGTCTTCAA    2049        C  CA
                    TTGAAGACT TTC GAGA
                    ||||||||| ||| ||||
                    AACTTCTGA AAG CTCT
                      _  A_
GAM62   SIAT8C   5' TCTTGGAAGAATCTCAA    1648     A C    G
                    TTGA GA TCTTCCA AGA
                    |||| || ||||||| |||
                    AACT CT AGAAGGT TCT
                      _  A   _
GAM62   LOC149706 3' ATCACCTCTGGAGCCCTTTCA 3313     ACTC     AC
                     TGAAG  TTCCAGAG GAT
                     |||||  |||||||| |||
```

```
                          ACTTT   GAGGTCTC  CTA
                          CCC_        CA
GAM62    LOC160292 3' CTCTGGAAAGCCTTCAA    3399       A  C
                          TTGAAG CT TTCCAGAG
                          ||||||| || |||||||||
                          AACTTC GA AAGGTCTC
                               C  _
GAM62    LOC203378 3' GTTTCTAAAGAGTCTTCAA    3491           CC
                          TTGAAGACTCTT AGAGAC
                          |||||||||||| ||||||
                          AACTTCTGAGAA TCTTTG
                                  A_
GAM62    LOC204200 5' CTCTGGAAAGGTCTCCAA    3493     A  TC
                          TTG AGAC  TTCCAGAG
                          ||| |||| |||||||||
                          AAC TCTG  AAGGTCTC
                               C  GA
GAM62    LOC255265 5' CGTACGGAAAAGTCTTCA    3672       C   AGAG
                          TGAAGACT TTCC   ACG
                          |||||||| ||||    |||
                          ACTTCTGA AAGG   TGC
                                 A  CA__
GAM63    FLJ10737  3' AGATGTTTTTATTTTATATTAT 1797           TCCCA_
         TA              TAATAATATAAAAT    ATCT
                          |||||||||||||    ||||
                          ATTATTATATTTTA    TAGA
                          TTTTTG
GAM64    COX15    3' AACAGTCCCAGAATGACCCCA 1104       C  AAATC  T
                          TGGGGTTA TCT   GCT GTT
                          |||||||| |||    ||| |||
                          ACCCCAGT AGA   TGA CAA
                               A  CCC__  _
GAM64    SH2D1A   3' AACAAGCCTCCTTTTAAAGTAA 920          C   TC___
         CCCTA             TGGGGTTACT TAAA   GCTTGTT
                          |||||||||| |||||   |||||||
                          ATCCCAATGA ATTT   CGAACAA
                               A  TCCTC
GAM64    FLJ12994  3' ACAAGCAAATGTAACTCCA 2017        TCTAAATC
                          TGGGGTTAC     GCTTGT
                          |||||||||     ||||||
                          ACCTCAATG     CGAACA
                          TAAA____
GAM64    FLJ12994  3' ACAAGCAAATGTAACTCCA 3081        TCTAAATC
                          TGGGGTTAC     GCTTGT
                          |||||||||     ||||||
                          ACCTCAATG     CGAACA
                          TAAA____
GAM65    FGFR2    3' ACCCTGTCATTACGTCAACGC 712          _  __
                          GCGT GGC  AATGACAGGGT
                          |||| |||  |||||||||||
```

```
                               CGCA CTG  TTACTGTCCCA
                                 A   CA
GAM65   FGFR2   3' ACCCTGTCATTACGTCAACGC  2023      _  __
                        GCGT GGC  AATGACAGGGT
                        |||| |||  |||||||||||
                        CGCA CTG  TTACTGTCCCA
                          A   CA
GAM65   FGFR2   3' ACCCTGTCATTACGTCAACGC  2024      _  __
                        GCGT GGC  AATGACAGGGT
                        |||| |||  |||||||||||
                        CGCA CTG  TTACTGTCCCA
                          A   CA
GAM65   FGFR2   3' ACCCTGTCATTACGTCAACGC  2026      _  __
                        GCGT GGC  AATGACAGGGT
                        |||| |||  |||||||||||
                        CGCA CTG  TTACTGTCCCA
                          A   CA
GAM65   FGFR2   3' ACCCTGTCATTACGTCAACGC  2027      _  __
                        GCGT GGC  AATGACAGGGT
                        |||| |||  |||||||||||
                        CGCA CTG  TTACTGTCCCA
                          A   CA
GAM65   FGFR2   3' ACCCTGTCATTACGTCAACGC  2028      _  __
                        GCGT GGC  AATGACAGGGT
                        |||| |||  |||||||||||
                        CGCA CTG  TTACTGTCCCA
                          A   CA
GAM65   MMP19   5' ACCAAGGCTGCCACGCTCTAA  2010      T      ATGACAG
                        TTAG AGCGTGGCA      GGT
                        |||| |||||||||      |||
                        AATC TCGCACCGT      CCA
                         _       CGGAA__
GAM66   ARHGEF12 3' AATAATGTCATTCTCAATTAA  1619          TA
                        TTAATTG AATGATATTATT
                        ||||||| ||||||||||||
                        AATTAAC TTACTGTAATAA
                            TC
GAM66   OS4     3' AATATTTGTATTACTTACAATT  1239          A    TAT
              AA            TTAATTGTAA TGATAT  TATT
                        |||||||||| |||||| ||||
                        AATTAACATT ATTATG  ATAA
                            C      TTT
GAM66   LOC148289 3' AATAATAACATATACAATTAA  3300        A  A
                        TTAATTGTA ATG TATTATT
                        ||||||||| ||| |||||||
                        AATTAACAT TAC ATAATAA
                            A  A
GAM66   LOC253160 3' AATAATAACATATACAATTAA  3714        A  A
                        TTAATTGTA ATG TATTATT
                        ||||||||| ||| |||||||
```

```
                     AATTAACAT TAC ATAATAA
                          A   A
GAM67   GAN      3' TGAGTGTGGTACATTAACT  1975     A  CA      _
                   AG TAA  TACCACAC CA
                   || ||| ||||||||| ||
                   TC ATT  ATGGTGTG GT
                      A  AC      A
GAM67   IDH3A    3' AAAGAGTGAATGTGGTATATTT 1222     TAAC      C_
             CT           AGA   ATACCACA CATTTTT
                          |||   |||||||| ||||||||
                          TCT   TATGGTGT GTGAGAAA
                          TTA_      AA
GAM67   PEX1     3' AAAAAATGGTGTCTATGAATTT 749      TAA_  CC
             CT           AGA   CATA ACACCATTTTT
                          |||   |||| |||||||||||
                          TCT   GTAT TGTGGTAAAAAA
                          TTAA   C_
GAM67   PYGO2    3' AAAAATTGGGATATGTTATCT 2676        CCACA  T
                   AGATAACATA   CCA TTTTT
                   ||||||||||   ||| |||||
                   TCTATTGTAT   GGT AAAAA
                        AG___  T
GAM67   FLJ21477 3' TGGCGTGAGATGTTATCT   2142       AC  A
                   AGATAACAT CAC CCA
                   ||||||||| ||| |||
                   TCTATTGTA GTG GGT
                        GA   C
GAM67   NS1-BP   3' AAAAAATGGTGTTTTATCT  2953      CATACC
                   AGATAA    ACACCATTTTT
                   ||||||    |||||||||||
                   TCTATT    TGTGGTAAAAAA
                        T_____
GAM67   UNC5D    5' AAAAAAGCTGTAATATGTTATC 2391        CC  CCA
              T          AGATAACATA ACA  TTTTTT
                         |||||||||| |||  ||||||
                         TCTATTGTAT TGT  AAAAAA
                              AA  CG_
GAM67   LOC257451 3' AAAAATTGGGATATGTTATCT 3678        CCACA  T
                   AGATAACATA   CCA TTTTT
                   ||||||||||   ||| |||||
                   TCTATTGTAT   GGT AAAAA
                        AG___  T
GAM68   CHAC     3' TGCCCATATGTCCATTTAT  1612            AGAT
                   ATAAGTGGACATAT  GCA
                   ||||||||||||||  |||
                   TATTTACCTGTATA  CGT
                        CC__
GAM68   GGCX     3' CTGCACCCTGCCACTTGT   778       A TATAGA
                   ATAAGTGG CA    TGCAG
                   |||||||| ||    |||||
```

```
                          TGTTCACC GT    ACGTC
                        _ CCC___
GAM68   ITPKB   3' TCTGCATCTGTCCAC    911         TATA
                        GTGGACA   GATGCAGA
                        |||||||   ||||||||
                        CACCTGT   CTACGTCT
                           ____
GAM68   KCNAB1  3' TCTAATGTTATGTCCACTTA 2584              ____
                        TAAGTGGACATA   TAGA
                        |||||||||||  ||||
                        ATTCACCTGTAT   ATCT
                           TGTA
GAM68   KLRC4   5' CTGTCAAAATATACACCACTTA 1451        ACA   GA_ _
                T              ATAAGTGG   TATA   TG CAG
                        ||||||||  ||||  || |||
                        TATTCACC   ATAT   AC GTC
                         AC_   AAA  T
GAM68   MLF2    3' TCTGCATCTACTGACTTG   1212      _ ACATA
                        TAAGT GG   TAGATGCAGA
                        |||||| ||   ||||||||||
                        GTTCA TC   ATCTACGTCT
                           G _____
GAM68   NR1I2   3' TCTGCATCCATTTGAACAC  1067    GA  T A
                        GTG  CA AT GATGCAGA
                        ||| || || |||||||||
                        CAC  GT TA CTACGTCT
                         AA  T C
GAM68   NR1I2   3' TCTGCATCCATTTGAACAC  1971    GA  T A
                        GTG  CA AT GATGCAGA
                        ||| || || |||||||||
                        CAC  GT TA CTACGTCT
                         AA  T C
GAM68   CEP3    3' TTCTACATCAGATGTTGTCACT 1304         __    ATA   C
            TAT               ATAAGTG  GACAT   GATG AGAA
                        ||||||| |||||  |||| ||||
                        TATTCAC  TTGTA   CTAC TCTT
                         TG   GA_  A
GAM68   FHX     3' TCATGGATCATGTCCAC     1825       ATA  G _
                        GTGGACAT  GAT CA GA
                        ||||||||  ||| || ||
                        CACCTGTA  CTA GT CT
                           ___  G A
GAM68   FLJ10352 3' TTCTGCATCTACAACTCAACAT 2233      GACATA__
            TTA             TAAGTG    TAGATGCAGAA
                        ||||||       |||||||||||
                        ATTTAC       ATCTACGTCTT
                         AACTCAAC
GAM68   FLJ22127 3' TCGAGTCCATATGTCCAC   2008       A  GCA
                        GTGGACATAT GAT  GA
                        |||||||||| ||| ||
```

```
                            CACCTGTATA CTG  CT
                              C  AG_
GAM68   GDAP1L1 3' TCTGCATCCATGCCAC    2043      A  ATA
                            GTGG CAT  GATGCAGA
                            |||| ||| ||||||||
                            CACC GTA  CTACGTCT
                              _  C__
GAM68   H-L(3)MBT 3' TCTGCTCTCTACCCACT    2230      ACA T  T
                            AGTGG  TA AGA GCAGA
                            |||||  || ||| |||||
                            TCACC  AT TCT CGTCT
                               C__ C  _
GAM68   KIAA1340 3' TCTAAGCTATGCCCATTTAT 2846          A   ___
                            ATAAGTGG CATA  TAGA
                            |||||||| ||||  ||||
                            TATTTACC GTAT  ATCT
                               C  CGA
GAM68   KNSL7   3' TTCTGCATCCATATACACCCT 1905    T AC_  A
                            AG GG  ATAT GATGCAGAA
                            || ||  |||| |||||||||
                            TC CC  TATA CTACGTCTT
                              _ ACA   C
GAM68   P5-1    3' CTCCATTTATGTACCCAC    1322    AC      C
                            GTGG  ATATAGATG AG
                            ||||  ||||||||| ||
                            CACC  TGTATTTAC TC
                               CA      C
GAM68   PP1044  5' CTGCATCTTTACCTATATCCAT 1956       C  T____
            TTA              TAAGTGGA ATA   AGATGCAG
                            ||||||||| |||   ||||||||
                            ATTTACCT TAT    TCTACGTC
                              A  CCATT
GAM68   SIRPB1  3' TGCATGTGTCCACTTA      1272          ATAG
                            TAAGTGGACAT   ATGCA
                            |||||||||||   |||||
                            ATTCACCTGTG   TACGT
                               ____
GAM68   LOC148811 3' CTGCATCTCTCCCCTTA    3126     T  CATAT
                            TAAG GGA   AGATGCAG
                            |||| |||   ||||||||
                            ATTC CCT   TCTACGTC
                               C  C____
GAM68   LOC149711 3' TCCATATGTCTATCCACTTA 3315         ____  A
                            TAAGTGGA  CATAT GA
                            ||||||||  ||||| ||
                            ATTCACCT  GTATA CT
                              ATCT    C
GAM68   LOC150630 5' CTGCATCTTCTGCCACT    3332      A TAT
                            AGTGG CA  AGATGCAG
                            ||||| ||  ||||||||
```

```
                              TCACC GT  TCTACGTC
                              _  CT_
GAM68   LOC150819 5' CTGCATTTTAGTCCAACT   3333    _  ATAT
                        AGT GGAC   AGATGCAG
                        ||| |||  ||||||||
                        TCA CCTG   TTTACGTC
                         A  AT__
GAM68   LOC154877 3' TCTGCATCCATTCCACT   3373      CAT A
                        AGTGGA  AT GATGCAGA
                        ||||||  || ||||||||
                        TCACCT  TA CTACGTCT
                            ___ C
GAM68   LOC158327 3' TTCTGCAGGGACACCACTTAT 3216       ACATATAGA
                        ATAAGTGG    TGCAGAA
                        ||||||||    |||||||
                        TATTCACC    ACGTCTT
                          ACAGGG___
GAM68   LOC196540 3' TCTGCATCCATGTACTCC   3467    C_  A
                        GGA  ATAT GATGCAGA
                        |||  |||| |||||||||
                        CCT  TGTA CTACGTCT
                         CA   C
GAM68   LOC220394 5' TCTCAGAATATGTCCAT   3581        AGA  C
                        GTGGACATAT  TG AGA
                        ||||||||||  || |||
                        TACCTGTATA  AC TCT
                            AG_  _
GAM68   LOC254428 3' CTGTTGACCCATGTCCACCTAT 3677    A      ATAGAT
                        ATA GTGGACAT    GCAG
                        ||| |||||||||    ||||
                        TAT CACCTGTA    TGTC
                          C      CCCAGT
GAM68   LOC92405 3' TTCTGTTACACATGTCTACTTA 2848          ATAGAT
                        TAAGTGGACAT    GCAGAA
                        ||||||||||||    ||||||
                        ATTCATCTGTA    TGTCTT
                          CACAT_
GAM69   DKFZP434G1411 3' TAGGTTGATACATGTATCA  3554           AA
                        TGATACATGTATTAA  TA
                        |||||||||||||||  ||
                        ACTATGTACATAGTT  AT
                            GG
GAM69   DKFZP564I052 3' GAAAGTATTCCTATCATGTAT  2760      T TAA
                        ATACATG AT  AATACTTTC
                        ||||||| ||  |||||||||
                        TATGTAC TA  TTATGAAAG
                          _ TCC
GAM69   KLHL8   3' AAAGTATTTGTTACATAATCA  2639    AC   TTA
                        TGAT ATGTA  AAATACTTT
                        |||| |||||  ||||||||||
```

```
                          ACTA TACAT TTTATGAAA
                          A_    TG_
GAM69   XLKD1    3' AAAGTGCCATTAACAAATGTAT 1323      GTA  AA_
           CA              TGATACAT TTAA TACTTT
                           ||||||| |||| ||||||
                           ACTATGTA AATT GTGAAA
                                AAC   ACC
GAM69   LOC51003 3' GAGGCACTTAATACATGTAT 1658            AATA
                        ATACATGTATTAA  CTT
                        |||||||||||| |||
                        TATGTACATAATT  GAG
                               CACG
GAM70   NEU3     3' ATGATTTGTTCCATTTTTA 1319        TA
                       TAAAAAT AACAAATCGT
                       ||||||| |||||||||
                       ATTTTTA TTGTTTAGTA
                              CC
GAM70   CHPT1    3' AACATTTGTTTAATTTTTA 1906            C
                      TAAAAATTAAACAAAT GTT
                      ||||||||||||||| |||
                      ATTTTTAATTTGTTTA CAA
                               _
GAM70   LOC143310 3' AATTTGTGATTTGTTTAATTT 3057           TT_
                      AAATTAAACAAATCG ATT
                      |||||||||||||| |||
                      TTTAATTTGTTTAGT TAA
                             GTT
GAM70   LOC152578 5' TAATAACAAATGTTTAATTTTT 3361          AATC
           A             TAAAAATTAAACA  GTTATTA
                         ||||||||||||  |||||||
                         ATTTTTAATTTGT  CAATAAT
                             AAA_
GAM71   HNF3A    3' ACAGCATAATAAAATCC    2543      C GTT
                      GGATT TGT  TATGCTGT
                      ||||| ||| ||||||||
                      CCTAA ATA  ATACGACA
                            A  ___
GAM71   MUC12    3' AGCTGCAAACACAGAGCCCA 3643     AT    TA T
                       TGG  TCTGTGTT TGC GTT
                       |||  |||||||| ||| |||
                       ACC  AGACACAA ACG CGA
                            CG      __  T
GAM71   OGN      3' ACAGCATTACAAAATCC    2307      C  TTT
                      GGATT TGTG  ATGCTGT
                      ||||| |||| |||||||
                      CCTAA ACAT  TACGACA
                            A  ___
GAM71   OGN      3' ACAGCATTACAAAATCC    1467      C  TTT
                      GGATT TGTG  ATGCTGT
                      ||||| |||| |||||||
```

```
                              CCTAA ACAT  TACGACA
                                 A      ___
GAM71    OGN     3' ACAGCATTACAAAATCC    2059     C   TTT
                              GGATT TGTG  ATGCTGT
                              ||||| ||||  |||||||
                              CCTAA ACAT  TACGACA
                                 A      ___
GAM71    PTPRA   3' AGATAAACACAAAATCCAT  962        C        G
                              ATGGATT TGTGTTTAT CT
                              ||||||| ||||||||| ||
                              TACCTAA ACACAAATA GA
                                 A        _
GAM71    PTPRA   3' AGATAAACACAAAATCCAT  2389       C        G
                              ATGGATT TGTGTTTAT CT
                              ||||||| ||||||||| ||
                              TACCTAA ACACAAATA GA
                                 A        _
GAM71    PTPRA   3' AGATAAACACAAAATCCAT  2390       C        G
                              ATGGATT TGTGTTTAT CT
                              ||||||| ||||||||| ||
                              TACCTAA ACACAAATA GA
                                 A        _
GAM71    TIRAP   3' AGCTAGAAACAGAAAACCCAT 2344     A__    G   T
                              ATGG  TTCTGT TTTA GCT
                              ||||  |||||| |||| |||
                              TACC  AAGACA AGAT CGA
                                CAA      A    _
GAM71    ATF3    3' AGCGTTAACACAAAATCCAT  1080       C    T
                              ATGGATT TGTGTT ATGCT
                              ||||||| |||||| |||||
                              TACCTAA ACACAA TGCGA
                                 A    T
GAM71    FLJ22457 3' AACATCTTCAACACAGAACACA 2106    GA       TATGC
                              TG TTCTGTGTT   TGTT
                              || |||||||||   ||||
                              AC AAGACACAA   ACAA
                                AC    CTTCT
GAM71    LIPG    3' AGCCTAAACACAAAATTCAT   1266      C     T
                              ATGGATT TGTGTTTA GCT
                              ||||||| |||||||| |||
                              TACTTAA ACACAAAT CGA
                                 A       C
GAM71    MGC4643  3' AACAGCATAAACAGCTGGACC  2271    A T _
                              GG TTC G TGTTTATGCTGTT
                              || ||| | |||||||||||||
                              CC AGG C ACAAATACGACAA
                                _  T G
GAM71    LOC143888 3' AGTCTAAACACAAAATTCAT  3064      C    T
                              ATGGATT TGTGTTTA GCT
                              ||||||| |||||||| |||
```

```
                                 TACTTAA ACACAAAT TGA
                                  A          C
GAM71   LOC149619 5'  AACATCTTCAACACAGAACACA 3311      GA        TATGC
                          TG TTCTGTGTT    TGTT
                          II IIIIIIIII    IIII
                          AC AAGACACAA    ACAA
                           AC         CTTCT
GAM71   LOC91464 5'  AACAGCATAAAGGACCCCA  2740      AT  GTG
                          TGG TCT  TTTATGCTGTT
                          III III  IIIIIIIIIII
                          ACC AGG  AAATACGACAA
                            CC  ___
GAM72   CLDN1    3'  ATATTAATTAGTTTATATTA  1940            _
                          TAATATAAACTAAT AATAT
                          IIIIIIIIIIIII IIIII
                          ATTATATTTGATTA TTATA
                              A
GAM72   KIAA1706 3'  ACAGTGTTCATAGTTTATATTA 3577           ATAAT
                          TAATATAAACTA    ATATTGT
                          IIIIIIIIIII    IIIIIII
                          ATTATATTTGAT    TGTGACA
                             ACT__
GAM73   B3GALT5  3'  GTGCTGAAATCCACGCCAGA  2317    A    A_ T
                          TCT GCGTGGAT CAG CAC
                          III IIIIIIII III III
                          AGA CGCACCTA GTC GTG
                             C    AA  _
GAM73   B3GALT5  3'  GTGCTGAAATCCACGCCAGA  1268    A    A_ T
                          TCT GCGTGGAT CAG CAC
                          III IIIIIIII III III
                          AGA CGCACCTA GTC GTG
                             C    AA  _
GAM73   B3GALT5  3'  GTGCTGAAATCCACGCCAGA  2318    A    A_ T
                          TCT GCGTGGAT CAG CAC
                          III IIIIIIII III III
                          AGA CGCACCTA GTC GTG
                             C    AA  _
GAM73   B3GALT5  3'  GTGCTGAAATCCACGCCAGA  2319    A    A_ T
                          TCT GCGTGGAT CAG CAC
                          III IIIIIIII III III
                          AGA CGCACCTA GTC GTG
                             C    AA  _
GAM73   B3GALT5  3'  GTGCTGAAATCCACGCCAGA  2321    A    A_ T
                          TCT GCGTGGAT CAG CAC
                          III IIIIIIII III III
                          AGA CGCACCTA GTC GTG
                             C    AA  _
GAM73   MEF2A    3'  GTGACTGTAGTTACTTAAGA  1229    C  C  A
                          TCT TAG GTGG TACAGTCAC
                          III III IIII IIIIIIII
```

```
                    AGA ATT CATT ATGTCAGTG
                     _  _   G
GAM73  ORC2L    3' GTGAGAAGCCAGGCTAGAGA  1278        G  ATACAG
                   TCTCTAGC TGG    TCAC
                   |||||||| |||    ||||
                   AGAGATCG ACC    AGTG
                    G  GAAG__
GAM73  PART1    3' CGGTGACTATATGAGAATGGA  1699        GCGTGG  C
                   TCTA    ATA AGTCACCG
                   ||||    ||| ||||||||
                   AGGT    TAT TCAGTGGC
                    AAGAG_  A
GAM73  SLC10A1  3' GTGACTGTAAACTCTATG  989           ___
                   CGTGGA  TACAGTCAC
                   ||||||  |||||||||
                   GTATCT  ATGTCAGTG
                    CAA
GAM73  FUSIP1   3' GTGACTGTAATATACTAGAG  1314        CG GA
                   CTCTAG TG TACAGTCAC
                   |||||| || |||||||||
                   GAGATC AT ATGTCAGTG
                    AT A_
GAM73  RAI17    3' GTGACTGTGGAGCCTGAGA  3515       T C GGA
                   TCTC AG GT  TACAGTCAC
                   |||| || ||  |||||||||
                   AGAG TC CG  GTGTCAGTG
                    _ _ AG_
GAM73  LOC115811 5' GGTAACTGTGGCTAGGGA  2442         GTGGA    C
                   TCTCTAGC   TACAGT ACC
                   ||||||||   |||||| |||
                   AGGGATCG   GTGTCA TGG
                    _____       A
GAM73  LOC256946 3' GTGACTGTAATATACTAGAG  3657       CG GA
                   CTCTAG TG TACAGTCAC
                   |||||| || |||||||||
                   GAGATC AT ATGTCAGTG
                    AT A_
GAM74  PEX3     3' AATATAGATATTTTATATAC  1044        ___
                   GTATGTA  TATCTATATT
                   |||||||  ||||||||||
                   CATATAT  ATAGATATAA
                    TTT
GAM74  PKD2L2   3' TTAATATGAGACATACTG  1497         ATATC
                   CAGTATGT  TATATTAA
                   ||||||||  ||||||||
                   GTCATACA  GTATAATT
                    GA___
GAM74  BA108L7.2 3' ATGCATATACATACATGATA  2179     _      C
                   TATCA GTATGTATAT TAT
                   ||||| ||||||||||| |||
```

```
                              ATAGT CATACATATA GTA
                                  A         C
GAM74    IDI1     3' TTAATGTATTATATACACTGAT 2776        A    TC
      A                       TATCAGT TGTATA  TATATTAA
                              ||||||| |||||| ||||||||
                              ATAGTCA ATATAT  ATGTAATT
                                  C    T_
GAM74    PRO0899  5' AGTGTTTTACACATACTGAT 1846         A TCT
                              ATCAGTATGT TA  ATATT
                              ||||||||||| ||  |||||
                              TAGTCATACA AT  TGTGA
                                  C TT_
GAM74    SEC14L1  3' TGGTAATACAATACTGATA  980          _  AT
                              TATCAGTAT GTAT  CTA
                              ||||||||| ||||  |||
                              ATAGTCATA CATA  GGT
                                   A   AT
GAM74    LOC130074 3' TTAACATAGAATGTTTACTGAT 3045       TG  A   A
      A                       TATCAGTA TAT TCTAT TTAA
                              |||||||| ||| ||||| ||||
                              ATAGTCAT GTA AGATA AATT
                                  TT  _    C
GAM74    LOC222159 5' AGACCATGCATACTGATA    3633          A_
                              TATCAGTATGTAT TCT
                              ||||||||||||| |||
                              ATAGTCATACGTA AGA
                                   CC
GAM75    RNF28    3' AAGGAACTTTTGTATAATA  2263          A
                              TATTATACAAAA TTTTTT
                              |||||||||||| ||||||
                              ATAATATGTTTT AAGGAA
                                   C
GAM75    SWAP70   3' GAAATAAAAATTATTTGTATAA 2916        AAT
      T                       ATTATACAAA  TTTTTATTTC
                              ||||||||||  ||||||||||
                              TAATATGTTT  AAAAATAAAG
                                   ATT
GAM75    bA430M15.1 3' AAAAATTTTTGTATAATG   3072
                              TATTATACAAAAATTTTT
                              ||||||||||||||||||
                              GTAATATGTTTTTAAAAA


GAM76    PSG1     3' TTTGATTCGGATGTTATA   1337         GT
                              TATAACATC AATCAAA
                              |||||||||  |||||||
                              ATATTGTAG TTAGTTT
                                   GC
GAM76    RALB     3' TTTTGAACTACAGATGTTGTA 968          _  A_
                              TATAACATC GTA  TCAAAA
                              ||||||||| |||  ||||||
```

```
                          ATGTTGTAG CAT AGTTTT
                          A   CA
GAM76   CEACAM8  3' TTTGATTGGGATGTTATA   859          G
                          TATAACATC TAATCAAA
                          ||||||||| ||||||||
                          ATATTGTAG GTTAGTTT
                          G
GAM76   LAT1-3TM  3' TTTTGGTGGCTCGATGTTA   2183         TA__
                          TAACATCG   ATCAAAA
                          ||||||||   |||||||
                          ATTGTAGC   TGGTTTT
                          TCGG
GAM76   LAT1-3TM  5' TTTTGGTGGCTCGATGTTA   2827         TA__
                          TAACATCG   ATCAAAA
                          ||||||||   |||||||
                          ATTGTAGC   TGGTTTT
                          TCGG
GAM76   MCFP     5' TTTTGGCTACTGATGTTA   1863        _ AT
                          TAACATC GTA CAAAA
                          ||||||| ||| |||||
                          ATTGTAG CAT GTTTT
                          T   CG
GAM76   MGC26651 3' TTTTGATGTGAAAGATGTTATA 2489         GTA___
                          TATAACATC    ATCAAAA
                          |||||||||    |||||||
                          ATATTGTAG    TAGTTTT
                          AAAGTG
GAM76   LOC197423 5' TTTTGGTGGCTCGATGTTA  3090         TA__
                          TAACATCG   ATCAAAA
                          ||||||||   |||||||
                          ATTGTAGC   TGGTTTT
                          TCGG
GAM76   LOC220565 5' TTTTGGTGGCTCGATGTTA  3495         TA__
                          TAACATCG   ATCAAAA
                          ||||||||   |||||||
                          ATTGTAGC   TGGTTTT
                          TCGG
GAM77   FLJ13215 3' GAATATTCTACCTAAATAT   2126      G  A
                          ATA TTAG TAGAATATTC
                          ||| |||| ||||||||||
                          TAT AATC ATCTTATAAG
                          A   C
GAM77   PTP4A1   3' CTAATGAATTGAGCACATCTAA 1027        AGAAT__
             T              GTTAGAT   ATTCATTAG
                          ||||||||   |||||||||
                          TAATCTA    TAAGTAATC
                          CACGAGT
GAM77   SDFR1    3' TGGTAATATTCTATGCAACTAT 1430      AG      C
                          ATAGTT ATAGAATATT ATTA
                          |||||| |||||||||| ||||
```

```
                    TATCAA TATCTTATAA TGGT
                         CG          _
GAM77  SDFR1     3' TGGTAATATTCTATGCAACTAT 1718       AG      C
                    ATAGTT ATAGAATATT ATTA
                    ||||||| |||||||||| ||||
                    TATCAA TATCTTATAA TGGT
                         CG          _
GAM77  LOC221133 3' CTAATGAAGAGAATATTTAAC 3608          GAATA
                    GTTAGATA   TTCATTAG
                    |||||||||   ||||||||
                    CAATTTAT   AAGTAATC
                        AAGAG
GAM78  DJ667H12.2 3' TTATGCCATGAACATGCCA   1884             CGATAA
                    TGGTATGTTCA   GTATAA
                    |||||||||||   |||||
                    ACCGTACAAGT   CGTATT
                         AC____
GAM78  KIAA1799  3' TTATACTTAGAACTTACCA  3003     T  ACGA
                    TGGTA GTTC   TAAGTATAA
                    ||||| ||||   |||||||||
                    ACCAT CAAG   ATTCATATT
                        T    ____
GAM78  PPP1R3B  3' TTTATGTAAACATACCA    2071       C G
                    TGGTATGTT AC ATAAG
                    ||||||||| || |||||
                    ACCATACAA TG TATTT
                         A _
GAM78  LOC144840 3' ATTTCTCGTGAACACCCA   3071    TA      T
                    TGG TGTTCACGA AAGT
                    ||| |||||||||| ||||
                    ACC ACAAGTGCT TTTA
                     C_       C
GAM78  LOC158674 3' ATTTCCCGTGAACACCCA   3222    TA      AT
                    TGG TGTTCACG AAGT
                    ||| ||||||||| ||||
                    ACC ACAAGTGC TTTA
                     C_      CC
GAM78  LOC245757 3' ATTTCCCGTGAACACCCA   3496    TA      AT
                    TGG TGTTCACG AAGT
                    ||| ||||||||| ||||
                    ACC ACAAGTGC TTTA
                     C_      CC
GAM78  LOC81034 3' ATTTATCGTAAACATCCA   2164     T   C
                    TGG ATGTT ACGATAAGT
                    ||| ||||| |||||||||
                    ACC TACAA TGCTATTTA
                     _    A
GAM79  DTNB     3' CTAATATCCAGAATCTACAAAG 2316       TA  A G
       A              TCTTT AGA TT TGGATATTAG
                    ||||| ||| || ||||||||||
```

```
                             AGAAA TCT AA ACCTATAATC
                             CA   _ G
GAM79   SP100    3' AGTAAATACAATTTTTAAAA  993              GA
                        TTTTAAGAATTGTG TATT
                        IIIIIIIIIIIIII IIII
                        AAAATTTTTAACAT ATGA
                                   AA
GAM79   KIAA1229 3' AATATCCAGAATCTACAAAGA 2620      TA  A G
                        TCTTT AGA TT TGGATATT
                        IIIII III II IIIIIIII
                        AGAAA TCT AA ACCTATAA
                             CA   _ G
GAM79   LOC144776 3' AATATTCAATATTCTTAAAGA 3070      T    TG
                        TCTTT AAGAAT TGGATATT
                        IIIII IIIIII IIIIIIII
                        AGAAA TTCTTA ACTTATAA
                             _      TA
GAM79   LOC199775 5' CTAATTCTTCAATTCTTAA  3432      T  T
                        TTAAGAATTG GGA ATTAG
                        IIIIIIIIII III IIIII
                        AATTCTTAAC TCT TAATC
                             T  _
GAM79   LOC222236 3' GTCTACAATTCCCAAAAGA  3651      AA
                        TCTTTT GAATTGTGGAT
                        IIIIII IIIIIIIIIII
                        AGAAAA CTTAACATCTG
                             CC
GAM80   CHRNA1   3' TTATTATTGATGATAAGA    701       C    _
                        TCT ATCATCAG AATAA
                        III IIIIIIII IIIII
                        AGA TAGTAGTT TTATT
                            A    A
GAM80   TNFSF9   3' ATTTATTCTGAGCCTGAG   1062       TCA
                        CTCA TCAGAATAAAT
                        IIII IIIIIIIIIII
                        GAGT AGTCTTATTTA
                            CCG
GAM80   AKT3     3' ATTTATTTTTTAGTGATGAGAA 1214              C__
                        TTCTCATCAT AGAATAAAT
                        IIIIIIIIII IIIIIIIII
                        AAGAGTAGTG TTTTATTTA
                             ATT
GAM80   FLJ10103 3' TTGTTTACTGATGAGAA    1773              TCA
                        TTCTCATCA GAATAA
                        IIIIIIIII IIIIII
                        AAGAGTAGT TTTGTT
                             CA_
GAM80   FLJ22582 3' TTTTGTAAATGATGAGAA   2132              ___
                        TTCTCATCAT CAGAA
                        IIIIIIIIII IIIII
```

```
                         AAGAGTAGTA  GTTTT
                                AAT
GAM80   KIAA1371 3' ATTCTAGAAATGGTGAGAA  3454        __ _
                         TTCTCATCA  TC AGAAT
                         |||||||||| || |||||
                         AAGAGTGGT  AG TCTTA
                                AA  A
GAM80   MACF1    3' ATTTATTCTGAACGGGAGAA  2308      ATCA
                         TTCTC   TCAGAATAAAT
                         |||||   ||||||||||
                         AAGAG   AGTCTTATTTA
                              GGCA
GAM80   MACF1    3' ATTTATTCTGAACGGGAGAA  1403      ATCA
                         TTCTC   TCAGAATAAAT
                         |||||   ||||||||||
                         AAGAG   AGTCTTATTTA
                              GGCA
GAM80   MGC16824 3' TTATTCTGACAATGAAGA  1910      _ CA
                         TCT CAT  TCAGAATAA
                         ||| |||  |||||||||
                         AGA GTA  AGTCTTATT
                           A  AC
GAM80   NR2C1    3' ATTTATTCTTGGTGAAGA  1006     A    _
                         TC TCATCA GAATAAAT
                         || |||||| ||||||||
                         AG AGTGGT CTTATTTA
                           A    T
GAM80   P450RAI-2 3' ATTTATTCACTGATAGAGAA  1887     _ TCA
                         TTCTC ATCA  GAATAAAT
                         ||||| ||||  ||||||||
                         AAGAG TAGT  CTTATTTA
                           A   CA_
GAM80   LOC152715 5' ATTTGGCTGATGATGGAA  3174     T     AA
                         TTC CATCATCAG TAAAT
                         ||| ||||||||| |||||
                         AAG GTAGTAGTC GTTTA
                           _    G_
GAM80   LOC222166 3' ATTCTGTGGGCTGATGAGAA  3634          T____
                         TTCTCATCA   CAGAAT
                         ||||||||||   ||||||
                         AAGAGTAGT    GTCTTA
                                CGGGT
GAM80   LOC257042 3' ATTCTGAGTGATGATGAA  3719     _    _
                         TTC TCATCA TCAGAAT
                         ||| |||||| |||||||
                         AAG AGTAGT AGTCTTA
                           T   G
GAM81   CORO2B   5' TTCTGTTGCCCAAGCTGG  2694     _ GAG  TAAA
                         CC GCT  TGG   CAACAGAA
                         || ||| |||   |||||||
```

```
                              GG CGA  ACC   GTTGTCTT
                              T  ___  C___
GAM81   EFNB2   3' GTTCTGTTACCCAGGGCTCTGC 1084    T  ____    AACA
                              GC GAGT  GGTA   ACAGAAC
                              || |||| |||| |||||||
                              CG CTCG  CCAT  TGTCTTG
                              T  GGAC  ____
GAM81   GCGR    5' TCTGCTGCTCTGCCACTCAGC 714          AA_ A
                              GCTGAGTGGTA  CA CAGA
                              ||||||||||| || ||||
                              CGACTCACCGT  GT GTCT
                                    CTC  C
GAM81   HMOX1   3' GTTCTGTTGTTTTTATAGCAGG 901      G  AGTGGT
            G                 CC CTG   AAACAACAGAAC
                              || ||| |||||||||||
                              GG GAC   TTTGTTGTCTTG
                               _  GATATT
GAM81   HS3ST2  3' GTTCTGTTGCTATGAACACAGC 1267    A GGTAAA
                              GCTG GT   CAACAGAAC
                              |||| || ||||||||||
                              CGAC CA   GTTGTCTTG
                                A AGTATC
GAM81   PIM2    3' CTGTTGTTACCCCAAGG     2550    GC AGT   A
                              CC TG  GGTAA CAACAG
                              || || |||| ||||||
                              GG AC  CCATT GTTGTC
                                A_ C__    _
GAM81   PIP5K1B 5' TCTGTTGCTACTAAGC     1034     G  TAAA
                              GCT AGTGG   CAACAGA
                              ||| ||||| |||||||
                              CGA TCATC   GTTGTCT
                                A  ____
GAM81   RBM3    3' TTCTGTTGTGTCTCATACAG 2887     A  TAA
                              CTG GTGG  ACAACAGAA
                              ||| |||| |||||||||
                              GAC TACT  TGTTGTCTT
                                A  CTG
GAM81   SMAC    3' CTGTCTCCCCACTCAGTGG  1889          TAAACA
                              CCGCTGAGTGG   ACAG
                              |||||||||||   ||||
                              GGTGACTCACC   TGTC
                                  CCTC__
GAM81   SMAC    3' CTGTCTCCCCACTCAGTGG  2459          TAAACA
                              CCGCTGAGTGG   ACAG
                              |||||||||||   ||||
                              GGTGACTCACC   TGTC
                                  CCTC__
GAM81   SMAC    3' CTGTCTCCCCACTCAGTGG  2460          TAAACA
                              CCGCTGAGTGG   ACAG
                              |||||||||||   ||||
```

```
                    GGTGACTCACC    TGTC
                         CCTC__
GAM81   SOST    3'  TTCTGCCCACCACTCACGG 2148    C     AAACAA
                    CCG TGAGTGGT    CAGAA
                    ||| |||||||     |||||
                    GGC ACTCACCA    GTCTT
                     _      CCC___
GAM81   ZNF10   5'  TCTGCTGTCACTCAAGG  1626    GC    GTAA  A
                    CC TGAGTG   ACA CAGA
                    || ||||||   ||| ||||
                    GG ACTCAC   TGT GTCT
                     A_     ____    C
GAM81   ABCA10  5'  TTCTGTTAGTTACTCA    2373       GTAA  _
                    TGAGTG   AC AACAGAA
                    ||||||   || |||||||
                    ACTCAT   TG TTGTCTT
                       ____     A
GAM81   H2AFJ   3'  GTTCTGCTATTTACTCTGTGG 1807    T    TAAACAA
                    CCGC GAGTGG    CAGAAC
                    |||| ||||||    ||||||
                    GGTG CTCATT    GTCTTG
                       T    TATC___
GAM81   HSH2    3'  GTTCTGTTGTCTAAAAGC  2289    GAG  TAA
                    GCT  TGG  ACAACAGAAC
                    |||  |||  ||||||||||
                    CGA  ATC  TGTTGTCTTG
                     AA_     ___
GAM81   KIAA1024 3' TTCTGTTGTTCACCATTAAGGG 2841   G  G    A
          G              CC CT AGTGGT AACAACAGAA
                    || || |||||| ||||||||||
                    GG GA TTACCA TTGTTGTCTT
                      G  A    C
GAM81   KIAA1399 3' GTTCTGCTATTTCCAATCAGTC 2881   C   G  T  CAA
          A              C GCTGA TGG AAA  CAGAAC
                    | ||||| ||| |||  ||||||
                    A TGACT ACC TTT  GTCTTG
                     C   A  _  ATC
GAM81   MIC2L1  3'  TCTGTTGTCAGAGGCTCACGG 2205    C    GGTAA
                    CCG TGAGT    ACAACAGA
                    ||| |||||    ||||||||
                    GGC ACTCG    TGTTGTCT
                      _     GAGAC
GAM81   RASGRF2 3'  TTCTGTTAGAACTCAGGG  2590    G    GGTAAAC
                    CC CTGAGT    AACAGAA
                    || ||||||    |||||||
                    GG GACTCA    TTGTCTT
                     _    AGA____
GAM81   TJP2    3'  CTGTTACTTGCTTCAGTGG  2534       GT    AC
                    CCGCTGA GGTAA AACAG
                    ||||||| ||||| |||||
```

```
                              GGTGACT TCGTT TTGTC
                              __    CA
GAM81   LOC202020 3' TTCTGTTGCCTAAGGCAGC 3459     AG_ TAAA
                       GCTG TGG  CAACAGAA
                       |||| |||  ||||||||
                       CGAC ATC  GTTGTCTT
                        GGA C___
GAM81   LOC220766 5' TCTGGATTTCACCACTCAGAGG 3499    G      AAACAA
                      CC CTGAGTGGT    CAGA
                      || |||||||||    ||||
                      GG GACTCACCA    GTCT
                      A       CTTTAG
GAM81   LOC256277 3' CTGTTGTTCAGCAGTG     3664     AG TAA
                      CGCTG TGG  ACAACAG
                      ||||| |||  |||||||
                      GTGAC ACT  TGTTGTC
                        G_  ___
GAM81   LOC256337 3' CTGTTGTTCAGCAGTG     3663     AG TAA
                      CGCTG TGG  ACAACAG
                      ||||| |||  |||||||
                      GTGAC ACT  TGTTGTC
                        G_  ___
GAM82   PTCRA    3' ATGACTGAGAACATTAAA   2433      ATC
                     TTTAAT CTCAGTCAT
                     |||||| |||||||||
                     AAATTA GAGTCAGTA
                        CAA
GAM82   PUNC    3' ATGACTTGGAACTGAACTAAC 3469       ATA TC
                    GTTAGTTTA TCC AGTCAT
                    ||||||||| ||| ||||||
                    CAATCAAGT AGG TCAGTA
                      CA_ T_
GAM82   KIAA0940 3' ACTGATATATTATAAACTAAC 1586        __  CC
                     GTTAGTTTA ATAT TCAGT
                     ||||||||| |||| |||||
                     CAATCAAAT TATA AGTCA
                       AT  T_
GAM82   RGS18   3' ATGACTGAGAATAAGATCCAC 2398   TA AA C
                    GT GTTT TAT CTCAGTCAT
                    || |||| ||| |||||||||
                    CA TAGA ATA GAGTCAGTA
                     CC  __  A
GAM83   ATP12A  3' CCCTGCAGTGCAGACATCGTCA 846       A A C TT
          A               TTGATGAT TCT CAT GT GG
                          |||||||| ||| ||| || ||
                          AACTGCTA AGA GTG CG CC
                            C  C  A TC
GAM83   CRYGS   3' CCAAATAGGCATCATCAA    1722      AT ACATC
                    TTGATGAT CT  GTTTGG
                    |||||||| ||  ||||||
```

```
                          AACTACTA GA    TAAACC
                          CG    _____
GAM83   LPIN2    3' TCCAAAGTTAATTGTAAACATC 1514        ATC   TCG___
        ATCAG                  TTGATGAT TACA   TTTGGA
                          ||||||| |||   ||||||
                          GACTACTA ATGT   AAACCT
                           CAA   TAATTG
GAM83   KIAA1786 3' TCCATGCTGTAGATACCA   2738      A     TC T
                        TG TATCTACA GT TGGA
                        || ||||||| || ||||
                        AC ATAGATGT CG ACCT
                         C     __ T
GAM83   LOC222008 3' CCAAGTTAGATGTCATCAA   3629           CATCG
                        TTGATGATATCTA   TTTGG
                        ||||||||||||   |||||
                        AACTACTGTAGAT   GAACC
                            T____
GAM83   LOC90639 5' TCTGAACACAGATATCATCAG 2663          ACATC  TG
                        TTGATGATATCT   GTT GA
                        |||||||||||   ||| ||
                        GACTACTATAGA   CAA CT
                           CA___   GT
GAM84   AP1B1    3' GTCAGGATTGAAAGCTG    803      C ATA
                        TAGCTTTCA TC  TGAC
                        ||||||||| ||  ||||
                        GTCGAAAGT AG  ACTG
                           T G__
GAM84   IQGAP1   3' GTCATTTAGAAGTGGAAGCTA 2840         _ AT_
                        TAGCTTTCACT C  ATGAC
                        ||||||||||| |  |||||
                        ATCGAAGGTGA G  TACTG
                         A ATT
GAM84   PDE6A    3' GTCATAGGATTTGAAAGCTG  744       C_ A
                        TAGCTTTCA TC TATGAC
                        ||||||||| || ||||||
                        GTCGAAAGT AG ATACTG
                         TT G
GAM84   PTEN     3' CATATAAATGTGGAGGCTA  728          TC__
                        TAGCTTTCAC  ATATG
                        ||||||||||  |||||
                        ATCGGAGGTG   TATAC
                          TAAA
GAM84   SH3GL2   3' TCATGTGGAGTGAAAGGC    985     _    _
                        GC TTTCACTC ATATGA
                        || ||||||||| ||||||
                        CG AAAGTGAG TGTACT
                          G     G
GAM84   C1orf16  3' CATGGGAAGTGAAAGCTG   1567         _ A
                        TAGCTTTCACT C TATG
                        |||||||||||| | ||||
```

```
                        GTCGAAAGTGA G GTAC
                            A G
GAM84   DKFZp547A023 3' GTCATATAAATGAGTGAAA  2956          ____
                        TTTCACTCA   TATGAC
                        |||||||||   ||||||
                        AAAGTGAGT   ATACTG
                            AAAT
GAM84   FLJ11850 5' GTCATATGTGGCAGCT    2001      T  TC
                        AGCT TCAC ATATGAC
                        |||| |||| |||||||
                        TCGA GGTG TATACTG
                            C  __
GAM84   FLJ12888 3' GTCATATTTTTGAAAGTTA  2115          CTC
                        TAGCTTTCA ATATGAC
                        ||||||||| |||||||
                        ATTGAAAGT TATACTG
                            TTT
GAM84   FLJ21596 3' GTCATTGCATGGTGAAAGC  2092      T  ___
                        GCTTTCAC CAT  ATGAC
                        |||||||| ||| |||||
                        CGAAAGTG GTA  TACTG
                          _  CGT
GAM84   KIAA1878 3' GTCACAGATTTTGAAAGCTA  3539      C__ ATA
                        TAGCTTTCA TC  TGAC
                        ||||||||| ||  ||||
                        ATCGAAAGT AG  ACTG
                          TTT AC_
GAM84   NXPH3   3' GTCATGGGAGGAAGCTA   2728      A  TA
                        TAGCTTTC CTCA  TGAC
                        |||||||| |||| ||||
                        ATCGAAGG GGGT  ACTG
                          A   __
GAM84   SS18L1  3' GTCATATGAATGTTGAGC   2719      T_  C
                        GCTT  CA TCATATGAC
                        ||||  || |||||||||
                        CGAG  GT AGTATACTG
                          TT  A
GAM84   SYT13   3' CAGATGCAGAGAAAGCTA   3605      A  _  A
                        TAGCTTTC CT CAT TG
                        |||||||| || ||| ||
                        ATCGAAAG GA GTA AC
                          A  C  G
GAM84   LOC134301 3' GTCATATGTTAAAGAGCTA  3016          CACT
                        TAGCTTT  CATATGAC
                        |||||||  ||||||||
                        ATCGAGA  GTATACTG
                          AATT
GAM84   LOC151438 3' GTCATTTCTGATGAAAGCTG  3346      C  T__
                        TAGCTTTCA TCA  ATGAC
                        ||||||||| |||  |||||
```

```
                            GTCGAAAGT AGT   TACTG
                            _         CTT
GAM84   LOC158696 3' TCATATGAAGAAAGCTA     3223        AC
                     TAGCTTTC TCATATGA
                     |||||||| ||||||||
                     ATCGAAAG AGTATACT
                            A_
GAM84   LOC221975 3' GTCATATGACAGGGCTG     3570        CAC
                     TAGCTTT  TCATATGAC
                     |||||||  |||||||||
                     GTCGGGA  AGTATACTG
                            C__
GAM84   LOC84549 3' GTCAAGTGGAAAGCTA       2256        ACT   A
                    TAGCTTTC  CAT TGAC
                    ||||||||  ||| ||||
                    ATCGAAAG  GTG ACTG
                           ___     A
GAM84   LOC90459 3' TCATATAGGGTGAAAAGC     2644         _     _
                    GCTTT CACTC ATATGA
                    ||||| ||||| ||||||
                    CGAAA GTGGG TATACT
                        A     A
GAM84   LOC90529 3' GTCTACTGGGCGAAAGCTA    2652        A   TAT
                    TAGCTTTC CTCA  GAC
                    |||||||| ||||  |||
                    ATCGAAAG GGGT  CTG
                         C   CAT
GAM85   F2RL3   3' TGGTGAAATCCTATCTCT      1074     AG      ATGTAA
                  AGA TAGGATT    CATCA
                  ||| |||||||    |||||
                  TCT ATCCTAA    GTGGT
                      CT   A_____
GAM85   RAP1B   3' ATGTTACAACTACTTT        1642        GATTA
                  GAAGTAG   TGTAACAT
                  |||||||   ||||||||
                  TTTCATC   ACATTGTA
                       A____
GAM85   SLC6A12 3' TTGCCATCCTGCTTCT        988          TAT
                  AGAAGTAGGAT GTAA
                  ||||||||||| ||||
                  TCTTCGTCCTA CGTT
                         C__
GAM85   ALDH5A1 3' TGCAAATCCTACCCCTG       799     AA    A
                  CAG GTAGGATT TGTA
                  ||| |||||||| ||||
                  GTC CATCCTAA ACGT
                     CC      _
GAM85   C20orf112 3' TGATGTTAGAATCCCAC     2379    A  ATG
                     GT GGATT  TAACATCA
                     || |||||  ||||||||
```

```
                             CA CCTAA  ATTGTAGT
                              C    G__
GAM85   DICER1    3' GATGCCACATAGTCTTGC  2152          AA
                             GTAGGATTATGT CATC
                             |||||||||| ||||
                             CGTTCTGATACA GTAG
                                  CC
GAM85   DKFZP566G1424 5' TGATGTTAGAATCCCAC    3320    A   ATG
                             GT GGATT  TAACATCA
                             || ||||| ||||||||
                             CA CCTAA  ATTGTAGT
                              C    G__
GAM85   FLJ10858   3' ATGTTTGGTCCTCCTCTG   1805     A T    TGT
                             CAGA G AGGATTA  AACAT
                             |||| | |||||||  |||||
                             GTCT C TCCTGGT  TTGTA
                              _  C      ___
GAM85   FLJ13265   3' TGATGTTACTTGCCACCTACTT 2100          ATTAT_
            C                GAAGTAGG   GTAACATCA
                             ||||||||   |||||||||
                             CTTCATCC   CATTGTAGT
                               ACCGTT
GAM85   FLJ22282   3' TGATGTGGAAACCTACTTCTG 2089         A ATGTA
                             CAGAAGTAGG TT   ACATCA
                             |||||||||| ||   |||||
                             GTCTTCATCC AA   TGTAGT
                               A GG___
GAM85   GBTS1     3' GATGTTGCCTCCTCTCCTG   2516    A T   TTAT
                             CAG AG AGGA   GTAACATC
                             ||| || ||||   ||||||||
                             GTC TC TCCT   CGTTGTAG
                              C _  C___
GAM85   KIAA0193   3' TGATGTCCTAGTCCTACCACT 1545    AA      TGTA
                             AG GTAGGATTA  ACATCA
                             || |||||||||  ||||||
                             TC CATCCTGAT  TGTAGT
                              AC      CC__
GAM85   KIAA1030   3' TGATGCCCTGTCCTCACCTCTG 3597    A _   TATGTAA
                             CAGA GT AGGAT    CATCA
                             |||| || |||||    |||||
                             GTCT CA TCCTG    GTAGT
                              C  C  TCCC___
GAM85   OR7C1     3' ATGTTTCATGCATCCATACTTC 1719         _  _   T
            TG               CAGAAGTA GGAT TATG AACAT
                             |||||||| |||| |||| |||||
                             GTCTTCAT CCTA GTAC TTGTA
                              A   C  T
GAM85   PRO2214   3' TATGTAAATCCTACTTTTG   1834            _
                             CAGAAGTAGGATT ATGTA
                             ||||||||||||| |||||
```

```
                        GTTTTCATCCTAA TGTAT
                        A
GAM85   SMCR5    3' ACATGGGGAGATCCTACCTCT 2502      A        _____
                        AGA GTAGGATT    ATGT
                        ||| ||||||||    ||||
                        TCT CATCCTAG    TACA
                        C       AGGGG
GAM85   SSH1     3' ACATTAAGTCCTACCTCTG 1869       A       __
                        CAGA GTAGGATT ATGT
                        |||| |||||||| ||||
                        GTCT CATCCTGA TACA
                        C       AT
GAM85   TERA     3' TGGATCATCTCTACTTCTG 1948        _ T G
                        CAGAAGTAG GAT AT TA
                        ||||||||| ||| || ||
                        GTCTTCATC CTA TA GT
                        T   C G
GAM85   WBSCR23  5' ATATAGTGAGACCCTATTTCT 2131           _____
                        AGAAGTAGG    ATTATGT
                        |||||||||    |||||||
                        TCTTTATCC    TGATATA
                        CAGAG
GAM85   LOC134637 3' ATGTTACATGCACCTTC    3017    AGT  AT
                        GA  AGG  TATGTAACAT
                        ||  |||  ||||||||||
                        CT  TCC  GTACATTGTA
                        ___    AC
GAM85   LOC146745 5' GATGCCGAGGACATCTTACTCC 3098    A       TATGTAA_
        TG                CAG AGTAGGAT    CATC
                        ||| ||||||||    ||||
                        GTC TCATTCTA    GTAG
                        C       CAGGAGCC
GAM85   LOC153416 3' ATGTTACAACTACTTT     2573         GATTA
                        GAAGTAG   TGTAACAT
                        |||||||   ||||||||
                        TTTCATC   ACATTGTA
                        A____
GAM85   LOC157867 5' TGATTCAACAATCTTACTCCTG 3383   A    TA  AAC
                        CAG AGTAGGAT TGT ATCA
                        ||| |||||||| ||| ||||
                        GTC TCATTCTA ACA TAGT
                        C       __  ACT
GAM85   LOC201243 5' GATGCCGAGGACATCTTACTCC 3425    A       TATGTAA_
        TG                CAG AGTAGGAT    CATC
                        ||| ||||||||    ||||
                        GTC TCATTCTA    GTAG
                        C       CAGGAGCC
GAM86   OSR1     3' CGTTAGTAAACTTACTTCATA 1188          AG_ CT
                        TATGAAGTAA TAT ACG
                        |||||||||| ||| |||
```

```
                              ATACTTCATT ATG TGC
                              CAA     AT
GAM86   PACE4    5' CGCAGGCCCTTTACTTCA   2435          TA  A
                   TGAAGTAAAG TCT CG
                   |||||||||| ||| ||
                   ACTTCATTTC GGA GC
                              CC  C
GAM86   KIAA1462 3' CGTATGATTTTATTTCATA   3522          ATC
                   TATGAAGTAAAGT TACG
                   ||||||||||| ||||
                   ATACTTTATTTTA ATGC
                              GT_
GAM86   LOC145945 3' TCATAGATACAATACTTTA   3280      AA    C
                   TGAAGTA GTATCTA GA
                   ||||||| ||||||| ||
                   ATTTCAT CATAGAT CT
                          AA    A
GAM86   LOC219401 5' TCGTGGGCCCGCACTTCATA   3580          AAAGTA
                   TATGAAGT   TCTACGA
                   ||||||||   |||||||
                   ATACTTCA   GGGTGCT
                          CGCCC_
GAM87   ABCA1    3' TGGTGGCAGTAACATGCAAC   1219      T    CA
                   GTT GCATGTTAC CTATCA
                   ||| ||||||||| ||||||
                   CAA CGTACAATG GGTGGT
                       _        AC
GAM87   CD2AP    3' ATAATGGTAATAGGAAAAC   1408      GCA    C
                   GTTT TGTTACCA TAT
                   |||| |||||||| |||
                   CAAA ATAATGGT ATA
                        AGG      A
GAM87   HHIP     5' TGACACTGGCACAACTGCAAAC 1989       T A__  CTA
           GG              CCGTTTGCA GTT CCA TCA
                   ||||||||| ||| ||| |||
                   GGCAAACGT CAA GGT AGT
                       _ CAC  CAC
GAM87   AKAP7    3' TGATAGTGTCTGCACAAC   1159      _  TGTTAC
                   GTT TGCA     CACTATCA
                   ||| ||||     ||||||||
                   CAA ACGT     GTGATAGT
                        C   CT____
GAM87   AKAP7    3' TGATAGTGTCTGCACAAC   1683      _  TGTTAC
                   GTT TGCA     CACTATCA
                   ||| ||||     ||||||||
                   CAA ACGT     GTGATAGT
                        C   CT____
GAM87   AKAP7    3' TGATAGTGTCTGCACAAC   2446      _  TGTTAC
                   GTT TGCA     CACTATCA
                   ||| ||||     ||||||||
```

```
                         CAA ACGT    GTGATAGT
                          C   CT____
GAM87   ARHGAP5 3' TTGATAATGTTGTGCAAAGG 3077     G     TTAC  C
                         CC TTTGCATG   CA TATCAA
                         || ||||||||   || ||||||
                         GG AAACGTGT   GT ATAGTT
                          _         T___    A
GAM87   C22orf19 3' TGACAGTGCAGTGCAAAC  1048        GTTAC   A
                         GTTTGCAT   CACT TCA
                         ||||||||   |||| |||
                         CAAACGTG   GTGA AGT
                            AC___     C
GAM87   DKFZp566D234 3' GACAGTGGTAAGTAAA    2611      ATG    A
                         TTTGC  TTACCACT TC
                         |||||  |||||||| ||
                         AAATG  AATGGTGA AG
                          ___          C
GAM87   FLJ11160 3' TGACAGCGAGATGCAAGC  1815      G ACCA  A
                         GTTTGCAT TT  CT TCA
                         |||||||| ||  || |||
                         CGAACGTA AG  GA AGT
                          G C___  C
GAM87   FLJ13089 5' TTGACAATGGTAATAATAAAAT 2899      GCA      CTA
           GG              CCGTTT  TGTTACCA  TCAA
                         ||||||  ||||||||  ||||
                         GGTAAA  ATAATGGT  AGTT
                          ATA        AAC
GAM87   FLJ14297 3' ATAGTTTAAACATGCAAC  2107     T     ACC
                         GTT GCATGTT  ACTAT
                         ||| ||||||| |||||
                         CAA CGTACAA  TGATA
                          _     ATT
GAM87   HSPC065 3' TGACAGTGGTAGAATAAAGG  1483     G   CATG    A
                         CC TTTG   TTACCACT TCA
                         || ||||   |||||||| |||
                         GG AAAT   GATGGTGA AGT
                          _   AA__      C
GAM87   LOC150737 3' TGATAGTGGCATTTATCAAATG 3149        C  TTA_
           G              CCGTTTG ATG   CCACTATCA
                         |||||||| |||   |||||||||
                         GGTAAAC TAT   GGTGATAGT
                          _   TTAC
GAM87   LOC152185 3' ATAATGGTAATGCAAATCA  2498   C     GT   C
                         C GTTTGCAT TACCA TAT
                         | |||||||| ||||| |||
                         A TAAACGTA ATGGT ATA
                          C     __     A
GAM88   DAAM2   3' ACCAACTGGGGAACTGTG  3560           _  C
                         TACAGTTCCTT GTT GT
                         ||||||||||| ||| ||
```

```
                        GTGTCAAGGGG CAA CA
                            T   C
GAM88    FN14      3' TGACTAAGGAACTGCAGC   1703      A        TTC
                        GCT CAGTTCCTTG  GTCG
                        ||| |||||||||  ||||
                        CGA GTCAAGGAAT  CAGT
                            C        ___
GAM88    TM4SF2    3' TGTTTTAAAAAGGAACTGCAGC 1131     A       GTTCGTC
                        GCT CAGTTCCTT    GACA
                        ||| |||||||    ||||
                        CGA GTCAAGGAA    TTGT
                            C    AAATT__
GAM88    WNT3      3' GTCAGACAGCAAGGAACTGT   2159            C  _
                        ACAGTTCCTTGTT GTC GAC
                        ||||||||||||| ||| |||
                        TGTCAAGGAACGA CAG CTG
                            _    A
GAM88    GLTP      3' GCCAACGAGGAACACAGC   1686    ACA      C
                        GCT  GTTCCTTGTT GT
                        |||  |||||||||| ||
                        CGA  CAAGGAGCAA CG
                          CA_        C
GAM88    PRO0149   5' GTCCCAAAAAACTGTAGT    1473       CC  TTCGTC
                        GCTACAGTT TTG    GAC
                        ||||||||| |||    |||
                        TGATGTCAA AAC    CTG
                            AA  C_____
GAM89    LAMP2     3' AGTACTAAAATTAATGCA    1455            T
                        TGCATTAATTTT GTATT
                        |||||||||||| |||||
                        ACGTAATTAAAA CATGA
                            T
GAM89    DKFZp762K2015 3' AGAATCCATGCTAAAAATTAA 2949         _  T
                        TTAATTTTT GTAT GATTCT
                        ||||||||| |||| ||||||
                        AATTAAAAA CGTA CTAAGA
                            T   C
GAM89    FLJ10921  5' AGAATCAATACTACAACTGCA  1808      TTAATTTTT
                        TGCA      GTATTGATTCT
                        ||||      |||||||||||
                        ACGT      CATAACTAAGA
                          CAACAT___
GAM89    LOC91752  3' AATCAATACAATATATGC   2778     TAATTT
                        GCAT    TTGTATTGATT
                        ||||    |||||||||||
                        CGTA    AACATAACTAA
                          TAT___
GAM90    GLP1R     3' AGACACATGGCTATCCTAGAG  896      C       A
                        TTTTG GATAGCCATGT TCT
                        ||||| ||||||||||| |||
```

```
                               GAGAT CTATCGGTACA AGA
                                  C         C
GAM90   FLJ10891  3' TACAGCCATTGCAAAACA    1806        A CA
                     TGTTTTGCGAT GC  TGTA
                     |||||||||| || ||||
                     ACAAAACGTTA CG  ACAT
                               C __
GAM90   KIAA0781  3' CAAGGCCATCACAAAGCA    2793       C A A
                     TGTTTTG GAT GCC TG
                     ||||||| ||| ||| ||
                     ACGAAAC CTA CGG AC
                           A   C   A
GAM90   KIAA1077  3' CATGGCCACCGCAGAACA    2963        ATA
                     TGTTTTGCG  GCCATG
                     |||||||||  ||||||
                     ACAAGACGC  CGGTAC
                           CAC
GAM90   PELI2     3' ATACATGGGACTTCACAAACA 1950      T C TAG_
                     TGTTT G GA   CCATGTAT
                     ||||| | ||   ||||||||
                     ACAAA C CT   GGTACATA
                     _ A TCAG
GAM91   GPRK6     3' GAGGAGCCACTGCCAAACT   898         CTA AGA
                     AGTTTGGCAG  GC  TTC
                     |||||||||| || |||
                     TCAAACCGTC  CG  GAG
                        AC_ AG_
GAM91   WWP1      5' GTTTCTAGTGCCAAACTTA   3164        G   C
                     TAAGTTTGGCA CTAG AGAT
                     |||||||||| |||| ||||
                     ATTCAAACCGT GATC TTTG

                          _    _
GAM91   LOC144559 5' TGAATCTGCCAGCACCATAACT 3067     _ CA  A
           T           AAGTT TGG  GCT GCAGATTCA
                       ||||| ||| ||| |||||||||
                       TTCAA ACC  CGA CGTCTAAGT
                         T  A_   C
GAM91   LOC200163 3' TGCTAATGCCAAACTTA     3440        GC
                     TAAGTTTGGCA TAGCA
                     |||||||||| |||||
                     ATTCAAACCGT ATCGT
                           A_
GAM91   LOC219918 5' TGAATCTGCCAGCACCAGAACT 3531     _ CA  A
           T           AAGT TTGG  GCT GCAGATTCA
                       |||| |||| ||| |||||||||
                       TTCA GACC  CGA CGTCTAAGT
                         A  A_   C
GAM91   LOC220071 5' TGAATCTGCCAGCAGCAGAACT 3603     G A  A
           T           AAGTTT GC GCT GCAGATTCA
                       |||||| || ||| |||||||||
```

```
                           TTCAAG CG CGA CGTCTAAGT
                             A  A   C
GAM91   LOC255515 3' TGAATCTGCCAACACCAGAACT 3689      _    CAGCTA
            T                AAGT TTGG    GCAGATTCA
                         |||| ||||   |||||||||
                           TTCA GACC    CGTCTAAGT
                             A  ACAAC_
GAM92   BCL11B   3' ACAAATATCATAAAGGA    2020     CC G
                        TCCT TA GATATTTGT
                        |||| || |||||||||
                        AGGA AT CTATAAACA
                          AA A
GAM92   M17S2    5' GATACCTACAACTCCTAGGAAG 2213    C      TAT   A_
            A                TC TCCTAGGA  TTGTA TATC
                         || |||||||| ||||| ||||
                         AG AGGATCCT  AACAT ATAG
                          A    C__   CC
GAM92   CRFG     3' ATATTACAAATATTTTGAG  2775    CT
                        CTC AGGATATTTGTAATAT
                        ||| ||||||||||||||||
                        GAG TTTTATAAACATTATA
                          __
GAM92   FLJ23360 5' ATATTGCATCCCTAGAGA   2030     _    ATATT
                        TC CTAGG   TGTAATAT
                        || |||||   ||||||||
                        AG GATCC   ACGTTATA
                         A  CT___
GAM92   KIAA0349 3' ATATCACAGAGCCTGGGAG  3561        ATA   A
                        CTCCTAGG  TTTGT ATAT
                        ||||||||  ||||| ||||
                        GAGGGTCC  AGACA TATA
                           G__  C
GAM92   PRO2325  5' GATATTAACAGTCATCCTAG  1836       AT  _
                        CTAGGAT  TTGT AATATC
                        |||||||  |||| ||||||
                        GATCCTA  GACA TTATAG
                          CT  A
GAM92   SCYA16   3' ATATTTCTCAATCTTAGGAGG 1130            ATTTGT
            A                TCCTCCTAGGAT    AATAT
                         ||||||||||||    |||||
                         AGGAGGATTCTA    TTATA
                           ACTCTT
GAM93   DJ-1     3' CGTTAGGAATCCATTCTCA  1375     ACTAAA
                        TGAGAAT   ATTCCTAACG
                        |||||||   |||||||||||
                        ACTCTTA   TAAGGATTGC
                          CC____
GAM93   FLJ10535 3' TAGGAATTTTTATTCCCA   1787   A   CT
                        TG GAATA AAAATTCCTA
                        || ||||| |||||||||
```

```
                             AC CTTAT  TTTTAAGGAT
                             C     __
GAM93   FLJ10539 3'  AGGATTTTAGTATCCTCA    1788      A        T
                             TGAG ATACTAAAAT CCT
                             |||| ||||||||| |||
                             ACTC TATGATTTTA GGA
                             C        _
GAM93   PIB5PA   3'  TTAGGAATTAAATTCTC     2739      ACTAA
                             GAGAAT    AATTCCTAA
                             ||||||    |||||||||
                             CTCTTA    TTAAGGATT
                                  AA___
GAM93   LOC149351 3'  AGGAGTTTAGTATCCTTA   3130      A        A
                             TGAG ATACTAAA TTCCT
                             |||| |||||||| |||||
                             ATTC TATGATTT GAGGA
                             C        _
GAM93   LOC157858 5'  AGGGGAGTGTTCTCA      3384           AAAA
                             TGAGAATACT  TTCCT
                             ||||||||||  |||||
                             ACTCTTGTGA  GGGGA

                               _____
GAM94   DLG5    5'  TGATACAGCACAATAACT     3265      CCAC     C
                             AGTTA  GTGCTGTA CA
                             |||||  |||||||| ||
                             TCAAT  CACGACAT GT
                                 AA__      A
GAM94   DVL3    3'  CAATAAATGGTAGCTATTA    1112           CG  C
                             TAATAGTTACCA TG TG
                             |||||||||||| || ||
                             ATTATCGATGGT AT AC
                                   AA  A
GAM94   ENPP3   3'  GTACACACAGTGACTATTA    1173           CAC  C
                             TAATAGTTAC  GTG TGTAC
                             ||||||||||  ||| |||||
                             ATTATCAGTG  CAC ACATG
                                   A__  _
GAM94   FANCF   3'  TGGTACAACCCAGGGGTAAACT 1998        _  ACGTGC_
         ATTA                TAATAGTT ACC    TGTACCA
                             |||||||| |||    |||||||
                             ATTATCAA TGG    ACATGGT
                              A  GGACCCA
GAM94   PCDH11X 3'  ACAGCACACAAGTGGCTATTG  2298           CAC_
                             TAATAGTTAC  GTGCTGT
                             ||||||||||  |||||||
                             GTTATCGGTG  CACGACA
                                  AACA
GAM94   PCDH11X 3'  ACAGCACACAAGTGGCTATTG  2300           CAC_
                             TAATAGTTAC  GTGCTGT
                             ||||||||||  |||||||
```

```
                    GTTATCGGTG   CACGACA
                         AACA
GAM94   PCDH11Y  3' ACAGCACACAAGTGGCTATTG 2302        CAC_
                    TAATAGTTAC   GTGCTGT
                    |||||||||    |||||||
                    GTTATCGGTG   CACGACA
                         AACA
GAM94   FLJ10539  3' TACAGTATGACAACTATT  1789        ACCA
                    AATAGTT   CGTGCTGTA
                    |||||||   |||||||||
                    TTATCAA   GTATGACAT
                         CA__
GAM94   FLJ10898  3' TAGTCATTCGTGGTAACTA  2528            T___
                    TAGTTACCACG   GCTG
                    |||||||||||   ||||
                    ATCAATGGTGC   TGAT
                         TTAC
GAM94   KIAA0680  3' TGGTACAGTATAGTACCATTA 1530     A T CAC
                    TAAT GT AC   GTGCTGTACCA
                    |||| || ||   |||||||||||
                    ATTA CA TG   TATGACATGGT
                         C _ A__
GAM94   KIAA1804  3' GCAGTACAGTACTATTA    2868       T CAC
                    TAATAGT AC   GTGCTGT
                    ||||||| ||   |||||||
                    ATTATCA TG   CATGACG
                          _ A__
GAM94   MO25     3' TAGTAGTATGTAACTATTA  1677        C_ G
                    TAATAGTTAC AC TGCTG
                    |||||||||| || |||||
                    ATTATCAATG TG ATGAT
                         TA _
GAM94   RAB33B   3' ACAGCTGTAGTAACTAT    2190        C  T
                    ATAGTTAC ACG GCTGT
                    |||||||| ||| |||||
                    TATCAATG TGT CGACA
                         A    _
GAM94   RoXaN    3' TGGTACAGCACACATGTGAGC 2128       AC C__
                    GTT CA   GTGCTGTACCA
                    ||| ||   |||||||||||
                    CGA GT   CACGACATGGT
                     GT ACA
GAM95   KIF13A   3' ACCGCAACAACTTGGTAGGA 1979      ATAG AT
                    TCC   TAC AGTTGTTGCGGT
                    |||   ||| |||||||||||
                    AGG   ATG TCAACAACGCCA
                    ____   GT
GAM95   LOXL3    3' ACTCATCAGACCATGCACTATG 2264        A  A  GT_ C
            GA              TCCATAGT CAT GTT  TG GGT
                    |||||||| ||| ||| || |||
```

```
                    AGGTATCA GTA CAG  AC TCA
                      C  C  ACT _
GAM95   DKFZp547I014 5' CAGCTAACAATGTACTACAGA 1901    CA      A _
                    TC TAGTACAT GTT GTTG
                    || ||||||||| ||| ||||
                    AG ATCATGTA CAA CGAC
                      AC      A  T
GAM95   Spir-1  3' ACCATGAACTCGTACTATG  2699       AT  GTTGC
                    CATAGTAC AGTT   GGT
                    |||||||| ||||    |||
                    GTATCATG TCAA   CCA
                      C_  GTA__
GAM96   GCLC   3' AATTGTACAATACTTGCATTCC 833      CT___   C
                    GGA   AGTAT GTACAATT
                    |||    ||||| ||||||||
                    CCT   TCATA CATGTTAA
                      TACGT   A
GAM96   FLJ21324 5' AATTGTTGCCTAGTCCTGC 3513       TAT T
                    GTAGGACTAG  CG ACAATT
                    ||||||||||  || ||||||
                    CGTCCTGATC  GT TGTTAA
                      C__  _
GAM96   KIAA0193 3' AATTGTGATGTCCTAGTCCTAC 1543      T CG
                    GTAGGACTAG AT TACAATT
                    |||||||||| || |||||||
                    CATCCTGATC TG GTGTTAA
                      C TA
GAM96   LOC91097 3' AATTGTTGCCTAGTCCTGC  2705     TAT T
                    GTAGGACTAG  CG ACAATT
                    ||||||||||  || ||||||
                    CGTCCTGATC  GT TGTTAA
                      C__  _
GAM97   ADAMTS5 3' TTCAATAGATACCACGAA   1353       GG A
                    TTTGTGGTATT AT GAA
                    ||||||||||| || |||
                    AAGCACCATAG TA CTT
                      A_ A
GAM97   BCRP2   3' TTCTATCCAACATTCAA    2633    T A
                    TTG GGT TTGGATAGAA
                    ||| ||| |||||||||||
                    AAC TTA AACCTATCTT
                      _  C
GAM97   IL13RA1 3' TCTACTAAAACTACAAA    835       A A
                    TTTGTGGT TTGG TAGA
                    |||||||| |||| ||||
                    AAACATCA AATC ATCT
                      A  _
GAM97   IL1A   3' TCTACCCATATTACAGA   2634       T A
                    TTTGTGGTAT GG TAGA
                    ||||||||| || ||||
```

```
                          AGACATTATA CC ATCT
                          C _
GAM97   ISL1    3' TCTATTTTGCCACAAG     906        TT
                          TTTGTGGTA GGATAGA
                          ||||||||| |||||||
                          GAACACCGT TTTATCT
                          __
GAM97   MITF    3' TTCTATTTTACAACTACAAA 721        ATT_
                          TTTGTGGT  GGATAGAA
                          ||||||||  ||||||||
                          AAACATCA  TTTATCTT
                          ACAT
GAM97   NCF2    3' TTCTGTGTCATACCACAA   742        T _
                          TTGTGGTAT GG ATAGAA
                          ||||||||| || ||||||
                          AACACCATA CT TGTCTT
                          _ G
GAM97   NEDD4L  3' TTCTACTCAACTACAAA    1618       AT GA
                          TTTGTGGT TG TAGAA
                          |||||||| || |||||
                          AAACATCA AC ATCTT
                          __ TC
GAM97   NR3C1   3' TTCTATCCTACAACAAG    717        G TT
                          TTTGT GTA GGATAGAA
                          ||||| ||| ||||||||
                          GAACA CAT CCTATCTT
                          A __
GAM97   PDK4    3' TTCTATTTTCCCCACAAA   3733       TATT
                          TTTGTGG  GGATAGAA
                          |||||||  ||||||||
                          AAACACC  TTTATCTT
                          CCT_
GAM97   PSEN1   3' TTCTACTTTGCCACAGA    1393       TT A
                          TTTGTGGTA GG TAGAA
                          ||||||||| || |||||
                          AGACACCGT TC ATCTT
                          T_ _
GAM97   RAG1    3' TTCTTTCCACCACAAA     746        ATT T
                          TTTGTGGT GGA AGAA
                          |||||||| ||| ||||
                          AAACACCA CCT TCTT
                          ___ T
GAM97   SYNGR1  3' TTCTGTGCCCACCACAAG   1148       ATT _
                          TTTGTGGT GG ATAGAA
                          |||||||| || ||||||
                          GAACACCA CC TGTCTT
                          C__ G
GAM97   TOX     5' TTCTTAAACAAACCACAAA  1534       A GAT_
                          TTTGTGGT TTG AGAA
                          |||||||| ||| ||||
```

```
                          AAACACCA AAC   TCTT
                           _     AAAT
GAM97   TRPC6    3' TTCTATCCTTCTACCCAAA  1135      T  TT_
                          TTTG GGTA  GGATAGAA
                          |||| ||||  ||||||||
                          AAAC CCAT  CCTATCTT
                           _    CTT
GAM97   AF9Q34   3' TTCTACACACTCAGCCACAAA 2258        AT__ GA
                          TTTGTGGT  TG TAGAA
                          ||||||||  || |||||
                          AAACACCG  AC ATCTT
                           ACTC AC
GAM97   C1QR1    3' TTCCATCCTCATCACAAG   1402       ATT  A
                          TTTGTGGT GGAT GAA
                          |||||||| |||| |||
                          GAACACTA CCTA CTT
                           CT_  C
GAM97   FLJ10193 3' TCTGACAGATACCACGAA   1775         GGA
                          TTTGTGGTATT TAGA
                          ||||||||||| ||||
                          AAGCACCATAG GTCT
                           ACA
GAM97   FLJ10989 3' CTATTTACTGATCACAAA   1810       AT_
                          TTTGTGGT TGGATAG
                          |||||||| |||||||
                          AAACACTA ATTTATC
                           GTC
GAM97   FLJ20700 3' TTCTACCAAAACTACAAA   1767      A  A
                          TTTGTGGT TTGG TAGAA
                          |||||||| |||| |||||
                          AAACATCA AACC ATCTT
                           A  _
GAM97   FLJ31101 3' TTCTATCTAGCACAA      1772      GTA
                          TTGTG TTGGATAGAA
                          ||||| ||||||||||
                          AACAC GATCTATCTT
                           ___
GAM97   KIAA0252 3' TCTACTAAAACTACAAA    2638      A  A
                          TTTGTGGT TTGG TAGA
                          |||||||| |||| ||||
                          AAACATCA AATC ATCT
                           A  _
GAM97   KIAA0416 3' TCATTTCAAACCACAAA    1638      A  TA
                          TTTGTGGT TTGGA GA
                          |||||||| ||||| ||
                          AAACACCA AACTT CT
                           _   TA
GAM97   KIAA0445 5' TCTACTAAAACTACAAA    1519      A  A
                          TTTGTGGT TTGG TAGA
                          |||||||| |||| ||||
```

```
                         AAACATCA AATC ATCT
                              A   _
GAM97  KIAA0493 5' TTCTACTTCCACCACAAG  2683       ATT  __
                   TTTGTGGT  GGA TAGAA
                   |||||||| ||| |||||
                   GAACACCA  CCT ATCTT
                        ___    TC
GAM97  KIAA0753 3' TCTATTTCATACCACAAA   1553       TG
                   TTTGTGGTAT GATAGA
                   |||||||||| ||||||
                   AAACACCATA TTATCT
                        CT
GAM97  KIAA0781 3' TTCTGCCCCACCACAAA    2794       ATT A
                   TTTGTGGT  GG TAGAA
                   |||||||| || |||||
                   AAACACCA  CC GTCTT
                        CC_ _
GAM97  KIAA0825 3' TTCTATCTAACACATAA    2589       GTA
                   TTGTG  TTGGATAGAA
                   |||||  ||||||||||
                   AATAC  AATCTATCTT
                        AC_
GAM97  KIAA0831 3' TTCTATCCGGTAGTCACAAA  1590       _
                   TTTGTGG TATTGGATAGAA
                   ||||||| |||||||||||
                   AAACACT ATGGCCTATCTT
                        G
GAM97  KIAA1172 3' TTCTATTTAAAAATAGCCACAA 2897       A____
              A          TTTGTGGT   TTGGATAGAA
                   ||||||||   ||||||||||
                   AAACACCG   AATTTATCTT
                        ATAAA
GAM97  KR18     3' TTCTATCCAATTTGTGAA    2325       TG T
                   TTTG G ATTGGATAGAA
                   |||| | |||||||||||
                   AAGT T TAACCTATCTT
                        GT _
GAM97  MAPK13   3' TCTAACGAATTACCACAAA   953         __ GA
                   TTTGTGGTA TTG TAGA
                   ||||||||| ||| ||||
                   AAACACCAT AGC ATCT
                        TA A_
GAM97  MGC11386 3' TCTACTAAAACTACAAA    2296       A A
                   TTTGTGGT TTGG TAGA
                   |||||||| |||| ||||
                   AAACATCA AATC ATCT
                        A _
GAM97  PRO0641  3' TCTGCCAATAACCACAAA   1477       _   A
                   TTTGTGGT ATTGG TAGA
                   |||||||| ||||| ||||
```

```
                          AAACACCA TAACC GTCT
                           A        _
GAM97   PRO0902   3' TCTACCTTTGCCACAAG    2358       TT A
                    TTTGTGGTA GG TAGA
                    |||||||||| || ||||
                    GAACACCGT CC ATCT
                           TT  _
GAM97   SMAP-5    3' TCTACTAAAACTACAAA    2168       A   A
                    TTTGTGGT TTGG TAGA
                    |||||||| |||| ||||
                    AAACATCA AATC ATCT
                           A  _
GAM97   SPRY4     3' TCTACTAAACTACAAA     2177     A   A
                    TTTGTGGT TTGG TAGA
                    |||||||| |||| ||||
                    AAACATCA AATC ATCT

                        _    _
GAM97   USP24     3' TCTACGATGCTACAAA     3512         GA
                    TTTGTGGTATTG TAGA
                    ||||||||||||| ||||
                    AAACATCGTAGC ATCT

                        __
GAM97   ZNF304    3' TTCATTGTATACCACAA    1921       TG  A
                    TTGTGGTAT GAT GAA
                    ||||||||| ||| |||
                    AACACCATA TTA CTT
                        TG  _
GAM97   LOC121344 3' TCTACCTCAGTTTGCCACAAA 2990          TT____ A
                    TTTGTGGTA    GG TAGA
                    |||||||||    || ||||
                    AAACACCGT    CC ATCT
                        TTGACT _
GAM97   LOC144266 5' TTCTGTCCCACCAGAAA     3065     G   ATT
                    TTT TGGT  GGATAGAA
                    ||| ||||  ||||||||
                    AAA ACCA  CCTGTCTT
                        G   C__
GAM97   LOC145241 3' CTTACGTCAGTACCACAAA   2640            AT__
                    TTTGTGGTATTGG  AG
                    |||||||||||||  ||
                    AAACACCATGACT  TC
                         GCAT
GAM97   LOC148545 5' TCTACCTCTTCTGCCACAAA  3120           TT  __
                    TTTGTGGTA GGA TAGA
                    |||||||| ||| ||||
                    AAACACCGT TCT ATCT
                        CT CC
GAM97   LOC149073 5' TTCTGATGACAAACCACAAA  3305         A  GA__
                    TTTGTGGT TTG  TAGAA
                    |||||||| ||| |||||
```

```
                              AAACACCA AAC   GTCTT
                              _   AGTA
GAM97   LOC149448 3'  CTGTAACAAAATACCACAAA  3309           GG___
                      TTTGTGGTATT    ATAG
                      |||||||||| ||||
                      AAACACCATAA   TGTC
                              AACAA
GAM97   LOC149579 5'  TCTACTAAAACTACAAA     2907        A   A
                      TTTGTGGT TTGG TAGA
                      |||||||| |||| ||||
                      AAACATCA AATC ATCT
                          A   _
GAM97   LOC152641 5'  TTCTAGGGAAACCACAAA    3173        A  GGA
                      TTTGTGGT TT  TAGAA
                      |||||||| ||  |||||
                      AAACACCA AG   ATCTT
                          A  GG_
GAM97   LOC169966 3'  TTCTATCATCATCTACTACAAA 3253           TTG___
                      TTTGTGGTA   GATAGAA
                      ||||||||    |||||||
                      AAACATCAT   CTATCTT
                            CTACTA
GAM97   LOC222234 3'  TCTGTAACAAATTACCACAAA 3647           __  G_
                      TTTGTGGTA TTG ATAGA
                      ||||||||| ||| |||||
                      AAACACCAT AAC TGTCT
                          TA  AA
GAM97   LOC254058 3'  TTCTAACCACCACAAG       3735        ATT A
                      TTTGTGGT  GG TAGAA
                      ||||||||  || |||||
                      GAACACCA  CC ATCTT
                           ___  A
GAM97   LOC51110 3'  TTCTGGTATACCACAAA       1657          TGGA
                      TTTGTGGTAT   TAGAA
                      |||||||||| |||||
                      AAACACCATA   GTCTT
                            TG__
GAM97   LOC51292 3'  TCTATCTGCACACACAAA      1698        _  ATT
                      TTTGTG GT  GGATAGA
                      |||||| ||  |||||||
                      AAACAC CA   TCTATCT
                          A  CG_
GAM97   LOC92573 5'  TTCTGGCCACCACAGA        2870        ATT A
                      TTTGTGGT  GG TAGAA
                      |||||||| || |||||
                      AGACACCA  CC GTCTT
                            ___  G
GAM98   AVP      5'  AGCTCCTAGGCCAGGGCCTGTC 752          A AGA_
                      GACAG CC   CCTAGGAGCT
                      ||||| ||    |||||||||
```

```
                         CTGTC GG   GGATCCTCGA
                         C  GACC
GAM98   HTRA3     3' CTGCAGGTCTGGGCTGCCA  3457     A  A    A_
                         TG CAG CCAGACCT  GG
                         || ||| |||||||| ||
                         AC GTC GGTCTGGA  TC
                          C   G    CG
GAM98   LGALS3BP  3' AGCCCCTGGTCAGTCTG   2851      CA   T  A
                         CAGAC GACC AGG GCT
                         ||||| |||| ||| |||
                         GTCTG CTGG TCC CGA
                            A_  _  C
GAM98   MAD2L1    3' TAGCTCCTTTTGACCTTCA  921      C  AC   CCT
                         TGA AG CAGA  AGGAGCTA
                         ||| || |||| ||||||||
                         ACT TC GTTT  TCCTCGAT
                          _  CA  ___
GAM98   PYGM      5' TAGCTCCCTGAGCTGCCA   1230    A  AC  ACCTA
                         TG CAG CAG   GGAGCTA
                         || ||| |||   |||||||
                         AC GTC GTC   CCTCGAT
                          C  GA  _____
GAM98   SLC35A3   3' TTCTGGGTCTGATCTGTCA  1418        C
                         TGACAGA CAGACCTAGGA
                         ||||||| |||||||||||
                         ACTGTCT GTCTGGGTCTT
                               A
GAM98   ATPAF1    3' ATAGCTCCCAAATGATGAGTTT 2583       _ GACCTA_
         GTCA              TGACAGAC CA    GGAGCTAT
                         |||||||| ||    ||||||||
                         ACTGTTTG GT    CCTCGATA
                          A AGTAAAC
GAM98   C7orf13   3' CTTAAGTCTGGTCCCTCA   2265    CA     C
                         TGA GACCAGAC TAGG
                         ||| ||||||||| ||||
                         ACT CTGGTCTG ATTC
                          CC     A
GAM98   CBLC      3' CTGCCAAGCCTGGTCTGTCA  1407         AC A _
                         TGACAGACCAG CT GG AG
                         ||||||||||| || || ||
                         ACTGTCTGGTC GA CC TC
                          C_  A  G
GAM98   FLJ10241  3' AGCTCCTGTCACCCTGTCA  1776       ACCA CT
                         TGACAG  GAC AGGAGCT
                         ||||||  ||| |||||||
                         ACTGTC  CTG TCCTCGA
                          CCA_  __
GAM98   FLJ20651  3' CCAAGCTTGGTCTGTCA    1761       AC A
                         TGACAGACCAG CT GG
                         ||||||||||| || ||
```

```
                          ACTGTCTGGTT GA CC
                             C_ A
GAM98   KIAA1203 3' CTTCAGATCCTGTCTGTCA  2922        CA C A
                         TGACAGAC GA CT GGAG
                         |||||||| || || ||||
                         ACTGTCTG CT GA CTTC
                            TC A _
GAM98   PL6     3' AGCTCCTGGGCCGGCCCTCA  1348     CAGA AGA
                         TGA  CC CCTAGGAGCT
                         ||| || |||||||||
                         ACT  GG GGGTCCTCGA
                           CCC_ CC_
GAM98   SRCRB4D 3' AGCTCCTACCTTGGGCCCTCA  2386     CAGA  ACC
                         TGA  CCAG TAGGAGCT
                         |||  |||| ||||||||
                         ACT  GGTT ATCCTCGA
                           CCCG  CC_
GAM98   SYNPO2  3' AGCAGCTCTGGTCTGTCA   2928         C AGGA
                         TGACAGACCAGA CT  GCT
                         |||||||||||| ||  |||
                         ACTGTCTGGTCT GA  CGA
                               C ____
GAM98   LOC145858 5' CCTAGGTCTGGCCTTCA    3085    C A
                         TGA AG CCAGACCTAGG
                         ||| || |||||||||||
                         ACT TC GGTCTGGATCC
                            _ C
GAM98   LOC151162 5' AGCTCCTAGAGGCTGCTCA  3338      _ A AGAC
                         TGA CAG CC  CTAGGAGCT
                         ||| ||| ||  ||||||||
                         ACT GTC GG  GATCCTCGA
                            C _ A___
GAM98   LOC196410 5' AGCTCAGAGCTGGTCTGCCA  3411    A    AC AG
                         TG CAGACCAG CT GAGCT
                         || |||||||| || |||||
                         AC GTCTGGTC GA CTCGA
                            C    __ GA
GAM98   LOC203339 5' AGCTCCTAGGAATTCTCTCA  3489    C CCAGA
                         TGA AGA   CCTAGGAGCT
                         ||| |||   ||||||||||
                         ACT TCT   GGATCCTCGA
                            C TAA__
GAM98   LOC203377 5' AGCTCCTAGAGGCTGCTCA  3490     _ A AGAC
                         TGA CAG CC  CTAGGAGCT
                         ||| ||| ||  ||||||||
                         ACT GTC GG  GATCCTCGA
                            C _ A___
GAM99   SEL1L   3' CAAGAAAATTTAAAACGATCCC 1179    AA       TT
         AA              TTG ATTGTTTT ATTTCTTG
                         ||| |||||||| ||||||||
```

```
                              AAC  TAGCAAAA  TAAAAGAAC
                               CC        TT
GAM99   DKFZP564O1863 3' AAAGTAAATACAATTTCAA  2826            TT
                         TTGAAATTGT TTTATTTT
                         |||||||||| ||||||||
                         AACTTTAACA AAATGAAA
                                  T_
GAM99   LOC129446 3' CAAGAAAAATGAGAACATTTTC 3042        T     TA
        AA                   TTGAAA TGTTTTT TTTTCTTG
                             |||||| ||||||| ||||||||
                             AACTTT ACAAGAG AAAAGAAC
                                 T     TA
GAM100  CYP19   3' AAAAAGCAGAGGCCAAGAGTTT 705       ATGAT_      C
           G              CAAA    GCCTCTGC TTTT
                          ||||    |||||||| ||||
                          GTTT    CGGAGACG AAAA
                            GAGAAC      A
GAM100  CYP19   3' AAAAAGCAGAGGCCAAGAGTTT 2185      ATGAT_      C
           G              CAAA    GCCTCTGC TTTT
                          ||||    |||||||| ||||
                          GTTT    CGGAGACG AAAA
                            GAGAAC      A
GAM100  F8      3' AAAGGCAAATCATTTGGA    707        A  GCCTC
                          TCCAAA TGAT    TGCCTTT
                          |||||| |||| |||||||
                          AGGTTT ACTA    ACGGAAA
                           _   A____
GAM100  MSR1    3' AAAAGGCAAAACCTTACCTTGG 2453      AA  TGCCTC
           A                  TCCAA TGA    TGCCTTTT
                              ||||| ||| |||||||||
                              AGGTT ATT    ACGGAAAA
                               CC  CCAAA_
GAM100  MSR1    3' AAAAGGCAAAACCTTACCTTGG 2454      AA  TGCCTC
           A                  TCCAA TGA    TGCCTTTT
                              ||||| ||| |||||||||
                              AGGTT ATT    ACGGAAAA
                               CC  CCAAA_
GAM100  PCDHB16 3' AAAAGGCAAAGGTATTAT    1931          C
                          ATGATGCCT TGCCTTTT
                          ||||||||| ||||||||
                          TATTATGGA ACGGAAAA
                                  A
GAM100  QPCT    3' AAAAGTCAAGGCATCATTT    1428        C C
                          AAATGATGCCT TG CTTTT
                          |||||||||| || |||||
                          TTTACTACGGA AC GAAAA
                                 _  T
GAM100  TWIST   3' AAAGGAAAGGCATCACTATGGA 750       AAA      CTG
                          TCCA TGATGCCT CCTTT
                          |||| |||||||| |||||
```

```
                        AGGT  ACTACGGA  GGAAA
                        ATC        AA_
GAM100  ATP9A    3' AAAGGCAGAGGCATCTTTCGGA 2617     A   T
                        TCC AAA GATGCCTCTGCCTTT
                        ||| ||| |||||||||||||
                        AGG TTT CTACGGAGACGGAAA
                        C   _
GAM100  CALN1    3' CAGAAATATCATCTTGGA   2207      A    CC
                        TCCAA ATGATG  TCTG
                        ||||| ||||||  ||||
                        AGGTT TACTAT  AGAC
                        C     AA
GAM100  FLJ23277 3' AAAAGGCAGAAATCCATTCA 2238     _  CC__
                        TGA TG   TCTGCCTTTT
                        ||| ||   ||||||||||
                        ACT AC   AGACGGAAAA
                        T   CTAA
GAM100  KIAA0992 3' AAAAGGCAGAAACATACCTTG 1661      ATG  CC
                        CAAA  ATG TCTGCCTTTT
                        ||||  ||| ||||||||||
                        GTTT  TAC AGACGGAAAA
                        CCA   AA
GAM100  KIAA1045 3' AAAAGGCAGAACAGTTTTG   2906      GA CC
                        CAAAAT TG TCTGCCTTTT
                        |||||| || ||||||||||
                        GTTTTG AC AGACGGAAAA
                        __  A_
GAM100  KIAA1056 3' AAAGGCAGAGAGGCCAGGA  1575     AAAA AT     __
                        TCC  TG GCCTCT GCCTTT
                        |||  || |||||| ||||||
                        AGG  AC CGGAGA CGGAAA
                        ____ __   GA
GAM100  KIAA1323 3' AGGGGAGAGGCACATTT    2646      A    G
                        AAAATG TGCCTCT CCTT
                        |||||| ||||||| ||||
                        TTTTAC ACGGAGA GGGA
                        _     G
GAM100  LMOD1    3' AGGTGAAAGGCATCTTTCTG 1409     A T    CT_
                        CA AA GATGCCT  GCCT
                        || || |||||||  ||||
                        GT TT CTACGGA  TGGA
                        C  T     AAG
GAM100  RNF32    3' AAAAGTTTACCATCATTTTGG 2172          CCTCT C
                A              TCCAAAATGATG   GC TTTT
                        ||||||||||   || ||||
                        AGGTTTTACTAC   TG AAAA
                        CATT_ A
GAM100  SS-56    3' AAAAAGCAGAGGCCCAGTCA  2535      ___      C
                        TGAT  GCCTCTGC TTTT
                        ||||  |||||||| ||||
```

```
                        ACTG  CGGAGACG AAAA
                        ACC       A
GAM100  LOC122792 3' AAAAGTGCCTTGCATCATTT 2518         CTCT _
                     AAATGATGC   GC CTTTT
                     |||||||||   || |||||
                     TTTACTACG   CG GAAAA
                        TTC_ T
GAM100  LOC146512 3' GCAGTGCAAACATCATTTTGGA 3094          CCT___
                     TCCAAAATGATG    CTGC
                     ||||||||||||    ||||
                     AGGTTTTACTAC    GACG
                        AAACGT
GAM100  LOC201633 3' CAGAGGCATCTTCTGGA    3483     A  T
                     TCCA AA GATGCCTCTG
                     |||| || ||||||||||
                     AGGT TT CTACGGAGAC
                        C _
GAM100  LOC202126 3' AAAAAGCAAGTATCATTTGGA 3486       A    CTC  C
                     TCCAAA TGATGC  TGC TTTT
                     |||||| ||||||  ||| ||||
                     AGGTTT ACTATG  ACG AAAA
                        _   A__  A
GAM100  LOC221755 3' CAGAGGCGCCATCTTGGA    3563     A  A
                     TCCAA ATG TGCCTCTG
                     ||||| ||| ||||||||
                     AGGTT TAC GCGGAGAC
                        C  C
GAM100  LOC257334 3' GCAGAGGCACCATCTTGG    3734     A  A
                     CCAA ATG TGCCTCTGC
                     |||| ||| |||||||||
                     GGTT TAC ACGGAGACG
                        C  C
GAM101  ANGPT1   3' ACTGAAACATGCTTACCAGATT 804         CATCTC_
          CA              TGAATC   TATGTTTCAGT
                     ||||||     |||||||||||
                     ACTTAG     GTACAAAGTCA
                        ACCATTC
GAM101  GPR61    5' ACTGAAATTCAGAAGATTCAC 3123        CATC  AT
                     GTGAATC   TCT GTTTCAGT
                     |||||||   ||| ||||||||
                     CACTTAG   AGA TAAAGTCA
                        A___   CT
GAM101  PPP1R12B 3' ACTGAAACCCGGAACAGATTC 2228        CATC  AT
                     GAATC   TCT GTTTCAGT
                     |||||   ||| ||||||||
                     CTTAG   AGG CAAAGTCA
                        ACA_  CC
GAM101  TRIM9    3' ACTTCTATATAGAGATAGACTT 1610     A  C       TTC
          AC               GTGA TC ATCTCTATGT  AGT
                     |||| || |||||||| |||
```

```
                         CATT AG TAGAGATATA  TCA
                          C A        TCT
GAM101  YWHAE     3' ACTGAAACACAGCATGGAATTA 1329    A   CT A
                         TGA TCCAT  CT TGTTTCAGT
                         ||| ||||| || ||||||||||
                         ATT AGGTA  GA ACAAAGTCA
                          A    C_ C
GAM101  AKAP9     3' ACTGAAATAAAAATGACTTCAC 1242      TC  CTCTA
                         GTGAA CAT   TGTTTCAGT
                         ||||| |||   |||||||||
                         CACTT GTA   ATAAAGTCA
                          CA  AAA__
GAM101  LOC166824 3' ACTGAAACATAATCAATGGATT 3259         CTC_
          CA               TGAATCCAT  TATGTTTCAGT
                         ||||||||| ||||||||||
                         ACTTAGGTA  ATACAAAGTCA
                         ACTA
GAM101  LOC254835 3' TGAAGCAAGAGACAGACCCAC 3722    AA CA   A
                         GTG TC TCTCT TGTTTCA
                         ||| || ||||| |||||||
                         CAC AG AGAGA ACGAAGT
                          CC AC   _
GAM102  PNPASE   3' CTGAGGCAGAAGAATCACTTC 2900          GATG G
                         GAAGTGATTCTTT  GT TCAG
                         |||||||||||||  || ||||
                         CTTCACTAAGAAG  CG AGTC
                          A___ G
GAM102  SEC24D   3' CAGTATCAATAAATCACTTC 1559     CT   G
                         GAAGTGATT TTGATG TG
                         ||||||||| |||||| ||
                         CTTCACTAA AACTAT AC
                          AT    G
GAM102  LOC131000 3' CTGACCTTGAAATAAATCACTT 3037      CT GAT T
          C               GAAGTGATT TT  GG GTCAG
                         ||||||||| ||  || |||||
                         CTTCACTAA AA  TC CAGTC
                          AT  AGT _
GAM102  LOC151658 5' GAAGTCTCAAAGCATCACTTC 3349      T    T TG
                         GAAGTGAT CTTTGA GG  TC
                         |||||||| |||||| || ||
                         CTTCACTA GAAACT CT  AG
                          C    _ GA
GAM102  LOC257428 3' GCACTTTCAAAGAATCATCC 3649    A        T
                         A GTGATTCTTTGA GGTGT
                         | ||||||||||| |||||
                         C TACTAAGAAACT TCACG
                          C       T
GAM103  CARD15   3' GTAAATAATCAGAGGGGAATAA 1983      GGA TC
          A               TTTGTT  T CTGATTATTTAC
                         ||||||  | ||||||||||
```

```
                         AAATAA  G GACTAATAAATG
                           GG_ GA
GAM103  CLCN4     3' AAATAACAGAAAACCCAGCAAA 861            ATTC_  A
                         TTTGTTGG   CTG TTATTT
                         |||||||   ||| ||||||
                         AAACGACC   GAC AATAAA
                            CAAAA  _
GAM103  FGF2      3' TAAATAATTTTATAATTCAACA 885           CCT_
        AA                 TTTGTTGGATT  GATTATTTA
                         ||||||||||  |||||||||
                         AAACAACTTAA  TTAATAAAT
                            TATT
GAM103  ZNF135    3' TGGTGAGAAACCCAACAAA  1022         A C G
                         TTTGTTGG TT CT ATTA
                         |||||||| || || ||||
                         AAACAACC AA GA TGGT
                           C A G
GAM103  SEC15B    3' AATTAAAAATCCAACAAA   2757         CC
                         TTTGTTGGATT TGATT
                         ||||||||||| |||||
                         AAACAACCTAA ATTAA
                              AA
GAM103  ZNF334    3' AAGTAATAAATTCCAACAAA  1780        TTCCTG
                         TTTGTTGGA    ATTATTT
                         |||||||||    |||||||
                         AAACAACCT    TAATGAA
                            TAAA__
GAM103  LOC158954 3' TGGTGAGAAATCCAACAAA  2567         C G
                         TTTGTTGGATT CT ATTA
                         ||||||||||| || ||||
                         AAACAACCTAA GA TGGT
                            A G
GAM103  LOC219686 3' GTAATTGGAAAAAATCCAATAA 3500           C___TG
        A                  TTTGTTGGATT  C ATTAT
                         |||||||||||  | |||||
                         AAATAACCTAA   G TAATG
                            AAAA GT
GAM103  LOC221510 3' AAATAATCAAAACCCAACA   3508       A CC
                         TGTTGG TT TGATTATTT
                         |||||| || |||||||||
                         ACAACC AA ACTAATAAA
                            C A_
GAM104  PLN       3' TAATAGCCTACTATTGACC  947    C         _
                         GG CAATAGTAG CTATTA
                         || ||||||||| |||||
                         CC GTTATCATC GATAAT
                            A        C
GAM104  PRRG1     3' GTAATAGCTCTATCAGCC  789       CA  T
                         GGC ATAG AGCTATTAC
                         ||| |||| |||||||||
```

```
                          CCG  TATC TCGATAATG
                          AC    _
GAM104  LOC149320 3' GCGGCAGCTACTACTGCC  2892    CAA      ATTA
                          GGC  TAGTAGCT  CCGT
                          ||| |||||||  ||||
                          CCG  ATCATCGA  GGCG
                          TC_      C___
GAM104  LOC163782 5' ACGGATGCCACTATTGGGC  3234    G    A TATTA
                          G CCAATAGT GC   CCGT
                          | |||||||| ||   ||||
                          C GGTTATCA CG   GGCA
                          G    C TA___
GAM105  FLJ12668 3' ACTTGAGCAAATAATTGGGATG 2123          CCAA AG
                  A             TTATCCCAATTA  CT AAGT
                          ||||||||||| || ||||
                          AGTAGGGTTAAT  GA TTCA
                          AAAC G_
GAM105  KIAA0016 3' ACTTTTAAGGTAACTGGGATGA 1542        A   AAC
                          TTATCCCA TTACC  TAGAAGT
                          |||||||| |||||  |||||||
                          AGTAGGGT AATGG  ATTTTCA
                          C   A__
GAM105  ZAK     3' ACTTCCAGTTTTTGGATTGGGA 1708        ACC_  A
                          TCCCAATT   AACT GAAGT
                          ||||||||   |||| |||||
                          AGGGTTAG   TTGA CTTCA
                          GTTT   C
GAM105  LOC58489 3' TGGTTGGTAATGGAATAA   2952    C  A
                          TTAT CCA TTACCAACTA
                          |||| ||| ||||||||||
                          AATA GGT AATGGTTGGT
                          A  _
GAM106  IL1R1   3' AGAACATCCTCCAATTCC   782        CG  A
                          GGAATTGGAGG ATG TCT
                          ||||||||||| ||| |||
                          CCTTAACCTCC TAC AGA
                          __  A
GAM106  SUFU    3' ATCAGTTCGCCTCCATTCC  1668     T     __
                          GGAAT GGAGGCGA TGAT
                          ||||| |||||||| ||||
                          CCTTA CCTCCGCT ACTA
                          _       TG
GAM106  CGRP-RCP 5' AAGATCATCGCACCCCC    1503    AATT AG
                          GG  GG GCGATGATCTT
                          ||  || ||||||||||
                          CC  CC CGCTACTAGAA
                          ____  CA
GAM106  LOC152348 5' ATCAGTCACCACCAATTCC  3358        A C _
                          GGAATTGG GG GA TGAT
                          |||||||| || || ||||
```

```
                                 CCTTAACC CC CT ACTA
                                  A     A   G
GAM106   LOC158219 3' ATCATTGCCCCCAACTCC   3214     A   A
                         GGA TTGG GGCGATGAT
                         ||| |||| |||||||||
                         CCT AACC CCGTTACTA
                             C    C
GAM106   LOC255177 3' AGAATCACCTCTAATCC    3711     A     C  GA
                         GGA TTGGAGG GAT  TCT
                         ||| |||||||| ||| |||
                         CCT AATCTCC CTA  AGA
                         _        A   __
GAM106   LOC90522  3' AGGCACCGCCTCCATCC    2651     AT    A A
                         GGA  TGGAGGCG TG TCT
                         |||  |||||||| || |||
                         CCT  ACCTCCGC AC GGA
                         __        C _
GAM107   CEACAM4   3' CTCTGAGTCCTGAGGAG    860      CC  TCGT
                         CTCC TAG  ACTCAGAG
                         |||| |||  ||||||||
                         GAGG GTC  TGAGTCTC
                            A_  C___
GAM107   MGC11115  3' CTCTGAGGCCCAGGGGAGC  2244       AGTC A
                         GCTCCCCT  GT CTCAGAG
                         ||||||||  || |||||||
                         CGAGGGGA  CG GAGTCTC
                            CC__ _
GAM107   PRO2714   5' CTCTAAGCAACAAGGGGAGCG 1837      A C ACTC
                         CGCTCCCCT GT GT  AGAG
                         ||||||||| || ||  ||||
                         GCGAGGGGA CA CG  TCTC
                            A A AA__
GAM107   LOC147057 3' CTCTGAGTATTGGGAAGAGAGG 3288   G_  C_  GTC
                  C              GC CTC CCTA  GTACTCAGAG
                         || ||| |||| ||||||||||
                         CG GAG GGGT  TATGAGTCTC
                          GA AA    ___
GAM107   LOC147976 3' CTCTGGTGTGACTAAGGAAAG 3114     CC  _    T
                         CT CCT AGTCGTAC CAGAG
                         || ||| |||||||| |||||
                         GA GGA TCAGTGTG GTCTC
                          AA A      _
GAM107   LOC57100  3' CTCTGAGTACCCTGGCGGGAGG 1917    G   _  TC
                  C              GC CTCCC CTAG  GTACTCAGAG
                         || ||||| |||| |||||||||
                         CG GAGGG GGTC  CATGAGTCTC
                          _  C  C_
GAM108   E2F3      3' ACAAACCTCGAAACGAACAGTT 875          TCA A A
               AA               TTAGCTGTTT  TC AG TTTGT
                         ||||||||||| || || |||||
```

```
                        AATTGACAAG  AG TC AAACA
                        CAA  C C
GAM108  SCML1    3' ACAGAGAACCAAAACAGCTAA 1328           CATCAAGA
                   TTAGCTGTTTT     TTTGT
                   ||||||||||     |||||
                   AATCGACAAAA     AGACA
                        CCAAG___
GAM108  KIAA1468 3' ACAAATCCTACAGTCAATAGCT 3541          TTCATCAA
            AA              TTAGCTGTT     GATTTGT
                   |||||||||     |||||||
                   AATCGATAA     CTAAACA
                        CTGACATC
GAM108  MGC16025 3' ACAAATCTCCAAGAAAACAGCT 2295           ATCA
                   AGCTGTTTC   AGATTTGT
                   |||||||||   |||||||
                   TCGACAAAAG   TCTAAACA
                        AACC
GAM108  LOC148545 3' CTTGATAAAAACAACTAA    3119      C    C
                   TTAG TGTTTT ATCAAG
                   |||| |||||| ||||||
                   AATC ACAAAA TAGTTC
                        A    A
GAM108  LOC163669 5' ACAAATCTTGACGAACAC    3233     T  A
                   GT TTC TCAAGATTTGT
                   || ||| |||||||||||
                   CA AAG AGTTCTAAACA
                        C  C
GAM108  LOC51652  3' ACAAATAAGGAAAACAGCT   1660          ATCAAG
                   AGCTGTTTC   ATTTGT
                   |||||||||   ||||||
                   TCGACAAAAG   TAAACA
                        GAA___
GAM109  CXCL13    3' GTTATTCAGTTATAAGTAATA 1299               T
                   TATTATTTATAACTGA GTAAC
                   ||||||||||||||| |||||
                   ATAATGAATATTGACT TATTG
                        _
GAM109  RASGRP1   3' ATCAGTGGCTTAAATAATA   1241          TA__
                   TATTATTTA  ACTGAT
                   |||||||||  ||||||
                   ATAATAAAT  TGACTA
                        TCGG
GAM109  HTGN29    3' GGGTCATTATCACTTAAATAAT 1899     TAAC   TA_
            A            TATTATTTA  TGATG  ACCC
                   |||||||||  |||||  ||||
                   ATAATAAAT  ACTAT  TGGG
                        TC__   TAC
GAM109  KIAA1430 3' GGACCACATCAGTTGCAAA    3179    A      AA_
                   TTT TAACTGATGT  CC
                   ||| |||||||||| ||
```

```
                        AAA GTTGACTACA  GG
                        C      CCA
GAM109  KIAA1764 5'  GCTTCAGTTATAAATAGTA  2850              T
                        TATTATTTATAACTGA GT
                        ||||||||||||||| ||
                        ATGATAAATATTGACT CG
                                 T
GAM109  ZAK       3'  TATCAGTTTCAAATAATA  2428         AT
                        TATTATTT AACTGATG
                        |||||||| ||||||||
                        ATAATAAA TTGACTAT
                                 CT
GAM109  LOC151571 5'  GGTTATATACATCATAAATGA  3348          AACTG
                        TTATTTAT   ATGTAACC
                        ||||||||   ||||||||
                        AGTAAATA   TATATTGG
                              CTACA
GAM109  LOC196989 3'  GGGCACATAGAGCTATAAATAA  3470        A  G_   AA
                        TTATTTATA CT ATGT CC
                        ||||||||| || |||| ||
                        AATAAATAT GA TACA GG
                              C GA   CG
GAM109  LOC221431 3'  TATATCAGGTCATAAATAATA  3553          AA_
                        TATTATTTAT CTGATGTA
                        |||||||||| ||||||||
                        ATAATAAATA GACTATAT
                              CTG
GAM110  COL12A1  3'  AACCTCCTTGTTTTAGACAC  1102          CTAGT
                        GTGTCTAA    GGAGGTT
                        ||||||||    |||||||
                        CACAGATT    CCTCCAA
                              TTGTT
GAM110  COL12A1  3'  AACCTCCTTGTTTTAGACAC  2380          CTAGT
                        GTGTCTAA    GGAGGTT
                        ||||||||    |||||||
                        CACAGATT    CCTCCAA
                              TTGTT
GAM110  FLJ25473 5'  AACCTCCGAAAGCTCAGCACAC  2496      _ AA_ AG
                        GTGT CT  CT TGGAGGTT
                        |||| || || ||||||||
                        CACA GA  GA GCCTCCAA
                              C CTC AA
GAM111  ANK1     5'  CAGCCCCAGCTGCTCCTCCTC  699        A TC C A
                        GAGGAGGA TA GT GG GCTG
                        |||||||| || || || ||||
                        CTCCTCCT GT CG CC CGAC
                              C __ A C
GAM111  ANK1     5'  CAGCCCCAGCTGCTCCTCCTC  1918       A TC C A
                        GAGGAGGA TA GT GG GCTG
                        |||||||| || || || ||||
```

```
                          CTCCTCCT GT  CG CC CGAC
                          C __   A  C
GAM111  CDH5    3' CAGCCCAGCACCCCTTCCTCG  857         AATATC C A
                          CGAGGAGG   GT GG GCTG
                          ||||||||   || || ||||
                          GCTCCTTC   CG CC CGAC
                              CCCA__ A  _
GAM111  DSP     5' CAGCTCCGACGCAGCTCCTC  1110         GAATAT
                          GAGGAG   CGTCGGAGCTG
                          ||||||   |||||||||||
                          CTCCTC   GCAGCCTCGAC
                              GAC___
GAM111  GDF5    3' AGCCCACCATTTCTCCTC  755            ATC C A
                          GAGGAGGAAT  GT GG GCT
                          ||||||||||  || || |||
                          CTCCTCTTTA  CA CC CGA
                              C__ _ _
GAM111  OGDH    3' CAGCTCTGGCCACAATCCTCC  3510        ATATC
                          GGAGGA   GTCGGAGCTG
                          ||||||   ||||||||||
                          CCTCCT   CGGTCTCGAC
                              AACAC
GAM111  RFX2    3' CAGCCCCGGCCGGCGCCTCCTC 765         AATATC   A
         G                CGAGGAGG   GTCGG GCTG
                          ||||||||   ||||| ||||
                          GCTCCTCC   CGGCC CGAC
                              GCGGC_   C
GAM111  SET7    5' CAGCCCCGACTGCTCCTCCTC  2153        A TC   A
                          GAGGAGGA TA  GTCGG GCTG
                          |||||||| ||  ||||| ||||
                          CTCCTCCT GT  CAGCC CGAC
                              C __   C
GAM111  C17orf31 3' CAGCTCCCCCTTCACCCCTCCT  1723      AATATCGTC
         TG               CGAGGAGG    GGAGCTG
                          ||||||||    |||||||
                          GTTCCTCC    CCTCGAC
                              CCACTTCCC
GAM111  caspr5  5' CAGCTCCGAAGAATCCCCCG  2396   A A ATA G
                          CG GG GGA  TC TCGGAGCTG
                          || || |||  || ||||||||||
                          GC CC CCT  AG AGCCTCGAC
                              _ _ A__ A
GAM111  caspr5  5' CAGCTCCGAAGAATCCCCCG  2462   A A ATA G
                          CG GG GGA  TC TCGGAGCTG
                          || || |||  || ||||||||||
                          GC CC CCT  AG AGCCTCGAC
                              _ _ A__ A
GAM111  CECR2   5' AGCCCCGCCCCCTCCTCG  2192           AATATC T A
                          CGAGGAGG   G CGG GCT
                          ||||||||   | ||| |||
```

```
                    GCTCCTCC   C GCC CGA
                  CC____ _   C
GAM111  DKFZP434P0111 3' CAGCCCCGGCCCATTCCTCC 2790      ATC   A
                  GGAGGAAT GTCGG GCTG
                  ||||||||  ||||| ||||
                  CCTCCTTA  CGGCC CGAC
                     CC_    C
GAM111  FLJ10634 3' CAGCTCCAGCCATCCACCCCTC 1791      A AAT C  C
                  GAGG GG  AT GT GGAGCTG
                  |||| ||  || || |||||||
                  CTCC CC  TA CG CCTCGAC
                    _ ACC  C  A
GAM111  FLJ32334 3' CTCCAAAACGCTATTCCTTC 2483       T  C__
                  GGAGGAATA CGT  GGAG
                  ||||||||| |||  ||||
                  CTTCCTTAT GCA  CCTC
                     C  AAA
GAM111  FLJ32894 3' CTCTGGTTTCCTCCTC    2491       TATCG
                  GAGGAGGAA   TCGGAG
                  |||||||||   ||||||
                  CTCCTCCTT   GGTCTC
                     T____
GAM111  KIAA0711 5' AGTTGGACACACCCCTCCTCG 1572      AATATC  G  G
                  CGAGGAGG   GTC GA CT
                  ||||||||   ||| || ||
                  GCTCCTCC   CAG TT GA
                  CCACA_  G  _
GAM111  KIAA1649 3' CAGCTGGAAGACATTCCTCC 2245      A G GG
                  GGAGGAAT TC TC  AGCTG
                  |||||||| || ||  |||||
                  CCTCCTTA AG AG  TCGAC
                    C A G_
GAM111  KIAA1649 3' CAGCTGGAAGACATTCCTCC 2770      A G GG
                  GGAGGAAT TC TC  AGCTG
                  |||||||| || ||  |||||
                  CCTCCTTA AG AG  TCGAC
                    C A G_
GAM111  MGC30052 3' AGTACATCATTCCTCCTC   2500      ATC CGGA
                  GAGGAGGAAT GT   GCT
                  ||||||||||  ||   |||
                  CTCCTCCTTA  CA   TGA
                    CTA ____
GAM111  MGC4737 3' CAGCCCCATCTCCTCCTCCTC 2206      ATATC C  A
                  GAGGAGGA   GT GG GCTG
                  ||||||||   || || ||||
                  CTCCTCCT   TA CC CGAC
                    CCTC_ C  _
GAM111  LOC115110 5' AGCCCCGGTTCCTCCCCG   2923    A   ATCGT A
                  CG GGAGGAAT   CGG GCT
                  || |||||||    ||| |||
```

```
                          GC CCTCCTTG    GCC CGA
                           C      ____      C
GAM111  LOC123242 5' CAGCTCCACCATATTTCTCC 3029       C  C
                     GGAGGAATAT GT GGAGCTG
                     |||||||||| || |||||||
                     CCTCTTTATA CA CCTCGAC
                               C _
GAM111  LOC146237 3' CAGCTCTCACATTCCTTC   3282       ATC  C
                     GGAGGAAT  GT GGAGCTG
                     ||||||||  || |||||||
                     CTTCCTTA  CA TCTCGAC
                             ___ C
GAM111  LOC147160 5' CAGCCCCACTCACTCCTTCTC 3291      ATATC  C  A
                     GAGGAGGA   GT GG GCTG
                     ||||||||   || || ||||
                     CTCTTCCT   CA CC CGAC
                          CACT_ C _
GAM111  LOC149670 5' CAGCCCTGCCACTCCTTCCTC 3138    _ ATATC  C  A
                     GAGGA GGA   GT GG GCTG
                     ||||| |||   || || ||||
                     CTCCT CCT   CG CC CGAC
                        T  CAC__ T _
GAM111  LOC155072 3' CAGCTCCGACCACACCATCCTC 3374    _ AATATC
                     GAGGA GG    GTCGGAGCTG
                     ||||| ||    ||||||||||
                     CTCCT CC    CAGCCTCGAC
                        A  ACAC__
GAM111  LOC158828 3' CAGCCCCGGAGCCATTCCTCC 3227      ATCG   A
                     GGAGGAAT   TCGG GCTG
                     ||||||||   |||| ||||
                     CCTCCTTA   GGCC CGAC
                          CCGA   C
GAM111  LOC202868 3' CAGCTCCGACCACACCATCCTC 3487    _ AATATC
                     GAGGA GG    GTCGGAGCTG
                     ||||| ||    ||||||||||
                     CTCCT CC    CAGCCTCGAC
                        A  ACAC__
GAM111  LOC253001 5' CAGCTCCACCATATTTCTCC 3697       C  C
                     GGAGGAATAT GT GGAGCTG
                     |||||||||| || |||||||
                     CCTCTTTATA CA CCTCGAC
                               C _
GAM111  LOC253841 5' CAGCCCCAGCTGCTCCTCCTC 3704     A TC  C  A
                     GAGGAGGA TA  GT GG GCTG
                     |||||||| ||  || || ||||
                     CTCCTCCT GT  CG CC CGAC
                          C __ A  C
GAM111  LOC51177 5' CAGCTCCGACGCCCTCCCG   1676    A   AATAT
                     CG GGAGG    CGTCGGAGCTG
                     || |||||    |||||||||||
```

```
                                GC CCTCC   GCAGCCTCGAC
                                _    C____
GAM111 LOC91408  3' CAGCTTTTGGTAATATTCTTCC 2735          CG   _
         TC                GAGGAGGAATAT TCGGA GCTG
                           ||||||||||| ||||| ||||
                           CTCCTTCTTATA GGTTT CGAC
                                AT    T
GAM112 KIAA1265 3' CCATATGAATTTTGGTATA 2896          A__
                   TATACCAGAATT ATGG
                   |||||||||||| ||||
                   ATATGGTTTTAA TACC
                        GTA
GAM112 MGC2731  3' CCACTGATTGGCTGGTGTA 2050        __   A
                   TATACCAG AATTA TGG
                   |||||||| ||||| |||
                   ATGTGGTC TTAGT ACC
                      GG    C
GAM113 C3AR1    3' ACTGTCAAAGAATCAATCCA 1081    A       GA__
                   TG ATTGATTCTT  GGT
                   || |||||||||   |||
                   AC TAACTAAGAA   TCA
                      C       ACTG
GAM113 GABARAPL3 3' TATACCTCTCACTCATTCA 2260    T TTCTT
                   TGAAT GA   GAGGTATA
                   ||||| ||   ||||||||
                   ACTTA CT   CTCCATAT
                    _ CACT_
GAM113 GOLGA2LY 5' CTCAGTGAAAACATCAATTCA 2684        ____ _
                   TGAATTGAT  TC TTGAG
                   |||||||||  || |||||
                   ACTTAACTA  AG GACTC
                    CAAA  T
GAM113 PEG10    3' TACCTCAAGTATCAATTCA 1607        T
                   TGAATTGAT CTTGAGGTA
                   ||||||||| |||||||||
                   ACTTAACTA GAACTCCAT
                       T
GAM113 RNF13    3' TGTAACTCAAGCATCAATTCA 1376       T   G
                   TGAATTGAT CTTGAG TATA
                   ||||||||| |||||| ||||
                   ACTTAACTA GAACTC ATGT
                       C    A
GAM113 LOC143692 5' GCCTATCAGAAGTCAATTCA 3060       CT  __
                   TGAATTGATT TGA GGT
                   |||||||||| ||| |||
                   ACTTAACTGA ACT CCG
                       AG  AT
GAM113 LOC151201 5' GTTTATACCATTGGATTCAATT 3342      T TGA
         CA                TGAATTGA TCT GGTATAAAC
                          |||||| ||| |||||||||
```

```
                        ACTTAACT AGG   CCATATTTG
                          T   TTA
GAM113  LOC257431 5' CTCAGTGAAAACATCAATTCA 3231         ____ _
                        TGAATTGAT   TC TTGAG
                        ||||||||| || |||||
                        ACTTAACTA   AG GACTC
                          CAAA  T
GAM113  LOC93259  5' ATACCCAGGTCAATTC     2927      TT   A
                        GAATTGA  CTTG GGTAT
                        ||||||| |||| |||||
                        CTTAACT GGAC CCATA

                          __   _
GAM114  SAMHD1    3' CATCAAATCCTGCCCCCGT 2594        AA      T
                        ACGGG  CAGGGTTTG TG
                        ||||| ||||||||| ||
                        TGCCC  GTCCTAAAC AC
                          CC      T
GAM114  LOC150864 5' AATCAACAGGCTCCCG     3150      ACAGG
                        CGGGA   GTTTGTTGATT
                        |||||   |||||||||||
                        GCCCT   CGGACAACTAA

                          _____
GAM114  LOC257358 3' AATCAACACCCTTGCCCC    3731      AA  TT
                        GGG  CAGGG  TGTTGATT
                        ||| ||||| |||||||
                        CCC  GTTCC  ACAACTAA
                          C_   C_
GAM114  LOC90288  3' AATCTTGCTCTGTTCCC    2621          TTGTT
                        GGGAACAGGGT   GATT
                        |||||||||| ||||
                        CCCTTGTCTCG   CTAA
                          TT___
GAM115  GAD1      3' GGCTTAGTAATAGATCACGGCA 777     A A    A T
                        TGC CGT ATCTATTAT GA GCC
                        ||| ||| ||||||||| || |||
                        ACG GCA TAGATAATG TT CGG
                        _   C     A _
GAM115  KLHL2     3' TATAATAAATTATGTGCA    1371        C
                        TGCACGTAAT TATTATA
                        |||||||||| |||||||
                        ACGTGTATTA ATAATAT
                          A
GAM115  KIAA0276  3' CACTGTAATGTTACATGCA  2904     C  CT    A
                        TGCA GTAAT  ATTATAG TG
                        |||| ||||| ||||||| ||
                        ACGT CATTG  TAATGTC AC
                          A    __     _
GAM115  LOC130814 3' GGCACCTATAATAAATGAC  3012     A C    A
                        GT AT TATTATAG TGCC
                        || || ||||||| ||||
```

```
                          CA TA ATAATATC ACGG
                           G A      C
GAM116  TGFBR2   3' AATGCCTGTATATAAATATGAA 1002         TAG   C_
                    TTCATATTTAT  ATAC GCATT
                    |||||||||||  |||| |||||
                    AAGTATAAATA  TATG CGTAA
                                  TC
GAM116  KIAA1223 3' AATGAGTCTATTAATAAATATG 2908          ATACCG
         AA             TTCATATTTATTAG   CATT
                    |||||||||||||   ||||
                    AAGTATAAATAATT   GTAA
                         ATCTGA
GAM116  PRO2859  5' CGGTATGTAAATATGAA    1840        TAG
                    TTCATATTTAT ATACCG
                    ||||||||||| ||||||
                    AAGTATAAATG TATGGC

                         ___
GAM116  PSIP2    3' ATGCTTATACAATAAATATGAA 2324         AG  CC
                    TTCATATTTATT ATA GCAT
                    |||||||||||| ||| ||||
                    AAGTATAAATAA TAT CGTA
                         CA  T_
GAM116  LOC152185 3' AATGCAAATCAAATAAATATGA 2497        A  ACC
                    TCATATTTATT GAT  GCATT
                    |||||||||| ||| |||||
                    AGTATAAATAA CTA  CGTAA
                         A  AA_
GAM116  LOC89953 3' ATGCTACTCTAATAAATAT  2437        TACC
                    ATATTTATTAGA   GCAT
                    |||||||||||   ||||
                    TATAAATAATCT   CGTA
                         CAT_
GAM116  LOC90509 5' GTGTTTAATAAATATGAA    2649
                    TTCATATTTATTAGATAC
                    ||||||||||||||||||
                    AAGTATAAATAATTTGTG


GAM117  BPNT1    3' CAATGAGAGAGATTATA    2702     TCC
                    TATGA TCTCTCATTG
                    ||||| |||||||||
                    ATATT AGAGAGTAAC

                         ___
GAM117  FLJ21709 3' CAATGAGGGTGTCATG    2235       CCT
                    TATGAT CTCTCATTG
                    |||||| |||||||||
                    GTACTG GGGAGTAAC
                         T__
GAM117  MGC13007 5' CAATGAGAAAGGAGAGTA 2246      GA  C
                    TAT TCCT TCTCATTG
                    ||| |||| |||||||||
```

```
                          ATG  AGGA AGAGTAAC
                           AG   A
GAM117  MGC14407  5' CAATGGGGGGAGACATA    2294      ATC
                       TATG  CTCTCTCATTG
                       ||||  |||||||||||
                       ATAC  GAGGGGGTAAC
                          A__
GAM117  LOC151201 3' CAATGGGGCGGTCATA     3341      T T T
                       TATGA CC CTC CATTG
                       ||||| || ||| |||||
                       ATACT GG GGG GTAAC
                         _  C  _
GAM117  LOC197131 3' CAATGAGTGGATCATG     3419      TCT
                       TATGATCC  CTCATTG
                       ||||||||  |||||||
                       GTACTAGG  GAGTAAC
                          T__
GAM117  LOC219942 3' CAACAAGCGGGGGGGTCATA  3598        _ CA
                       TATGATCCTCT CT  TTG
                       |||||||||||| || |||
                       ATACTGGGGGG GA  AAC
                          C  AC
GAM118  B3GAT1    5' CAGTTGGGCCGGACTCTCC   1855      ACTA
                       GGAGAGTT  GGCCCAACTG
                       ||||||||  ||||||||||
                       CCTCTCAG  CCGGGTTGAC
                            G___
GAM118  B3GAT1    5' CAGTTGGGCCGGACTCTCC   2362      ACTA
                       GGAGAGTT  GGCCCAACTG
                       ||||||||  ||||||||||
                       CCTCTCAG  CCGGGTTGAC
                            G___
GAM118  GALNT7    3' AGTTGAGAAACTCTCCTG    2365      A AGGCC
                       TAGGAGAGTT CT    CAACT
                       |||||||||| ||    |||||
                       GTCCTCTCAA GA    GTTGA
                            A _____
GAM118  ZNF76     3' CAGCTGGGCGCCCACTCTCCT 1019      TACTAG   A
                       AGGAGAGT    GCCCA CTG
                       ||||||||    ||||| |||
                       TCCTCTCA    CGGGT GAC
                         CCCG__    C
GAM118  DKFZp434M0331 5' CAGTTGAGCCTCATGGCTCTCC 1727    CT  C
                       GGAGAGTTA AGGC CAACTG
                       ||||||||| |||| ||||||
                       CCTCTCGGT TCCG GTTGAC
                          AC   A
GAM118  FLJ20666  5' CAGTCACCTGATGACTCTCC  1763      C  CCCA
                       GGAGAGTTA TAGG   ACTG
                       ||||||||| ||||   ||||
```

```
                        CCTCTCAGT GTCC   TGAC
                          A   AC__
GAM118  FYCO1    3' CAGTCAGGCCCCAGGTTCTTCC 2064     G  TTA A_   CA
                        GGA AG  CT GGCC  ACTG
                        ||| ||  || |||| ||||
                        CCT TC  GA CCGG  TGAC
                         _  TTG CC   AC
GAM118  ILF3     5' CAGTTGAACCCAGCAGCCCGCC 1121    AGA  A A CC
                        GG  GTT CT GG  CAACTG
                        ||  ||| || ||  ||||||
                        CC  CGA GA CC  GTTGAC
                         GCC  C C  AA
GAM118  KIAA0193 3' CAGTTGGGCCTAATCCTGCCTC 1544     A  TAC__
                        GAG GT    TAGGCCCAACTG
                        ||| ||    |||||||||||
                        CTC CG    ATCCGGGTTGAC
                         _  TCCTA
GAM118  KIAA1163 3' CAGCTGGACCTAGCTGATTCTC 3121         _   C  A
                        GAGAGTTA CTAGG CCA CTG
                        |||||||| ||||| ||| |||
                        CTCTTAGT GATCC GGT GAC
                           C     A   C
GAM118  KIAA1247 3' GGCTCCCTAGCAACTCCCTA 2609     A   A   C__
                        TAGG GAGTT CTAGG  CC
                        |||| ||||| |||||  ||
                        ATCC CTCAA GATCC  GG
                         _    C    CTC
GAM118  KIAA1870 5' CAGCTGGGCCTGCAGTTCCTCC 2293    A  TT __    A
            C           GG GAG ACT AGGCCCA CTG
                        || ||| ||| ||||||| |||
                        CC CTC TGA TCCGGGT GAC
                         _ CT  CG      C
GAM118  LOC146517 3' CAGTTAAACCTAGATCCCTCCC 3095    A  TTA_   CCC
        T               AGG GAG  CTAGG  AACTG
                        ||| |||  |||||  |||||
                        TCC CTC  GATCC  TTGAC
                         _  CCTA    AAA
GAM118  LOC162083 5' CAGCTGGGCTCCATAGACCCTC 3242    A  ACTA_    A
        C                   GGAG GTT   GGCCCA CTG
                            |||| |||   |||||| |||
                            CCTC CAG   TCGGGT GAC
                             C   ATACC    C
GAM118  LOC220477 5' CAGTTGGGCCCTGTACCATCCC 3041    A  GT_ TA
                        GG GA  TAC GGCCCAACTG
                        || ||  ||| |||||||||
                        CC CT  ATG CCGGGTTGAC
                         _ ACC  TC
GAM118  LOC222237 3' AGCTGGGCCTAGTCAACT   3650      _       A
                        AGTT ACTAGGCCCA CT
                        |||| |||||||||| ||
```

```
                          TCAA TGATCCGGGT GA
                             C        C
GAM118  LOC255096 5' TGGGCCAGCAGATTCTCC    3745        A_  A
                     GGAGAGTT  CT GGCCCA
                     |||||||| || ||||||
                     CCTCTTAG  GA CCGGGT
                           AC  _
GAM118  LOC92340  3' CAGCCAGGCCCTCTTCTCCTG 2837         TTACTA   CAA
                     TAGGAGAG   GGCC  CTG
                     ||||||||   |||| |||
                     GTCCTCTT   CCGG  GAC
                           CTC___    ACC
GAM119  ARG1     3' TAACTTGGCAAAAGACTTA  700           ___
                     TAAGTCTT  CCAAGTTG
                     ||||||||  ||||||||
                     ATTCAGAA  GGTTCAAT
                          AAC
GAM119  BACH2    3' TGATGCTGCAGTGGAAAAC  1964    C    AGT
                     GT TTCCA  TGGCATCA
                     || |||||  ||||||||
                     CA AAGGT  GTCGTAGT
                        A    GAC
GAM119  CDR1     3' TGATTTACTGGAAGACTTG  1083        A TGGC
                     TAAGTCTTCCA GT   ATCA
                     ||||||||||| ||   ||||
                     GTTCAGAAGGT CA   TAGT
                          _  TT__
GAM119  CNTN3    3' GCATTATTTGGAAGACTTA  2758          TG_
                     TAAGTCTTCCAAGT  GC
                     ||||||||||||| ||
                     ATTCAGAAGGTTTA  CG
                              TTA
GAM119  ESRRG    3' GATGTCGAAGAAACTTA   2748    C  CAAG
                     TAAGT TTC  TTGGCATC
                     ||||| |||  ||||||||
                     ATTCA AAG   AGCTGTAG
                          _  A___
GAM119  FSTL1    3' GATGCCAGAGAGAACTTA  1357    CT CAAG
                     TAAGT TC  TTGGCATC
                     ||||| ||  ||||||||
                     ATTCA AG   GACCGTAG
                          AG A___
GAM119  GABRB2   3' TGATGTAGGACTTGGAAAAC 1967   C      G_
                     GT TTCCAAGTT GCATCA
                     || ||||||||| ||||||
                     CA AAGGTTCAG TGTAGT
                        A     GA
GAM119  GABRB2   3' TGATGTAGGACTTGGAAAAC 776    C      G_
                     GT TTCCAAGTT GCATCA
                     || ||||||||| ||||||
```

```
                           CA AAGGTTCAG TGTAGT
                            A      GA
GAM119  MCP      3' ATGCCAACTCTTAAGATT  925       CCA
                           AGTCTT AGTTGGCAT
                           |||||| |||||||||
                           TTAGAA TCAACCGTA
                                 TTC
GAM119  NRIP1    3' ATGCCAACAAAGCTTA  2548      T CCAA
                           TAAG CTT  GTTGGCAT
                           |||| ||| |||||||||
                           ATTC GAA  CAACCGTA
                             _  A___
GAM119  OPHN1    3' GATGCAAACATTGGAAGATT  936       _ G
                           AGTCTTCCAA GTT GCATC
                           |||||||||| ||| |||||
                           TTAGAAGGTT CAA CGTAG
                                A  A
GAM119  PTPRO    3' GAAGCACCGGGAAGACTTA  964      AA TG A
                           TAAGTCTTCC GT GC TC
                           |||||||||| || || ||
                           ATTCAGAAGG CA CG AG
                            GC __  A
GAM119  PTPRO    3' GAAGCACCGGGAAGACTTA  2155     AA TG A
                           TAAGTCTTCC GT GC TC
                           |||||||||| || || ||
                           ATTCAGAAGG CA CG AG
                            GC __  A
GAM119  PTPRO    3' GAAGCACCGGGAAGACTTA  2156     AA TG A
                           TAAGTCTTCC GT GC TC
                           |||||||||| || || ||
                           ATTCAGAAGG CA CG AG
                            GC __  A
GAM119  PTPRO    3' GAAGCACCGGGAAGACTTA  2157     AA TG A
                           TAAGTCTTCC GT GC TC
                           |||||||||| || || ||
                           ATTCAGAAGG CA CG AG
                            GC __  A
GAM119  PTPRO    3' GAAGCACCGGGAAGACTTA  2158     AA TG A
                           TAAGTCTTCC GT GC TC
                           |||||||||| || || ||
                           ATTCAGAAGG CA CG AG
                            GC __  A
GAM119  RAD50    5' TGATGTCAATGGAGAACTTA  2419     CT  AG
                           TAAGT TCCA TTGGCATCA
                           ||||| |||| |||||||||
                           ATTCA AGGT AACTGTAGT
                             AG   __
GAM119  RORB     3' GTGTTCATGAAGACTTA  1338      CAA TG
                           TAAGTCTTC GT GCAT
                           ||||||||| || ||||
```

```
                          ATTCAGAAG  TA  TGTG
                              ___  CT
GAM119  SORD     3' TAACTTCATGAAGACTTA   990          C__
                   TAAGTCTTC  AAGTTG
                   |||||||||  ||||||
                   ATTCAGAAG  TTCAAT
                              TAC
GAM119  SULT1C1  3' ATGCCACCCTTTTGGAAGC  797      T      T___
                   G CTTCCAAG   TGGCAT
                   | ||||||||   ||||||
                   C GAAGGTTT   ACCGTA
                   _     TCCC
GAM119  WRB      3' GTTCTTTGAAGACTTA      1137        C  TT
                   TAAGTCTTC AAG  GGC
                   ||||||||| ||| |||
                   ATTCAGAAG TTC  TTG
                      T  __
GAM119  ANKRD5   5' TGATCGCCCGGAAGACT     1978        AAGTT  _
                   AGTCTTCC   GGC ATCA
                   ||||||||   ||| ||||
                   TCAGAAGG   CCG TAGT
                     C____  C
GAM119  C7orf10  3' TGATACCACTAAGAAGAAGATT 2084        CA___  T C
        TA                TAAGTCTTC   AGT GG ATCA
                   |||||||||   ||| || ||||
                   ATTTAGAAG   TCA CC TAGT
                     AAGAA  _ A
GAM119  DKFZP727M111 5' TGATGCCAACTCAGAC   1633      TCCA
                   GTCT  AGTTGGCATCA
                   ||||  |||||||||||
                   CAGA  TCAACCGTAGT
                     C___
GAM119  FLJ13262 3' TGATGCCAACTCCCCCGCACTT 2113       CTTCCA_
                   AAGT    AGTTGGCATCA
                   ||||    |||||||||||
                   TTCA    TCAACCGTAGT
                     CGCCCC
GAM119  FLJ20425 5' TGACGGCTTTTTGACAAGACTT 1755        C_  TT A_
        A                TAAGTCTT CAAG GGC TCA
                   ||||||||| |||| ||| |||
                   ATTCAGAA GTTT TCG AGT
                     CA  T_ GC
GAM119  KIAA0953 3' TGGAAACTAGAAGACTTA    2763        CA  GG
                   TAAGTCTTC AGTT CA
                   ||||||||| |||| ||
                   ATTCAGAAG TCAA GT
                     A_  AG
GAM119  KIAA1450 3' TGATGCTTCATTGAAGACTTA 2732        C GTT
                   TAAGTCTTC AA  GGCATCA
                   ||||||||| ||  ||||||
```

```
                          ATTCAGAAG TT  TCGTAGT
                          _  ACT
GAM119  NEUROD6  5' TGAAAAGATTTGGAAGAC   2000          GGCA
                          GTCTTCCAAGTT   TCA
                          |||||||||||  |||
                          CAGAAGGTTTAG   AGT
                               AAA_
GAM119  PRO0255  3' GTTTCTTGAAAGACTTA   1475       C  TT
                          TAAGTCTT CAAG  GGC
                          ||||||||| ||||  |||
                          ATTCAGAA GTTC  TTG
                               A   T_
GAM119  UBE3B   5' TGATGCCGAGGAAAGACT   3069      _ AAG
                          AGTCTT CC  TTGGCATCA
                          |||||| ||  |||||||||
                          TCAGAA GG  AGCCGTAGT
                               A ___
GAM119  ZIM2   3' ATGTCAGTAGGAGACTTA   1623       CAAG
                          TAAGTCTTC  TTGGCAT
                          |||||||||  |||||||
                          ATTCAGAGG   GACTGTA
                               AT__
GAM119  LOC112868 3' TGTAGACATGAAGACTTA   2962       CAA  G
                          TAAGTCTTC  GTT GCA
                          ||||||||| |||  |||
                          ATTCAGAAG  CAG TGT
                               TA_  A
GAM119  LOC116166 3' TAACTTCATGAAGACTTA   2545         C__
                          TAAGTCTTC  AAGTTG
                          ||||||||| ||||||
                          ATTCAGAAG  TTCAAT
                               TAC
GAM119  LOC123855 3' TGAGCACGCTTGGAATAC   3033   C    TG A
                          GT TTCCAAGT  GC TCA
                          || ||||||||| || |||
                          CA AAGGTTCG  CG AGT
                            T    CA _
GAM119  LOC146818 5' GATGCCGAAGAAGGCT   3100         CAAG
                          AGTCTTC   TTGGCATC
                          |||||||   ||||||||
                          TCGGAAG   AGCCGTAG
                               A___
GAM119  LOC152190 5' TGACAACTGGAAGACTT   2864      A  G
                          AAGTCTTCCA GTTG CA
                          |||||||||| |||| ||
                          TTCAGAAGGT CAAC GT
                               _   A
GAM119  LOC153077 3' TGATACCAACTTGAGATAACTT 3366   CT _    C
                          AAGT TC CAAGTTGG ATCA
                          |||| || ||||||||| ||||
```

```
                         TTCA  AG GTTCAACC TAGT
                         AT A        A
GAM119  LOC158382 3' TGATAGCTGATAAGACTTA  3388          CCAA  TG _
                         TAAGTCTT   GT GC ATCA
                         |||||||  || || ||||
                         ATTCAGAA   TA CG TAGT
                         ____  GT  A
GAM119  LOC158476 3' TGATCTGTCAGGAGACTTA  3391          CAAGT   ___
                         TAAGTCTTC   TGGC ATCA
                         |||||||||   |||| ||||
                         ATTCAGAGG   ACTG TAGT
                         _____ CTC
GAM119  LOC164397 5' ATGTCTTCTGAAGACTTA   3249          CA TT
                         TAAGTCTTC AG GGCAT
                         ||||||||| || |||||
                         ATTCAGAAG TC CTGTA
                         __ TT
GAM119  LOC196510 3' TGATCTGGCTTGGCAGACTTA  3416        T    TG C
                         TAAGTCT CCAAGT G ATCA
                         ||||||| |||||| | ||||
                         ATTCAGA GGTTCG C TAGT
                         C    GT _
GAM119  LOC200220 3' TGATCTGGCTTGGCAGACTTA  3445        T    TG C
                         TAAGTCT CCAAGT G ATCA
                         ||||||| |||||| | ||||
                         ATTCAGA GGTTCG C TAGT
                         C    GT _
GAM119  LOC201477 5' CAACTGAGGTCTGTAAGACTTA 3472        _____ A_
                         TAAGTCTT   CC AGTTG
                         |||||||||   || |||||
                         ATTCAGAA   GG TCAAC
                         TGTCT AG
GAM119  LOC201696 5' TGATGCCATTGAAGACTT   2650          CAAGT
                         AAGTCTTC   TGGCATCA
                         ||||||||    ||||||||
                         TTCAGAAG   ACCGTAGT
                         TT___
GAM119  LOC220469 3' GATGGCCAGAAGATTTA   3049           CAAGT   _
                         TAAGTCTTC   TGGC ATC
                         |||||||||   |||| |||
                         ATTTAGAAG   ACCG TAG
                         _____  G
GAM119  LOC221272 3' TGACACCAACTTTTGAGATTTA 3615        CC    CA
                         TAAGTCTT AAGTTGG TCA
                         |||||||| ||||||| |||
                         ATTTAGAG TTCAACC AGT
                         TT    AC
GAM119  LOC222166 3' TGAGGCCCCAGAGGACTTA  3636          CAAGTT A
                         TAAGTCTTC   GGC TCA
                         |||||||||    ||| |||
```

```
                        ATTCAGGAG    CCG AGT
                         ACC___  G
GAM119  LOC253220 5' TGAGCAGCTCCTGGAAGAC  3706          __   G A
                        GTCTTCCA AGTTG C TCA
                        |||||||| ||||| | |||
                        CAGAAGGT  TCGAC G AGT
                          CC       _ _
GAM119  LOC51275  5' TGATGGAAGTGGAAGATT  1694         AG  GG
                        AGTCTTCCA TT CATCA
                        ||||||||| || |||||
                        TTAGAAGGT AG GTAGT
                             GA __
GAM119  LOC54505  5' GATTTCTGGAAGACTTA    2800          AGTT  C
                        TAAGTCTTCCA  GG ATC
                        |||||||||||  || |||
                        ATTCAGAAGGT  CT TAG
                             ___ T
GAM119  LOC90844  3' TGATTGCATTGGAAGATCA  2682   A      GTTG  _
                        A GTCTTCCAA  GCA TCA
                        | |||||||||  ||| |||
                        A TAGAAGGTT  CGT AGT
                          C    A___  T
GAM119  LOC92697  5' GATGCCACCAGACTTA    2882         TCCAA  T
                        TAAGTCT   GT GGCATC
                        |||||||   || ||||||
                        ATTCAGA   CA CCGTAG
                          C____  _
GAM120  KIF5C    3' ACAAATTCTATTGAAGTATTT 1122       AC
                        GAATAT TCAATAGAATTGT
                        |||||| |||||||||||||
                        TTTATG AGTTATCTTAAACA
                          A_
GAM120  DKFZP564M182 3' ACAATTGTCAAGTATATTCTG 3097         CA   AAT
                        TAGAATATACT ATAG TTGT
                        ||||||||||| |||| ||||
                        GTCTTATATGA TGTT AACA
                             AC    ___
GAM120  KIAA0852  5' ACAAATTCGTAAGTATCCTCTA 1594      AT   CAATA
                        TAGA ATACT   GAATTTGT
                        |||| |||||   ||||||||
                        ATCT TATGA   CTTAAACA
                          CC   ATG__
GAM120  PRO0097  5' CTATTGAGTAGTATTCTA  1472         _
                        TAGAATAT ACTCAATAG
                        |||||||| |||||||||
                        ATCTTATG TGAGTTATC
                           A
GAM120  LOC222161 5' TTGTATTAGTATATTCTA  3578        C  G
                        TAGAATATACT AATA AA
                        ||||||||||| |||| ||
```

```
                    ATCTTATATGA TTAT TT
                      _    G
GAM120   LOC255811 5'  ACAAAGATGGCTATCGGTATAT 3662            CA   AA___
       TCTA                TAGAATATACT ATAG    TTTGT
                    |||||||||| |||| |||||
                    ATCTTATATGG TATC   AAACA
                      C_   GGTAG
GAM121   DPYD    3' TATTAAGTAAAATCCCCTTC 2569    TAT
                    GA  GGGATTTACTTAATA
                    ||  ||||||||||||||
                    CT  CCCTAAAATGAATTAT
                     TC_
GAM121   KIAA1240 3' TATTAATGTTTAAATCCCATCT 2761    T      T_ _
         C              GA ATGGGATTT AC TTAATA
                    || |||||||| || |||||
                    CT TACCCTAAA TG AATTAT
                     C      TT T
GAM121   KIAA1843 3' TATTACAGAAAATCCCATATTC 2624   A         A _
         A               A GATATGGGATTT CT TAATA
                    | |||||||||||| || |||||
                    A TTATACCCTAAAA GA ATTAT
                     C      _ C
GAM121   LOC122786 3' ATTAAGTAATCCACCATTTCTT 2995     T   GATT
         A              TAAGA ATGG   TTACTTAAT
                    ||||| |||| |||||||||
                    ATTCT TACC   AATGAATTA
                      T   ACCT
GAM122   FGF12   3' AACTAAACTGTATTGTTATT 1935         TAG
                    AATAACAGT  TAGTTTAGTT
                    ||||||||| |||||||||
                    TTATTGTTA  GTCAAATCAA
                      T__
GAM122   FGG     3' AACTGCTAACTTCTATTGA 1965       AC
                    TCAATA AGTTAGTAGTT
                    |||||| |||||||||||
                    AGTTAT TCAATCGTCAA
                     CT
GAM122   NEBL    3' AACTAACTGTCAACTGTTG 1295         AG   T
                    TAACAGTT TAGTT AGTT
                    |||||||| ||||| ||||
                    GTTGTCAA GTCAA TCAA
                     CT    _
GAM122   RPE    3' AACTAAATATTTATAACTGTTC 2623    AT     GTA__
         TGA             TCA AACAGTTA   GTTTAGTT
                    ||| |||||||   |||||||||
                    AGT TTGTCAAT   TAAATCAA
                     C_    ATTTA
GAM122   TRHDE    3' AACTAAATTTCTCAACTGTTAT 1446    A    _ T
         GA              TCA TAACAGTT AG AGTTTAGTT
                    ||| |||||||| || |||||||||
```

```
                        AGT ATTGTCAA TC TTAAATCAA
                          _      C  T
GAM122   BCMP1      3' AACTAAACATTCTCTGTTCTGA 2197     AT    TT  A
                       TCA  AACAG  AGT GTTTAGTT
                       ||| ||||| ||| ||||||||
                       AGT  TTGTC  TTA CAAATCAA
                         C_      TC  _
GAM122   DKFZP434A0225 3' AACTAAACCTAATGCTGCTGTT 3624        T   ____
             A            TAACAGT AGTA   GTTTAGTT
                          |||||||| ||||   ||||||||
                          ATTGTCG TCGT   CAAATCAA
                             _   AATC
GAM122   FLJ12899   3' ACTAAAATACTGTTATTGG  2069           TAGTAG
                       TCAATAACAGT    TTTAGT
                       |||||||||| |    ||||||
                       GGTTATTGTCA    AAATCA
                                TA____
GAM122   PREI3      3' AACTAAACTACTAAGTTA  2747     AG
                       TAAC  TTAGTAGTTTAGTT
                       |||| ||||||||||||||
                       ATTG  AATCATCAAATCAA
                          __
GAM122   PSIP2      3' AATTAAGCAACTGACATTGA 2323     AACA   A
                          TCAAT   GTTAGT GTTTAGTT
                          ||||| |||||| ||||||||
                          AGTTA   CAGTCA CGAATTAA
                          ____        A
GAM122   LOC220963 3' AACTAAACTACTTGTTGTGTTG 3526      A TT
         A              TCAATA CAG  AGTAGTTTAGTT
                        |||||| ||| ||||||||||||
                        AGTTGT GTT TCATCAAATCAA
                           _  GT
GAM123   LOC143098 5' CGATGATCTGGCCGAAGAGCTT 3051      A_ _ TT
                       AAGCT TCG TCA GATCATCG
                       ||||| ||| ||| ||||||||
                       TTCGA AGC GGT CTAGTAGC
                          GA  C  __
GAM124   CALB2      3' AAAGAAGAGTTTACAGACAATA 853          ATTTA_
             A             TTATTGTCTG   TTTCTTT
                           |||||||||| ||||||||
                           AATAACAGAC   GAAGAAA
                                ATTTGA
GAM124   TRAF5      3' AAAGAAATAGGTTCACAACAGG 1133     A  CT
             A             TCTT TTGT GATTTATTTCTTT
                           |||| |||| |||||||||||||
                           AGGA AACA TTGGATAAAGAAA
                              C  C_
GAM124   C15orf5    3' AAAGAAAGGCACCATCAGACAA 2173     A       TTA___
         AAGA               TCTT TTGTCTGAT   TTTCTTT
                           |||| ||||||||     |||||||
```

```
                    AGAA AACAGACTA    AAAGAAA
                    _    CCACGG
GAM124  DKFZp761K1423 3' AAAGAAATAAATCCAACAA  1826      CT
                    TTGT GATTTATTTCTTT
                    |||| ||||||||||||
                    AACA CTAAATAAAGAAA
                      AC
GAM124  FLJ12892 5' AAAGAAACATCATCTTCAGATA 2801           TTTA____
          ATAAGA            CTTATTGTCTGA    TTTCTTT
                    ||||||||||    ||||||||
                    GAATAATAGACT    AAAGAAA
                      TCTACTAC
GAM124  MGC15437 3' AAAGAAATAAATGACAAT  2292       TG
                    ATTGTC ATTTATTTCTTT
                    |||||| |||||||||||
                    TAACAG TAAATAAAGAAA

                      __
GAM124  MGC27016 3' AAAGAAATGATGAGACAAAAG 2503      A    G  T
          A              TCTT TTGTCT ATT ATTTCTTT
                    |||| |||||| ||| ||||||||
                    AGAA AACAGA TAG TAAAGAAA
                     A    G  _
GAM124  LOC154089 3' AAGAAATATTACAATAAGG  3187       CTGATT
                    TCTTATTGT    TATTTCTT
                    |||||||||    ||||||||
                    GGAATAACA    ATAAAGAA
                      TT____
GAM124  LOC159053 3' AAAGAAATAAACTTTTGGACAG 3395      TG ___
                    TTGTC A  TTTATTTCTTT
                    ||||| |  |||||||||||
                    GACAG T  AAATAAAGAAA
                    GT TTC
GAM125  XPR1    3' CTGAGCATATCTCTCGTAACA 1152           AAATCA  A
                    TGTTACGA    ATAT TTCAG
                    ||||||||    |||| |||||
                    ACAATGCT    TATA GAGTC
                    CTC___   C
GAM126  DFNA5   3' TGCACGTTAAAAGTTGAC   1109       GC     A
                    GTCAAT TTTAACGT CA
                    |||||| ||||||||| ||
                    CAGTTG AAATTGCA GT
                    A_     C
GAM126  LRAT    3' TGTCTTTTAAAGCATTTACTAA 2557     C     CGT
                    TTAGT AATGCTTTAA  ACA
                    ||||| ||||||||||  |||
                    AATCA TTACGAAATT  TGT
                    T       TTC
GAM126  PKHD1   3' TACACTATAGCACTTTGACTAA 2449        __  T AC
                    TTAGTCAA TGCT TA GTA
                    |||||||| |||| || |||
```

```
                      AATCAGTT ACGA AT CAT
                        TC   T CA
GAM126  HSPC055   5' CGTTGAAGCACAACTAA   1480      CAA
                      TTAGT  TGCTTTAACG
                      IIIII IIIIIIIIII
                      AATCA  ACGAAGTTGC
                         AC_
GAM126  PRO0386   5' TACTTTGAGAAACATTGACTA 1845       C__   C
                      TAGTCAATG  TTTAA GTA
                      IIIIIIIII  IIIII III
                      ATCAGTTAC  GAGTT CAT
                           AAA    T
GAM126  LOC121441 3' TGTTTCTAAGCCATTGACTAA 2992        _  TAACGT
                      TTAGTCAATG CTT    ACA
                      IIIIIIIIII III    III
                      AATCAGTTAC GAA    TGT
                          C TCTT__
GAM127  ADAMTS5   3' ATTGGAAACTGAAATTCAGA 1351    CA  G    TG
                      TC AATT CAGTTTC GT
                      II IIII IIIIIII II
                      AG TTAA GTCAAAG TA
                      AC   A    GT
GAM127  BHLHB3    3' GATACCAGATAATCACAA   2161    CA  _
                      TTG GTT TCTGGTATC
                      III III IIIIIIIII
                      AAC TAA AGACCATAG
                      AC   T
GAM127  CCR2      3' GCTGAAAACTGCAACTTG   767     A    CT
                      CAA TTGCAGTTT GGT
                      III IIIIIIIII III
                      GTT AACGTCAAA TCG
                      C      AG
GAM127  DCN       3' ACCTAACTGCAATGTGGA   868     A    TCT
                      TCCA ATTGCAGTT GGT
                      IIII IIIIIIIII III
                      AGGT TAACGTCAA CCA
                        G     T__
GAM127  DCN       3' ACCTAACTGCAATGTGGA   2421    A    TCT
                      TCCA ATTGCAGTT GGT
                      IIII IIIIIIIII III
                      AGGT TAACGTCAA CCA
                        G     T__
GAM127  DCN       3' ACCTAACTGCAATGTGGA   2422    A    TCT
                      TCCA ATTGCAGTT GGT
                      IIII IIIIIIIII III
                      AGGT TAACGTCAA CCA
                        G     T__
GAM127  DCN       3' ACCTAACTGCAATGTGGA   2423    A    TCT
                      TCCA ATTGCAGTT GGT
                      IIII IIIIIIIII III
```

```
                     AGGT TAACGTCAA  CCA
                       G       T__
GAM127  DCN     3' ACCTAACTGCAATGTGGA  2424      A     TCT
                     TCCA ATTGCAGTT  GGT
                     |||| |||||||||  |||
                     AGGT TAACGTCAA  CCA
                       G       T__
GAM127  DCN     3' ACCTAACTGCAATGTGGA  2425      A     TCT
                     TCCA ATTGCAGTT  GGT
                     |||| |||||||||  |||
                     AGGT TAACGTCAA  CCA
                       G       T__
GAM127  EXTL1   5' GGACACGGCCCTGCATTCTGGA 1116      AAT    TTT GTA
                     TCCA  TGCAG  CTG  TCC
                     ||||  |||||  |||  |||
                     AGGT  ACGTC  GGC  AGG
                       CTT    CC_  AC_
GAM127  FASN    3' GGACACCAGAGCTGCCGACTTG 1088       A  _  T   A
              GA           TCCAA TTG CAGTT CTGGT TCC
                           ||||| ||| ||||| ||||| |||
                           AGGTT AGC GTCGA GACCA AGG
                             C   C    _    C
GAM127  INHBB   3' GTCAGAAACTGCCATTTG   905      T
                     CAAAT GCAGTTCTGGT
                     ||||| |||||||||||
                     GTTTA CGTCAAAGACTG
                               C
GAM127  NEDD4   3' GATGGAAAACTGAAATTTGGA 2875       G    CTGG
                     TCCAAATT CAGTTT   TATC
                     |||||||| ||||||   ||||
                     AGGTTTAA GTCAAA   GTAG
                          A     AG__
GAM127  NFYA    3' ACCAAAACTGCAATCAGGA  1955    AA      C
                     TCC ATTGCAGTTT TGGT
                     ||| |||||||||| ||||
                     AGG TAACGTCAAA ACCA
                      AC        _
GAM127  NFYA    3' ACCAAAACTGCAATCAGGA  933     AA      C
                     TCC ATTGCAGTTT TGGT
                     ||| |||||||||| ||||
                     AGG TAACGTCAAA ACCA
                      AC        _
GAM127  RAD17   5' ACCTGCAACTGTAATTTG   967           TCT
                     CAAATTGCAGTT  GGT
                     |||||||||||| |||
                     GTTTAATGTCAA  CCA
                           CGT
GAM127  RAD17   5' ACCTGCAACTGTAATTTG   2410          TCT
                     CAAATTGCAGTT  GGT
                     |||||||||||| |||
```

```
                        GTTTAATGTCAA  CCA
                                 CGT
GAM127  RAD17      5' ACCTGCAACTGTAATTTG    2411          TCT
                        CAAATTGCAGTT  GGT
                        |||||||||||  |||
                        GTTTAATGTCAA  CCA
                                 CGT
GAM127  RAD17      5' ACCTGCAACTGTAATTTG    2412          TCT
                        CAAATTGCAGTT  GGT
                        |||||||||||  |||
                        GTTTAATGTCAA  CCA
                                 CGT
GAM127  RAD17      5' ACCTGCAACTGTAATTTG    2413          TCT
                        CAAATTGCAGTT  GGT
                        |||||||||||  |||
                        GTTTAATGTCAA  CCA
                                 CGT
GAM127  RAD17      5' ACCTGCAACTGTAATTTG    2414          TCT
                        CAAATTGCAGTT  GGT
                        |||||||||||  |||
                        GTTTAATGTCAA  CCA
                                 CGT
GAM127  ZNF146     3' GGACACCAGAAAATTTGTA   1358      __      A
                        TGCAG  TTTCTGGT TCC
                        |||||  |||||||| |||
                        ATGTT  AAAGACCA AGG
                           TA      C
GAM127  CHST3      3' GGACACCAGAAGACGATTCAGA 1096   CA    CAG      A
                        TC AATTG  TTTCTGGT TCC
                        || |||||  |||||||| |||
                        AG TTAGC  GAAGACCA AGG
                         AC  A__       C
GAM127  DKFZp762E1511 3' ATGCTACTGAATTTGGA    2531        G   TTCT
                        TCCAAATT CAGT   GGTAT
                        |||||||| ||||   |||||
                        AGGTTTAA GTCA   TCGTA
                          _   ____
GAM127  EIF5       5' GATACCAAAAAGTTGCAAT    878         _   C
                        ATTGCAG TTT TGGTATC
                        ||||||| ||| |||||||
                        TAACGTT AAA ACCATAG
                           G   A
GAM127  LATS1      3' GGATACCACAGCCAATT      2563      CA  TC
                        AATTG GTT TGGTATCC
                        ||||| ||| ||||||||
                        TTAAC CGA ACCATAGG
                          __  C_
GAM127  MGC27277   3' CCAAAATTGCAATTCAGA     2505      CA        C
                        TC AATTGCAGTTT TGG
                        || ||||||||||| |||
```

```
                    AG  TTAACGTTAAA ACC
                    AC          _
GAM127  POLD3     3' ACTAAAACTGAATTTG    3538      G    C
                    CAAATT CAGTTT TGGT
                    |||||| |||||| ||||
                    GTTTAA GTCAAA ATCA


                          _      _
GAM127  TSLRP     5' GATACATCACTGAAATTTGGA 1435       G    TTCTG
                    TCCAAATT CAGT    GTATC
                    |||||||| ||||    |||||
                    AGGTTTAA GTCA    CATAG
                          A    CTA__
GAM127  LOC147463 3' ATACCAGTGGCAAATTTGGA 3108        _   AGTTT
                    TCCAAATT GC    CTGGTAT
                    |||||||| ||    |||||||
                    AGGTTTAA CG    GACCATA
                          A   GT___
GAM127  LOC161734 3' GGATACCGTTTTCAACTTGGA 3400     A  C TTTC
                    TCCAA TTG AG   TGGTATCC
                    ||||| ||| ||   ||||||||
                    AGGTT AAC TT   GCCATAGG
                        C  _  TT__
GAM127  LOC164173 3' GATATTGAACTGCATCTGGA 3235      AAT     CT
                    TCCA  TGCAGTTT GGTATC
                    ||||  |||||||| ||||||
                    AGGT  ACGTCAAG TTATAG
                          CT_    ___
GAM127  LOC199675 3' GCCAAAGCCACAACTTGGA 3429      A  CA   C
                    TCCAA TTG GTTT TGGT
                    ||||| ||| |||| ||||
                    AGGTT AAC CGAA ACCG
                        C  AC   _
GAM127  LOC200150 5' GCCAACTGCAGTTTG        3439          TTC
                    CAAATTGCAGT TGGT
                    ||||||||||| ||||
                    GTTTGACGTCA ACCG

                          ___
GAM127  LOC51185  3' ATACCAGAAACATCTACTTGGG 1679       ATTGCA
                    TCCAA    GTTTCTGGTAT
                    |||||    |||||||||||
                    GGGTT    CAAAGACCATA
                        CATCTA
GAM127  LOC90459  3' GCTGAAACTGCAATTGGA 2643      A     T
                    TCCAA TTGCAGTTTC GGT
                    ||||| |||||||||| |||
                    AGGTT AACGTCAAAG TCG
                        _      _
GAM127  LOC91694  5' ATACCAGAGGTCACTTCAG 2769    C  ___
                    TTG AGT  TTCTGGTAT
                    ||| |||  |||||||||
```

```
                          GAC TCA  GAGACCATA
                            T  CTG
GAM128  SCNN1G   3' ACCTGAACTATTAGCACGTC  793      __      CA
                          GA TGCTAATA TCAGGT
                          || |||||||| ||||||
                          CT ACGATTAT AGTCCA
                             GC     CA
GAM128  YY1      3' ACCTGATGTGTACATC   1016     CTA
                          GATG ATACATCAGGT
                          |||| |||||||||||
                          CTAC TGTGTAGTCCA
                             A__
GAM128  FLJ21940 3' CCTGATGTGTACCTTA    2014     A TAAT
                          TAAG TGC  ACATCAGG
                          |||| |||  ||||||||
                          ATTC ATG  TGTAGTCC
                             C  ____
GAM128  PRO0159  5' ACCTGATGTATTGCTCT   1474     T T
                          AGA GC AATACATCAGGT
                          ||| || |||||||||||
                          TCT CG TTATGTAGTCCA
                            _  _
GAM128  LOC200282 3' CCTGATGTAGGTCTTATT  3448       GCTAA
                          AATAAGAT  TACATCAGG
                          ||||||||  |||||||||
                          TTATTCTG  ATGTAGTCC
                              G____
GAM129  PCDH9    5' ACATAGGGGATAGTAGCCAAC 3262          G C
                          GTTGGCTACTATCTT TA GT
                          ||||||||||||||| || ||
                          CAACGATGATAGGG AT CA
                             G  A
GAM129  ERO1L    3' GTACAATAACAACTCA    1508     GC CTATC
                          TGAGTTG TA  TTGTAC
                          ||||||| ||  ||||||
                          ACTCAAC AT  AACATG
                             A_  _____
GAM129  LOC253287 5' AAGATAATGCCAACTCA   3740         TAC
                          TGAGTTGGC TATCTT
                          ||||||||| ||||||
                          ACTCAACCG ATAGAA
                             TA_
GAM129  LOC254268 5' ACAACTGACAGCAGCCAGCTCA 3674       A A __
                          TGAGTTGGCT CT TC  TTGT
                          |||||||||| || ||  ||||
                          ACTCGACCGA GA AG  AACA
                             C  C TC
GAM130  AP1B1    3' AGCCACAGAAGCTGTGCC   802              A
                          GGCATGGTTTCTGTG CT
                          ||||||||||||||| ||
```

```
                          CCGTGTCGAAGACAC GA
                                  C
GAM130   BBS2    5' AGCCACAGAAGGCGCCG   2214      AT G     A
                          CGGC  G TTTCTGTG CT
                          IIII I IIIIIIII II
                          GCCG  C GAAGACAC GA
                            __ G      C
GAM130   FRK     5' AGCCACAGAAAGCAAGCCG  890      A G     A
                          CGGC TG TTTCTGTG CT
                          IIII II IIIIIIII II
                          GCCG AC AAAGACAC GA
                             A G      C
GAM130   HSPD1   3' TAGTCACAGAAATTCC     2560    CAT
                          GG  GGTTTCTGTGACTA
                          II  IIIIIIIIIIII
                          CC  TTAAAGACACTGAT
                          __
GAM130   IL20RA  3' TAGGAACTAAACTATGCC   1501        CT GA
                          GGCATGGTTT GT CTA
                          IIIIIIIIII II III
                          CCGTATCAAA CA GAT
                            T_ AG
GAM130   LAMC3   3' TAGTCACACTCCCTGCCG   1269     T TTTC
                          CGGCA GG   TGTGACTA
                          IIIII II   IIIIIIII
                          GCCGT CC   ACACTGAT
                            C TC__
GAM130   MEST    3' TAGTCAAGTCACCATGCTG  2872        TT G
                          CGGCATGGT CT TGACTA
                          IIIIIIIII II IIIIII
                          GTCGTACCA GA ACTGAT
                            CT _
GAM130   MKI67   3' AGCCACAGGAGATGTC     927      GG    A
                          GGCAT TTTCTGTG CT
                          IIIII IIIIIIII II
                          CTGTA GAGGACAC GA
                            __      C
GAM130   MMP19   3' AGCCACAGAAACCACGTT   2011    A     A
                          GGC TGGTTTCTGTG CT
                          III IIIIIIIIIII II
                          TTG ACCAAAGACAC GA
                            C      C
GAM130   MMP19   3' AGCCACAGAAACCACGTT   2012    A     A
                          GGC TGGTTTCTGTG CT
                          III IIIIIIIIIII II
                          TTG ACCAAAGACAC GA
                            C      C
GAM130   MS4A8B  3' AGTCTAGGAAACCATGCTG  2200          GT
                          CGGCATGGTTTCT GACT
                          IIIIIIIIIIIII IIII
```

```
                          GTCGTACCAAAGG CTGA
                                 AT
GAM130   PSMD9    3' TAGCCACAGACATGCTG    957        GTT    A
                          CGGCATG  TCTGTG CTA
                          ||||||| |||||| |||
                          GTCGTAC  AGACAC GAT
                            ___        C
GAM130   SH3GL2   3' TAGTCACAGAACTGCTG    984        TGGT
                          CGGCA  TTCTGTGACTA
                          ||||| ||||||||||
                          GTCGT  AAGACACTGAT
                              C___
GAM130   SPTAN1   3' AGTCACAATCATCATGTC    994         TTC
                          GGCATGGT  TGTGACT
                          ||||||||  |||||||
                          CTGTACTA  ACACTGA
                             CTA
GAM130   SYNGR1   3' AGTCACAGACTGTCCTGCC   1146     T TT__
                          GGCA GG  TCTGTGACT
                          |||| ||  |||||||||
                          CCGT CC  AGACACTGA
                           _ TGTC
GAM130   TRIM9    3' AGTCACAGAACTGGGGGTC   2353     AT__  T
                          GGC  GGTT CTGTGACT
                          |||  |||| |||||||||
                          CTG  TCAA GACACTGA
                            GGGG  _
GAM130   TRPM2    5' AGTTGCGAAACCATGTCG    1011           T TG
                          CGGCATGGTTTC G ACT
                          |||||||||||| | |||
                          GCTGTACCAAAG C TGA
                              _ GT
GAM130   ATPAF1   3' AGTCACAGAGATGAGCC     2582     ATG
                          GGC  GTTTCTGTGACT
                          |||  ||||||||||||
                          CCG  TAGAGACACTGA
                            AG_
GAM130   CENTG2   3' TAGTCACGCGGCACGCGCCG  1587      A _ TC
                          CGGC TG GTT  TGTGACTA
                          |||| || |||  |||||||
                          GCCG GC CGG  GCACTGAT
                            C A  C_
GAM130   COL12A1  3' AGCCACAGAAGATGTC      2381     GG     A
                          GGCAT TTTCTGTG CT
                          ||||| ||||||||| ||
                          CTGTA GAAGACAC GA
                            __        C
GAM130   COL12A1  3' AGCCACAGAAGATGTC      1103     GG     A
                          GGCAT TTTCTGTG CT
                          ||||| ||||||||| ||
```

```
                              CTGTA GAAGACAC GA
                              __        C
GAM130 DKFZp547I224 3' AGCCGCTGCAAAATCATGCC  1902          CT__  A
                          GGCATGGTTT  GTG CT
                          ||||||||||  ||| ||
                          CCGTACTAAA  CGC GA
                              ACGT  C
GAM130 DKFZp566H0824 3' AGTGAGCTGAGACCATGCC  1721             T G_
                          GGCATGGTTTC GT ACT
                          |||||||||| || |||
                          CCGTACCAGAG CG TGA
                            T AG
GAM130 FLJ11726 3' AGTGAGCCGAGACCATGCC   2119          T G_
                          GGCATGGTTTC GT ACT
                          |||||||||| || |||
                          CCGTACCAGAG CG TGA
                            C AG
GAM130 FLJ12668 3' TAGTCACTTGCCACCATGCC  2124          TTCT_
                          GGCATGGT   GTGACTA
                          ||||||||   |||||||
                          CCGTACCA   CACTGAT
                            CCGTT
GAM130 FLJ13385 3' TAGTCACAAAGATAATACC  2098     C G  C
                          GG AT GTTT TGTGACTA
                          || || |||| |||||||
                          CC TA TAGA ACACTGAT
                            A  A   A
GAM130 FLJ14936 3' TAGTCACAGACACAGGAGCC  2243     ATG_ T
                          GGC  GT TCTGTGACTA
                          |||   || ||||||||||
                          CCG  CA AGACACTGAT
                            AGGA  C
GAM130 FLJ14957 3' AGTCACAGCTGGGCTTCC   2291     CAT   __
                          GG  GGTTT CTGTGACT
                          ||  ||||| ||||||||
                          CC  TCGGG GACACTGA
                            T__  TC
GAM130 HSU79275 3' TAGTCACAAGATTTACCAT  2746     T__  _
                          ATGGT  TCT GTGACTA
                          |||||  ||| |||||||
                          TACCA  AGA CACTGAT
                            TTT  A
GAM130 KALI    3' AGTGAGCCAAAATCATGCC  2346          CT G_
                          GGCATGGTTT GT ACT
                          |||||||||| || |||
                          CCGTACTAAA CG TGA
                            AC AG
GAM130 KIAA0121 3' TAGTCACAGAGTGGCTG    2957     ATGGT
                          CGGC  TTCTGTGACTA
                          ||||   |||||||||||
```

```
                        GTCG   GAGACACTGAT
                        GT___
GAM130  KIAA0254 3' AGTCACAGGGAAGTGCTG   1540      GG TT
                        CGGCAT T CTGTGACT
                        |||||| | ||||||||
                        GTCGTG A GACACTGA
                          A_ GG
GAM130  KIAA0820 3' AGCACAAACCATGTC      2838      TC   A
                        GGCATGGTT TGTG CT
                        ||||||||| |||| ||
                        CTGTACCAA ACAC GA
                              __  _
GAM130  KIAA0863 3' AGTCATGGAGACCAGCC    3669      A
                        GGC TGGTTTCTGTGACT
                        ||| |||||||||||||
                        CCG ACCAGAGGTACTGA
                          _
GAM130  KIAA1023 3' AGCCACAGGAGATGTC     1728      GG     A
                        GGCAT TTTCTGTG CT
                        ||||| ||||||||| ||
                        CTGTA GAGGACAC GA
                          __       C
GAM130  KIAA1161 5' AGTCACAGAACATCTCC    3213    CAT  _
                        GG  GGT TTCTGTGACT
                        ||   ||| ||||||||||
                        CC  CTA AAGACACTGA
                          T__  C
GAM130  KIAA1254 3' TCACAGAAAGTAAAGCCG   2876      A_ G
                        CGGC TG TTTCTGTGA
                        |||| || |||||||||
                        GCCG AT AAAGACACT
                          AA  G
GAM130  KIAA1805 3' TAGCTTGTGAAACCATTCC  3148    C     T TG _
                        GG ATGGTTTC G A CTA
                        || ||||||||| | | |||
                        CC TACCAAAG T T GAT
                         T    _ GT C
GAM130  KIAA1866 3' TCACAGGACCGTCATGCTG  2587          T__
                        CGGCATGG TTCTGTGA
                        |||||||| |||||||||
                        GTCGTACT AGGACACT
                           GCC
GAM130  KIAA1958 3' AGTGAGCCGAGACCATGCC  3218           T G_
                        GGCATGGTTTC GT ACT
                        |||||||||| || |||
                        CCGTACCAGAG CG TGA
                          C  AG
GAM130  LIMK2   5' AGTCACAGACGGATTTGC    1709    T   __
                        GCA GGTT TCTGTGACT
                        ||| |||| |||||||||
```

```
                      CGT TTAG AGACACTGA
                        _    GC
GAM130  MGC12921 5' AGTCACAGCAGCTGCC    2666      TG  T
                      GGCA GTT CTGTGACT
                      |||| ||| ||||||||
                      CCGT CGA GACACTGA
                           __  C
GAM130  MGC5149  3' TAGCCACAGAAATGTC    2939      GGT    A
                      GGCAT TTCTGTG CTA
                      ||||| ||||||| |||
                      CTGTA AAGACAC GAT
                          ___      C
GAM130  MOST2    5' AGCCACCTGGCCATGCTG  1909        TCT  A
                      CGGCATGGTT GTG CT
                      |||||||||| ||| ||
                      GTCGTACCGG CAC GA
                           TC_ C
GAM130  MRPL9    3' AGTAGACCGAAACCATCC  2195    C    T G_
                      GG ATGGTTTC GT ACT
                      || |||||||| || |||
                      CC TACCAAAG CA TGA
                       _       C GA
GAM130  NCBP2    3' AGTCACAGAAGGTTCC    1397    C GG
                      GG AT TTTCTGTGACT
                      || || |||||||||||
                      CC TG GAAGACACTGA
                       T __
GAM130  PCYT1B   3' TAGTCACAGGAGCTGC    1160      TG
                      GCA GTTTCTGTGACTA
                      ||| |||||||||||||
                      CGT CGAGGACACTGAT
                          __
GAM130  PIP3-E   3' AGTCACAAACAATGTC    2764        G  TC
                      GGCAT GTT TGTGACT
                      ||||| ||| |||||||
                      CTGTA CAA ACACTGA
                        A __
GAM130  PPP1R15B 5' AGTCGGAAAACCATCGCCG  2288    _    CTG
                      CGGC ATGGTTT TGACT
                      |||| ||||||| |||||
                      GCCG TACCAAA GCTGA
                        C    AG_
GAM130  TFIP11   3' TAGTCACAGTAATCCCC   1410    CAT   T
                      GG  GGTT CTGTGACTA
                      ||  |||| |||||||||
                      CC  CTAA GACACTGAT
                        C__  T
GAM130  LOC132617 3' AGTTTGAAATCATGCC   3039        TGT
                      GGCATGGTTTC GACT
                      ||||||||||| ||||
```

```
                              CCGTACTAAAG  TTGA
                                    T__
GAM130  LOC147660 3' AGTCACAGATCACGCC     3111      A  TT
                        GGC TGG  TCTGTGACT
                        ||| |||  |||||||||
                        CCG ACT  AGACACTGA
                          C   __
GAM130  LOC149302 5' AGTCACAGCAGCCGCC     3129      AT  T
                        GGC  GGTT CTGTGACT
                        |||  |||| |||||||||
                        CCG  CCGA GACACTGA
                           __  C
GAM130  LOC151720 5' AGTCACAAAAACCATGCTG  3160          C
                        CGGCATGGTTT TGTGACT
                        ||||||||||| |||||||
                        GTCGTACCAAA ACACTGA
                              A
GAM130  LOC152215 3' TAGTCACAAAGGGCTTACG  3167    GCAT   C_
                        CG   GGTTT TGTGACTA
                        ||   ||||| |||||||||
                        GC   TCGGG ACACTGAT
                         AT__    AA
GAM130  LOC152426 3' AGTCACAGGCAGGTGCC    3359      G_ TT
                        GGCAT GT CTGTGACT
                        ||||| || |||||||||
                        CCGTG CG GACACTGA
                          GA  __
GAM130  LOC155179 3' AGCCACAGGAGATGTC     3199      GG     A
                        GGCAT TTTCTGTG CT
                        ||||| ||||||||| ||
                        CTGTA GAGGACAC GA
                           __       C
GAM130  LOC157562 5' TAGTCACATGGCCACACC   3381    CA  TC
                        GG TGGTT TGTGACTA
                        || ||||| |||||||||
                        CC ACCGG ACACTGAT
                         AC   T_
GAM130  LOC163115 3' AGTCACAGATCCGATGTC   3244      _ TT
                        GGCAT GG TCTGTGACT
                        ||||| || |||||||||
                        CTGTA CC AGACACTGA
                          G T_
GAM130  LOC169026 3' TAGTCACAAAATTTTACC   3260    CAT  C
                        GG  GGTTT TGTGACTA
                        ||  ||||| |||||||||
                        CC  TTAAA ACACTGAT
                         ATT   _
GAM130  LOC170106 5' AGCCACAGGAAGTGTCC    3255    C  G     A
                        GG ATG TTTCTGTG CT
                        || ||| ||||||||| ||
```

```
                              CC TGT AAGGACAC GA
                              _  G        C
GAM130  LOC170425 5' TAGTCACAACCCAATGC    3048       __  TTC
                              GCAT GGT  TGTGACTA
                              |||| |||  ||||||||
                              CGTA CCA  ACACTGAT
                              AC      ___
GAM130  LOC197342 3' AGTCACAGAAGGACTCGCC  3423     AT   __
                              GGC GGTT TCTGTGACT
                              ||| |||| |||||||||
                              CCG TCAG AGACACTGA
                              C_  GA
GAM130  LOC200488 5' AGTCATGATCATGCCG     3477          TCT
                              CGGCATGGTT GTGACT
                              |||||||||| |||||
                              GCCGTACTAG TACTGA
                              ___
GAM130  LOC219667 3' TAGTCACAAATCAGAACTG  3517    CA_  TC
                              CGG  TGGTT TGTGACTA
                              |||  ||||| ||||||||
                              GTC  ACTAA ACACTGAT
                              AAG      __
GAM130  LOC220980 5' AGCCACGTGAGCCATGCC   3592         C A
                              GGCATGGTTT TGTG CT
                              |||||||||| |||| ||
                              CCGTACCGAG GCAC GA
                                T   C
GAM130  LOC253461 3' AGCCACAGAAAATATACC   3700    C G    A
                              GG ATG TTTCTGTG CT
                              || ||| |||||||| ||
                              CC TAT AAAGACAC GA
                                A A    C
GAM130  LOC253502 3' AGCCACAGAGGCCTGCC    3660    T     A
                              GGCA GGTTTCTGTG CT
                              |||| |||||||||| ||
                              CCGT CCGGAGACAC GA
                              _       C
GAM130  LOC254211 5' AGTCACAGAGAGGTGCC    3707        GG
                              GGCAT TTTCTGTGACT
                              ||||| |||||||||||
                              CCGTG AGAGACACTGA
                              G_
GAM130  LOC90785 3' AGTGAGCCGAGACCATACC   2677    C    T G_
                              GG ATGGTTC GT  ACT
                              || ||||||| || |||
                              CC TACCAGAG CG  TGA
                              A    C AG
GAM130  LOC91050 3' AGTCACAGAAATCATTCT    2701    C
                              GG ATGGTTTCTGTGACT
                              || |||||||||||||||
```

```
                       TC TACTAAAGACACTGA
                       T
GAM130  LOC91380  3' AGTGAGCCGAGACCATGCC  2733        T G_
                   GGCATGGTTTC GT  ACT
                   |||||||||| || |||
                   CCGTACCAGAG CG  TGA
                       C  AG
GAM131  EIF2C1    3' TTATTCCTCTCTGTCCACA  1414    A      T TACA
                   TG TGGACAGA GA   AATAA
                   || |||||||| ||   |||||
                   AC ACCTGTCT CT   TTATT
                   _    _ CC__
GAM131  PCDHA9    3' TATCTATATCTGTCTATCA  1461              ___
                   TGATGGACAGAT  GATA
                   ||||||||||| ||||
                   ACTATCTGTCTA  CTAT
                       TAT
GAM131  KIAA0923  3' TATTTGTGTTGTCCATT    1463        GATG
                   GATGGACA   ATACAAATA
                   |||||||    |||||||||
                   TTACCTGT   TGTGTTTAT
                       ____
GAM131  UBF-fl    3' ATTTGTATATCTATCTACCA 2287    A   C   A
                   TG TGGA AGATG TACAAAT
                   || |||| ||||| |||||||
                   AC ATCT TCTAT ATGTTTA
                       C   A   _
GAM131  LOC119548 3' CTTATCTGTTATGTGTTCATCA 2983        G    CAA
                   TGATGGACA ATGATA  ATAAG
                   ||||||||| |||||| |||||
                   ACTACTTGT TATTGT  TATTC
                        G    C__
GAM131  LOC120400 5' CTTATCCATCTCTGTCCATTA 3027        T ACAA
                   TGATGGACAGA GAT   ATAAG
                   ||||||||||| |||   |||||
                   ATTACCTGTCT CTA   TATTC
                       _  CC__
GAM132  NARS      3' AAAGTTCGGGGAAAATACC   1125        TA CAA
                   GGTATTTTT TGG  ACTTT
                   ||||||||| |||  |||||
                   CCATAAAAG GCT  TGAAA
                       GG   ___
GAM132  BFAR      3' TGCACATAAAAAATACCG    2581             _
                   CGGTATTTTTTATG GCA
                   ||||||||||||| |||
                   GCCATAAAAAATAC CGT
                        A
GAM132  HSNOV1    3' AAAGTTCAAAAGTAGAAATACC 1720        TATGGCA
                   GGTATTTTT    AACTTT
                   |||||||||    ||||||
```

```
                        CCATAAAGA    TTGAAA
                            TGAAAAC
GAM132  KIAA0628 3' AGGCTGCCATAACAAAATACC 1547          _      AA
                        GGTATTTT TTATGGCA CT
                        |||||||| |||||||| ||
                        CCATAAAA AATACCGT GA
                           C        CG
GAM132  KIAA1393 3' TAAAGTTTGATTGGAACATACC 2936      T    TGG
                        GGTAT TTTTA  CAAACTTTA
                        ||||| ||||| |||||||||
                        CCATA AAGGT  GTTTGAAAT
                          C    TA_
GAM132  LOC147054 5' TAAAGTTTACATGCTACAAAAA 3289          A    ____
           ATAC          GTATTTTTT TGGCA   AACTTTA
                        ||||||||| ||||| |||||||
                        CATAAAAAA ATCGT  TTGAAAT
                           C    ACAT
GAM133  TRIM    3' CAAATGTAAGGCCATGA    1684    AA  GAC
                        TCAT GCTT  TACATTTG
                        |||| |||| ||||||||
                        AGTA CGGA  ATGTAAAC
                           C_    ___
GAM133  MGC11296 3' CCAAATGTAAGTGCCATGA  2248     AA_ TGAC
                        TCAT GCT  TACATTTGG
                        |||| ||| |||||||||
                        AGTA TGA  ATGTAAACC
                          CCG    ____
GAM133  PRO2037 5' CAAATGCTGTTTATGATA   1853        TTGACTA
                        TATCATAAGC    CATTTG
                        ||||||||||    ||||||
                        ATAGTATTTG   GTAAAC
                           TC_____
GAM134  PMX1    3' TCTATAGTGATGAAACATT  1996    A    ACCGT
                        AATG TTTCATCA   TAGA
                        |||| |||||||| ||||
                        TTAC AAAGTAGT   ATCT
                         _      GAT__
GAM134  FLJ22557 3' TCTGGCATGATAAAATCATGGA 2083   A   C  ACC
                        TC ATGATTT ATCA  GTTAGA
                        || |||||||| |||| ||||||
                        AG TACTAAA TAGT  CGGTCT
                          G    A   A__
GAM134  KIAA0618 5' TCTAGTGGATGAGAATCA  1563      CA  A
                        TGATTT TCA CCGTTAGA
                        |||||| ||| |||||||||
                        ACTAAG AGT GGTGATCT
                          __   A
GAM134  LOC154215 3' AACGGTTGCCGGCCATTG  3188      ATT AT
                        CAATG TC CAACCGTT
                        ||||| || ||||||||
```

```
                    GTTAC  GG GTTGGCAA
                        C__  CC
GAM135  GARP     3' ATCAACAAATCTTCACTGAGC 1220      C TTA_
                    GCTC GT  ATTTGTTGAT
                    |||| ||  ||||||||||
                    CGAG CA  TAAACAACTA
                       T CTTC
GAM135  TEM8     3' AGGGAATTAAAGAAAGCCATG 1790      CCG    G
                    CATGGCT TTTAATTT TT
                    ||||||| |||||||| ||
                    GTACCGA AAATTAAG GA
                       AAG      G
GAM135  TRHR     3' ATCAACAAAAGGGAGAACATG 1009      G_  G AATT
                    CATG CTCC TTT  TGTTGAT
                    |||| |||| |||  |||||||
                    GTAC GAGG AAA  ACAACTA
                       AA  G  ____
GAM135  LGI2     3' ATCAACAAACAAATCAAAGCCA 1792      CC_  AA
                    TGGCT GTTT TTTGTTGAT
                    ||||| |||| |||||||||
                    ACCGA TAAA AAACAACTA
                       AAC  C_
GAM135  MGC4638  3' TCAACAAATGTGAGTCAT   2212      CGTTTA
                    ATGGCTC   ATTTGTTGA
                    |||||||   |||||||||
                    TACTGAG   TAAACAACT
                        TG____
GAM135  LOC139065 5' CAACAAACAAGAGCTATG   3035      CGTTTAA
                    CATGGCTC   TTTGTTG
                    ||||||||   |||||||
                    GTATCGAG   AAACAAC
                        AAC____
GAM135  LOC154282 3' ATCAACAAAAGGAGGACCA 3372      C  G AA
                    TGG TCC TTT  TTTGTTGAT
                    ||| ||| |||  |||||||||
                    ACC AGG AGG  AAACAACTA
                     _  _  AA
GAM135  LOC91516 5' CAACAAAAAGGAGCTAT   2745      GTTTAA
                    ATGGCTCC   TTTGTTG
                    ||||||||   |||||||
                    TATCGAGG   AAACAAC
                        AA____
GAM136  C20orf28 3' CCACTCCGGAGATCCGGGT 1629      G ATA_
                    ACTCGGATCT CT  TGG
                    |||||||||| ||  |||
                    TGGGCCTAGA GG  ACC
                        _ CCTC
GAM136  MGC5139  5' CCAAAGAAGATCCGAGTT   2994      G ATA
                    AACTCGGATCT CT  TGG
                    ||||||||||| ||  |||
```

```
                                 TTGAGCCTAGA GA  ACC
                                    A A__
GAM136  PRO0899  3' CCTGCAGCAGACCCGAGTTG 1847        A    A T
                    TAACTCGG TCTGCT TA GG
                    ||||||| |||||| || ||
                    GTTGAGCC AGACGA GT CC
                         C    C  _
GAM136  PRO1386  3' CCACATAGCAAGGTCTGA    2187        _    A
                    TCGGATCT GCTAT TGG
                    |||||||| ||||| |||
                    AGTCTGGA CGATA ACC
                          A    C
GAM136  PTPRT    3' CCATGTAAATCCGGGTTA    2399        CTGC
                    TAACTCGGAT   TATATGG
                    ||||||||||   |||||||
                    ATTGGGCCTA   ATGTACC
                          A___
GAM136  TCL6     3' CCATTGCAGATTCGAGT     1919        TAT
                    ACTCGGATCTGC  ATGG
                    |||||||||||| ||||
                    TGAGCTTAGACG  TACC
                        T__
GAM136  TCL6     3' CCATTGCAGATTCGAGT     1433        TAT
                    ACTCGGATCTGC  ATGG
                    |||||||||||| ||||
                    TGAGCTTAGACG  TACC
                        T__
GAM136  TEX27    3' CCATATAGCAAGTTTAGT    1968     C  TC
                    ACT GGA  TGCTATATGG
                    ||| ||| ||||||||||
                    TGA TTT  ACGATATACC
                     _   GA
GAM136  LOC255759 5' CCTGTCAGGATCCGAGT    3739        GCT  T
                    ACTCGGATCT  ATA GG
                    ||||||||| ||| ||
                    TGAGCCTAGG  TGT CC
                        AC_  _
GAM137  APXL     3' ACTTACTTATTTTTATCTA   842     CT C
                    TAGATAAA  AT AGTAAGT
                    |||||||| || |||||||
                    ATCTATTT  TA TCATTCA
                        T_ T
GAM137  CKN1     3' ACTTCTGTATAGTTTATTTAGT 702           _  T
             CA        TGACTAGATAAACTAT CAG AAGT
                    |||||||||||||| ||| ||||
                    ACTGATTTATTTGATA GTC TTCA
                         T  _
GAM137  HMGA2    3' ACCTACTAATAGTTTGTTGATC 1032     CTA      C  A
                    GA  GATAAACTAT AGTA GT
                    || ||||||||| |||| ||
```

```
                          CT  TTGTTTGATA TCAT CA
                          AG_      A   C
GAM137 ZNF36    3' ACTTAAGGATCCTTCTAGTCA 3626       TAAACT  AG
                          TGACTAGA    ATC TAAGT
                          ||||||||    ||| |||||
                          ACTGATCT    TAG ATTCA
                          TCC___    GA
GAM137 FLJ23191 3' GTTGATAGCCCTCTAGTCA  2065       TAAA
                          TGACTAGA   CTATCAGT
                          ||||||||   ||||||||
                          ACTGATCT   GATAGTTG
                          CCC_
GAM137 KIAA0841 3' ACTTACTGAAATTCCCAGTCA 2918     A_ TAAACTA
                          TGACT GA    TCAGTAAGT
                          ||||| ||    |||||||||
                          ACTGA CT    AGTCATTCA
                          CC TAA____
GAM137 KIAA1243 3' ACCTATGGGCAGTTTATCTG 2977       AT A  A
                          TAGATAAACT C GTA GT
                          |||||||||| | ||| ||
                          GTCTATTTGA G TAT CA
                          CG G  C
GAM137 RNF20    3' CTGTAGGACAGTTTATCAGTCA 1882   A    A AGTA
                          TGACT GATAAACT TC   AG
                          ||||| |||||||| ||   ||
                          ACTGA CTATTTGA AG   TC
                          _      C GATG
GAM137 LOC118851 3' ACTTTGGGAAATTCATCTGGTC 3025     A CTA AGT
              A           TGACTAGAT AA  TC  AAGT
                          ||||||||| ||  ||  ||||
                          ACTGGTCTA TT  AG  TTCA
                          C AA_ GGT
GAM137 LOC150005 3' ACTAGCTGCTTCTAGTCA  3322       TAAACTAT  A
                          TGACTAGA    CAGT AGT
                          ||||||||    |||| |||
                          ACTGATCT    GTCG TCA
                          TC_____    A
GAM137 LOC221036 3' ACTTACCGATAGTTTCAGT 3585    A TA    A
                          ACT GA  AACTATC GTAAGT
                          ||| ||  ||||||| ||||||
                          TGA CT  TTGATAG CATTCA
                          _ __      C
GAM138 COG7     3' AAAAGAGTTGTAAATTAAAGAT 2795       __ G
              G           TATCTTTAA TA AACTCTTTT
                          ||||||||| || |||||||||
                          GTAGAAATT AT TTGAGAAAA
                          AA G
GAM138 DUSP5    3' GAAAAGAGTTCTTCAGAT    1111    TTAAT
                          ATCT AGAACTCTTTTC
                          ||||  |||||||||||
```

```
                          TAGA    TCTTGAGAAAAG
                          CT___
GAM138  C6orf29  3' AAAAGATTTTATTAAAGATA 2278            C
                          TATCTTTAATAGAA TCTTTT
                          |||||||||||||| ||||||
                          ATAGAAATTATTTT AGAAAA


                                       _
GAM138  CGR19    3' GAAAAGTACACTTTCTACTAAA 1311          A   CT____
           GATG               TATCTTTA TAGAA   CTTTTC
                          |||||||| |||||    ||||||
                          GTAGAAAT ATCTT   GAAAAG
                            C   TCACAT
GAM138  DSCR6    3' GAAAAGAGTAACAGAAAGATAG 1865          AATAGA
                          CTATCTTT    ACTCTTTC
                          ||||||||    |||||||||
                          GATAGAAA    TGAGAAAAG
                            GACAA_
GAM138  ETL      3' GAAATAGTTCTGTCAAAAATAG 1982     C A    CT
              T              ACTAT TTT ATAGAACT TTTC
                          ||||| ||| ||||||||| ||||
                          TGATA AAA TGTCTTGA AAAG
                            A   C    T_
GAM138  FLJ21269 3' GAGGCTTATTAAAAATAGT 2138      C    AA
                          ACTAT TTTAATAG CTC
                          ||||| |||||||| |||
                          TGATA AAATTATT GAG
                            A        CG
GAM138  HNT      3' GAAAAGAGTTTTAAAAAAGA 1692       AA
                          TCTTT TAGAACTCTTTC
                          ||||| ||||||||||||
                          AGAAA ATTTTGAGAAAAG
                            AA
GAM138  KCNB2    3' AAAAGAGCTCTATTAGGA 3690       T    A
                          TCTT AATAGA CTCTTTT
                          |||| |||||| |||||||
                          AGGA TTATCT GAGAAAA
                            _    C
GAM138  KIAA0794 3' GAAAAGAACAAGAAAGATAG 3163          AATAGAAC
                          CTATCTTT     TCTTTTC
                          ||||||||     |||||||
                          GATAGAAA     AGAAAAG
                            GAACA___
GAM138  LOC123342 5' GAAAAGAGTTCTAAACATGGT 3031      C TAA
                          ACTAT TT TAGAACTCTTTTC
                          ||||| || |||||||||||||
                          TGGTA AA ATCTTGAGAAAAG
                            C ___
GAM138  LOC144920 3' AAAAGAGTTCTAAAGAAATAG 3270      C AA
                          CTAT TTT TAGAACTCTTTT
                          |||| ||| ||||||||||||
```

```
                              GATA AAG  ATCTTGAGAAAA
                               _    AA
GAM138  LOC153688 3' GAAAAGAGTTTCTGCAAGATA 3370      TAA      _
                          TATCTT  TAGAA CTCTTTTC
                          ||||||  ||||| ||||||||
                          ATAGAA  GTCTT GAGAAAAG
                             C__     T
GAM138  LOC51336 5' GAAAAGAATTCTGTTGAAATCA 1707      ATC       C
          GT            ACT  TTTAATAGAA TCTTTTC
                        |||  |||||||||| |||||||
                        TGA  AAGTTGTCTT AGAAAAG
                        CTA         A
GAM139  SCN1A    3' GAAAAACAAATTCTTAAATTTC 3451      TA_       C
          A              TGG  TTAAGAATT GTTTTTC
                        |||  |||||||||| |||||||
                        ACT  AATTCTTAA CAAAAAG
                        TTA         A
GAM139  FLJ13315 5' GAAAAACGGAGGATTAAAACCA 2127     A   GAA
                        TGGT TTAA  TTCGTTTTTC
                        |||| ||||  |||||||||
                        ACCA AATT  AGGCAAAAAG
                          A  AGG
GAM139  KIAA0940 3' AAAATGGTATTATTAATACCAT 1584          G  _
          A             TATGGTATTAA AAT TCGTTTT
                        ||||||||||| ||| |||||||
                        ATACCATAATT TTA GGTAAAA
                             A T
GAM139  SARM    3' GAAATATAATTCTTAATATCAT 1608          C T
          A             TATGGTATTAAGAATT GT TTTC
                        |||||||||||||||| || ||||
                        ATACTATAATTCTTAA TA AAAG
                             _ T
GAM139  LOC144231 5' TGTAATTCTTAATACCAT    3266        _
                        ATGGTATTAAGAATT CG
                        ||||||||||||||| ||
                        TACCATAATTCTTAA GT
                             T
GAM139  LOC148734 3' GAAAATGGGGCCCTTAATAC 3124        AA_
                        GTATTAAG  TTCGTTTTT
                        ||||||||  |||||||||
                        CATAATTC  GGGTAAAAG
                          CCG
GAM140  MBD1    3' TTAAATATGCATCTGGCCCAGG 924      C   TTTTA
          AA            TTCCT GGCCA    ATATTTAA
                        ||||| |||||    ||||||||
                        AAGGA CCGGT    TATAAATT
                          C   CTACG
GAM140  MBD1    3' TTAAATATGCATCTGGCCCAGG 1644     C   TTTTA
          AA            TTCCT GGCCA    ATATTTAA
                        ||||| |||||    ||||||||
```

```
                              AAGGA CCGGT    TATAAATT
                                C   CTACG
GAM140  MBD1      3' TTAAATATGCATCTGGCCCAGG 1645      C    TTTTA
     AA                    TTCCT GGCCA    ATATTTAA
                           ||||| |||||   ||||||||
                              AAGGA CCGGT    TATAAATT
                                C   CTACG
GAM140  MBD1      3' TTAAATATGCATCTGGCCCAGG 1646      C    TTTTA
     AA                    TTCCT GGCCA    ATATTTAA
                           ||||| |||||   ||||||||
                              AAGGA CCGGT    TATAAATT
                                C   CTACG
GAM140  LOC254734 3' TTAAATATTCAGAACCGAGGA 3666        CCA  T
                       TCCTCGG  TTT AATATTTAA
                       |||||||  ||| |||||||||
                       AGGAGCC  AGA TTATAAATT
                         A__  C
GAM140  LOC51026  3' AAGTATTAAAACCAAGGAA 1659      C CCA
                       TTCCT GG  TTTTAATATTT
                       ||||| ||  |||||||||||
                       AAGGA CC  AAAATTATGAA
                         A  ___
GAM141  AICDA     3' TTGCAAGGAAATTGTGCTTTAT 1923       C____   C
     C                     GATAAAGC   TTCCT GCAA
                           ||||||||   ||||| ||||
                           CTATTTCG   AAGGA CGTT
                             TGTTA    A
GAM141  GCG       3' GGAATAAAGTTTTATCAAA 895          C___
                       TTTGATAAAGC  TTCC
                       |||||||||||  ||||
                       AAACTATTTG  AAGG
                           AAAT
GAM141  PTPN1     3' TTGCATCAAGGGCTTTATCAAA 960             CCTC
                       TTTGATAAAGCCTT  GCAA
                       ||||||||||||||  ||||
                       AAACTATTTCGGGA  CGTT
                           ACTA
GAM141  SCO2      5' GCGAGGAGCATCAGA       1189       AAA CT
                       TTTGAT  GC TCCTCGC
                       ||||||  || |||||||
                       AGACTA  CG AGGAGCG
                         ___ __
GAM141  UNG       3' TGTGAGCTTTATCAGA     2394       CTTCC
                       TTTGATAAAGC   TCGCA
                       |||||||||||   |||||
                       AGACTATTTCG   AGTGT
                         ____
GAM141  UNG       3' TGTGAGCTTTATCAGA     1013       CTTCC
                       TTTGATAAAGC   TCGCA
                       |||||||||||   |||||
```

```
                        AGACTATTTCG    AGTGT
                        ‾‾‾‾‾
GAM141  BM046    3' TGCAAGAAAAAGGACTTATTAA 1831        AG  C__  C
          A                TTTGATAA  CCTT  CT GCA
                       |||||||| ||||  || |||
                       AAATTATT  GGAA  GA CGT
                         CA    AAA  A
GAM141  DKFZP761G1913 3' TGCCAGGCTTTGCCAAA    2209      A       TCCTC
                       TTTG TAAAGCCT    GCA
                       |||| ||||||||    |||
                       AAAC GTTTCGGA    CGT
                          C    C____
GAM141  KIAA0057 3' GTGAGGAAGACTTTACCAA 1422      A   C
                       TTG TAAAG CTTCCTCGC
                       ||| ||||| |||||||||
                       AAC ATTTC GAAGGAGTG
                         C   A
GAM141  RTCD1    3' TTGCTGAGAAGGCTTCATTAAA 1053        A       C _
                       TTTGAT AAGCCTTC TC GCAA
                       |||||| ||||||||| || ||||
                       AAATTA TTCGGAAG AG CGTT
                          C      _ T
GAM141  LOC127396 3' TGAGAAGGCCTTATTAAA 3005      A    C
                       TTTGATAA GCCTTC TCG
                       |||||||| |||||| |||
                       AAATTATT CGGAAG AGT
                          C       _
GAM141  LOC130074 3' TGAGAGGCTTTATGAAA 3044      G    TC
                       TTT ATAAAGCCT CTCG
                       ||| ||||||||| ||||
                       AAA TATTTCGGA GAGT
                         G      __
GAM141  LOC149134 5' TGCAGGAAAGTTTACCAAA 3308      ATA  C   C
                       TTTG  AAGC TTCCT GCA
                       ||||  |||| ||||| |||
                       AAAC  TTTG AAGGA CGT
                         CA_  A    _
GAM141  LOC219818 3' TTGCAAGGAAGGCCTAATCA 3503      AAA     C
                       TGAT  GCCTTCCT GCAA
                       ||||  |||||||| ||||
                       ACTA  CGGAAGGA CGTT
                         ATC       A
GAM141  LOC256714 3' TGCTGGGCTTTAGCAAA 3702      A    TCCTC
                       TTTG TAAAGCCT    GCA
                       |||| ||||||||    |||
                       AAAC ATTTCGGG    CGT
                          G    T____
GAM141  LOC91149 5' TGCAAAGAAGGTTTCCAGA 2714      ATA     CTC
                       TTTG AAGCCTTC GCA
                       |||| |||||||| |||
```

```
                         AGAC  TTTGGAAG  CGT
                         C__         AAA
GAM142  ACADSB  3' CCATCATTTGGAAAAATAAAGG 838        __   C TA
          C                   GCCTTTATT TCCA AT GATGG
                         ||||||||| |||| || |||||
                         CGGAAATAA AGGT TA CTACC
                               AA   T __
GAM142  EDAR    3' CCATTTAAATGGGAATAAA 1985         CA
                         TTTATTTCCA TTAGATGG
                         |||||||||| ||||||||
                         AAATAAGGGT AATTTACC
                              A_
GAM142  MAX     3' CCATTCCATGGAAATAAA    2515         CATTA
                         TTTATTTCCA    GATGG
                         ||||||||||    |||||
                         AAATAAAGGT    TTACC
                              ACC__
GAM142  MAX     3' CCATTCCATGGAAATAAA    923          CATTA
                         TTTATTTCCA    GATGG
                         ||||||||||    |||||
                         AAATAAAGGT    TTACC
                              ACC__
GAM142  MPO     3' AATGTTTATGATAATAAAGGC 722        _  C___
                         GCCTTTATT TC   ACATT
                         ||||||||| ||    |||||
                         CGGAAATAA AG   TGTAA
                               T TATT
GAM142  NEK4    3' TAATGTAGAGATAAAAGC    995    C     C
                         GC TTTATTTC ACATTA
                         || ||||||||| ||||||
                         CG AAATAGAG TGTAAT
                            A     A
GAM142  C20orf170 3' CCAAAATAATAATGAAAATAAA 2608      C C_  GA_
          GGC                GCCTTTATTT CA ATTA  TGG
                         ||||||||| || |||| |||
                         CGGAAATAAA GT TAAT  ACC
                               A AA   AAA
GAM142  FLJ20435 3' CCATCTGGAGGAAATAAA    1756         ACA
                         TTTATTTCC  TTAGATGG
                         |||||||||  ||||||||
                         AAATAAAGG  GGTCTACC
                              A__
GAM142  FLJ23071 3' CCATCTAATGTTTTAAAAGGC 2143         ATTTCC
                         GCCTTT    ACATTAGATGG
                         ||||||    |||||||||||
                         CGGAAA    TGTAATCTACC
                              ATTT__
GAM142  KIAA0562 3' CCACTATAGCAAGAAATAAAGG 1525           CACAT_  A
          C                    GCCTTTATTTC   TAG TGG
                         ||||||||||    ||| |||
```

```
                        CGGAAATAAAG    ATC ACC
                          AACGAT  _
GAM142  LRRFIP1  3'  CCACTTAATAAAAATAGAGGC  1151          CCAC    A
                     GCCTTTATTT  ATTAG TGG
                     |||||||||  ||||| |||
                     CGGAGATAAA  TAATT ACC
                       AA__    C
GAM142  P115    3'  CCATCTAATGTGATTGCTAAG  1051      TATTTC
                     CTT   CACATTAGATGG
                     |||   |||||||||||
                     GAA   GTGTAATCTACC
                      TCGTTA
GAM142  SDCCAG16 3'  CATTTTAAAAATAAAGGC    1316          CCACATT
                     GCCTTTATTT   AGATG
                     |||||||||    |||||
                     CGGAAATAAA   TTTAC
                       AAT____
GAM142  TIAF1   3'  GATGTATGGAAATAAAGGC  2370            __
                     GCCTTTATTTCC ACATT
                     |||||||||||| |||||
                     CGGAAATAAAGG TGTAG
                       TA
GAM142  LOC149711 3' CCAAAATAATAATGAAAATAAA 3314        C C_  GA_
          GGC             GCCTTTATTT CA ATTA  TGG
                     ||||||||| || |||| |||
                     CGGAAATAAA GT TAAT  ACC
                       A AA  AAA
GAM142  LOC169933 5' CCAGTAGGTGAAGATAAAGGC 3251         C  ATTAGA
                     GCCTTTATTT CAC    TGG
                     ||||||||| |||    |||
                     CGGAAATAGA GTG    ACC
                       A GATG__
GAM143  SNX9    3'  ACAAATTGTAAAGAATATGT  1673        CCG
                     ACATAT  TTACAATTTGT
                     ||||||  |||||||||||
                     TGTATA  AATGTTAAACA
                       AGA
GAM143  TOX     5'  AACAAACCACAAACGGATGTG  1533         ACAA_
                     CATATCCGTT   TTTGTT
                     ||||||||||   ||||||
                     GTGTAGGCAA   AAACAA
                       ACACC
GAM143  DKFZP434C212 3' AACAAATTGCATAGGAGTGT  2833     A  GTTA
                     ACAT TCC  CAATTTGTT
                     |||| |||  |||||||||
                     TGTG AGG   GTTAAACAA
                      _ ATAC
GAM143  LOC151438 5' AACAAACCAAAAACGGATATG  3345          ACAA_
                     CATATCCGTT   TTTGTT
                     ||||||||||   ||||||
```

```
                              GTATAGGCAA   AAACAA
                                  AAACC
GAM143  LOC221663 3' AACAAATTGCATGGATTTGT  3619     T     TA
                            ACA ATCCGT CAATTTGTT
                            ||| |||||| |||||||||
                            TGT TAGGTA GTTAAACAA
                              T     C_
GAM143  LOC257358 5' AACATGACTAACGGATATTC  3730   C        CAATT
                            A ATATCCGTTA   TGTT
                            | ||||||||||   ||||
                            C TATAGGCAAT   ACAA
                              T        CAGT_
GAM143  LOC56832  3' AACAAATTGTGGATCATG   2703      _   GTT
                            CAT ATCC  ACAATTTGTT
                            ||| ||||  ||||||||||
                            GTA TAGG  TGTTAAACAA
                              C    ___
GAM144  SOX9      3' ATGATCCTAAAAATAACCG   732     TG   C_
                            CG TGTTT AGGATCAT
                            || ||||| ||||||||
                            GC ATAAA TCCTAGTA
                              CA   AA
GAM144  FLJ14356  3' ATGAATGCAAACACATG    2171         _   GGA
                            CGTGTGTTT CA  TCAT
                            ||||||||| ||  ||||
                            GTACACAAA GT  AGTA
                              C A__
GAM144  KIAA0982  3' ATGACCCTGAAATGACTG   1464    C G      A
                            CA GT TGTTTCAGG TCAT
                            || || |||||||||| ||||
                            GT CA GTAAAGTCC AGTA
                              _ _       C
GAM144  KIAA1028  3' ATGATCCTGAAGAAAAGGTGA 3546       ACGTGTG
                            TCACC    TTTCAGGATCAT
                            |||||    ||||||||||||
                            AGTGG    GAAGTCCTAGTA
                               AAAAA__
GAM144  PCQAP     3' CCTTAAAACACACATGGGA  1649    A C      C_
                            TC CCA GTGTGTTT AGG
                            || ||| |||||||| |||
                            AG GGT CACACAAA TCC
                              _  A      AT
GAM144  PRKWNK2   3' GATCCTGAAATCAAGG     3488    ACG T
                            CC  TG GTTTCAGGATC
                            ||  || ||||||||||
                            GG  AC TAAAGTCCTAG
                              A__  _
GAM144  RCD-8     3' ATGACCCTGAGATCGTG    1491     TGT    A
                            CACG  GTTTCAGG TCAT
                            ||||  |||||||| ||||
```

```
                      GTGC   TAGAGTCC AGTA
                      ___            C
GAM144  SMOC2    3' ATGATCCTAAACTTTTTGG  2945     CGTGT   C
                      CCA    GTTT AGGATCAT
                      |||    |||| ||||||||
                      GGT    CAAA TCCTAGTA
                      TTTT_   _
GAM144  SYNJ2    3' ATCCTGAGCCATGGTG     2605     CG T  T
                      CACCA  TG GTT CAGGAT
                      |||||  || ||| ||||||
                      GTGGT  AC CGA GTCCTA

                      __ _ _
GAM144  TRABID   3' ATGACCCTAAAGTTAGTGTGGT 2823       GTG  C  A
         G              CACCACGT  TTT AGG TCAT
                      ||||||||  ||| ||| ||||
                      GTGGTGTG  GAA TCC AGTA
                        ATT  A  C
GAM144  TSGA14   3' CTGTGGACACACAAGGTGA   1861     AC       _
                      TCACC  GTGTGTTT CAG
                      |||||  |||||||| |||
                      AGTGG  CACACAGG GTC
                        AA       T
GAM144  LOC197201 3' TCTGGAAAACAACACACGGTGA 3421      AC      _____
                      TCACC  GTGTGT    TTCAGG
                      |||||  ||||||    ||||||
                      AGTGG  CACACA    AGGTCT
                        __      ACAAA
GAM144  LOC219401 3' ATGAAGCAAACACACGTAGG  3579    _       CAGGA
                      CC ACGTGTGTTT    TCAT
                      || ||||||||||    ||||
                      GG TGCACACAAA    AGTA
                        A      CGA__
GAM145  INHBA    3' ACTAGAACAACCCAAATAGCA  904       C C CCAG
                      TGCTATTT GG TG   AGT
                      |||||||| || ||   |||
                      ACGATAAA CC AC   TCA
                        C A AAGA
GAM145  TBXAS1   5' ACACTCTGAGAAAGAGCA   2182     A  GGCTGC
                      TGCT TTTC    CAGAGTGT
                      |||| ||||    ||||||||
                      ACGA AAAG    GTCTCACA
                        G  A_____
GAM145  TBXAS1   5' ACACTCTGAGAAAGAGCA   798      A  GGCTGC
                      TGCT TTTC    CAGAGTGT
                      |||| ||||    ||||||||
                      ACGA AAAG    GTCTCACA
                        G  A_____
GAM145  KIAA1056 5' ACACTTCAGCCGCAGCCAAATA 1576        C   CA___
         GCA            TGCTATTT GGCTGC   GAGTGT
                      |||||||| ||||||   ||||||
```

```
                    ACGATAAA CCGACG    TTCACA
                    _           CCGAC
GAM145 LOC197342 3' GACACCTGGCTGAGCCGGAACA 3424       A     __     A
         GCA                 TGCT TTTCGGCT GCCAG GTGTC
                    |||| ||||||||| ||||| |||||
                    ACGA AAGGCCGA CGGTC CACAG
                        C     GT   _
GAM145 LOC91752  5' GACACTCTAGATGAAA     2779      G GCC
                    TTTCG CT  AGAGTGTC
                    ||||| ||  ||||||||
                    AAAGT GA  TCTCACAG
                        A ___
GAM146 FLJ11838  3' ATGAATAAACATATCTTG    2078
                    TAAGATATGTTTATTCAT
                    ||||||||||||||||||
                    GTTCTATACAAATAAGTA


GAM147 ATP10C    3' AATACAGGAAACAAGAGGTAC 2062     T  __
                    GT CCTC GTTTCCTGTATT
                    || |||| |||||||||||||
                    CA GGAG CAAAGGACATAA
                     T   AA
GAM147 CASP10    3' ACAGGGAACAAAGAAACA    2304      C C_
                    TGTT CT  GTTTCCTGT
                    |||| ||  |||||||||
                    ACAA GA  CAAGGGACA
                      A  AA
GAM147 ZNF36     3' GGAAACAGAAACATAGA     3627      C C
                    TCTATGTT CT GTTTCC
                    |||||||| || ||||||
                    AGATACAA GA CAAAGG
                       A _
GAM147 DORFIN    3' AATACAGGAAATAGATAAACAT 1630       CC _
        G                 TATGTT TC GTTTCCTGTATT
                    |||||| || |||||||||||
                    GTACAA AG TAAAGGACATAA
                      AT A
GAM147 FLJ21313  3' AATACAGGATGAAAAACACTGA 2037    TA  CC TT
                    TC TGTT TCG TCCTGTATT
                    || |||| ||| |||||||||
                    AG ACAA AGT AGGACATAA
                      TC  AA  __
GAM147 KIAA1819  5' AATACAGGAGATAGAACCAGA 2865     AT  CTC
                    TCT GTTC GTTTCCTGTATT
                    ||| |||| |||||||||||||
                    AGA CAAG TAGAGGACATAA
                      C_  A__
GAM147 P37NB     3' ATGGGAAAAAAAACATAGA 1254        CCTCG
                    TCTATGTT  TTTCCTGT
                    ||||||||  ||||||||
```

```
                        AGATACAA   AAAGGGTA
                        AAA__
GAM147  RAP140    5' ATACAGATAGAAACATAGA 1613         CC GTTTC
                        TCTATGTT TC   CTGTAT
                        |||||||| ||   ||||||
                        AGATACAA AG   GACATA
                           __ ATA__
GAM147  LOC127002 3' AATATAAAAACAGAAACATAGA 3002        C C  CC
                        TCTATGTT CT GTTT TGTATT
                        |||||||| || |||| ||||||
                        AGATACAA GA CAAA ATATAA
                           A _  A_
GAM147  LOC132332 3' AATACAGTTGCAGAGGAGCATA 3046        _ TTC
                        TATGTTCCTC GT  CTGTATT
                        |||||||||| ||  |||||||
                        ATACGAGGAG CG  GACATAA
                           A TT_
GAM147  LOC145624 5' ACTAGAAGAGGAACATA    3276        GT  CT
                        TATGTTCCTC TTC GT
                        |||||||||| ||| ||
                        ATACAAGGAG AAG CA
                           __  AT
GAM148  NR4A2     3' AATAGTATTTCAGACACTATG 1277     A     CA
                        TATAGT TCTGAAAT TATT
                        |||||| |||||||| ||||
                        GTATCA AGACTTTA ATAA
                           C    TG
GAM148  PRKCN     3' ATGATTATTCCAGATACTGTA 1252        A___
                        TATAGTATCTG  AATCAT
                        |||||||||||  ||||||
                        ATGTCATAGAC  TTAGTA
                           CTTA
GAM148  BIVM      3' ATGGTGGGTGATTTCAGATAT 1739        AT_
                        GTATCTGAAATCAT TCAT
                        |||||||||||||| ||||
                        TATAGACTTTAGTG GGTA
                           GGT
GAM148  DCLRE1A   3' ATGAAGATTGTTCAGATACT 2843        ATCATA
                        AGTATCTGAA    TTCAT
                        ||||||||||    |||||
                        TCATAGACTT    AAGTA
                           GTTAG_
GAM148  EBF2      3' ATGAAGCCTTTCAGATAC 1995       TCATA
                        GTATCTGAAA   TTCAT
                        ||||||||||   |||||
                        CATAGACTTT   AAGTA
                           CCG__
GAM148  FLJ10852  3' GAATATTTTCAGATACTATA 1873       TC
                        TATAGTATCTGAAA ATATTC
                        |||||||||||||| ||||||
```

```
                        ATATCATAGACTTT TATAAG
                                  _

GAM148  FLJ20220 3'  ATGAATAACATTTCAGATAC  1742        CA
                     GTATCTGAAAT TATTCAT
                     |||||||||| ||||||
                     CATAGACTTTA ATAAGTA
                             CA
GAM148  FLJ21952 3'  ATGATATTCTAGATACTATA  1992        _  _
                     TATAGTATCT GAA ATCAT
                     |||||||||| ||| |||||
                     ATATCATAGA CTT TAGTA
                              T  A
GAM148  MGC10724 3'  ATGAAGACCCAGATACTA    2274        AAA ATA
                     TAGTATCTG  TC  TTCAT
                     |||||||||  ||  |||||
                     ATCATAGAC  AG  AAGTA
                            CC_  ___
GAM148  MGC4238  3'  ATGGAAGGACTTCAGATAC   2247        A ATA
                     GTATCTGAA TC  TTCAT
                     ||||||||| ||  |||||
                     CATAGACTT AG  AGGTA
                            C GA_
GAM148  Rab11-FIP2 3' ATGACAGTATCTGCAGATACTA 1581           AAATCATAT
            TA           TATAGTATCTG    TCAT
                         |||||||||||    ||||
                         ATATCATAGAC    AGTA
                            GTCTATGAC
GAM148  LOC90768 3'  ATGAAGGTGTGTCCCAGATATT 2674        AAAT_ A
            A            TAGTATCTG   CAT TTCAT
                         |||||||||   ||| |||||
                         ATTATAGAC   GTG AAGTA
                            CCTGT  G
GAM149  ANPEP    3'  CTAAATCTGAGGAATCAAC   805        CT  TA
                     GTTGAT CTCA GATTTAG
                     |||||| |||| |||||||
                     CAACTA GAGT CTAAATC
                            AG   __
GAM149  NP       3'  TCTAAATCACCAGAGACCAAAC 724     GA_  CATA
                     GTT TCTCT  GATTTAGA
                     ||| |||||  |||||||||
                     CAA AGAGA  CTAAATCT
                         ACC    CCA_
GAM149  TFAP2C   3'  CTAGATCAACAGATCAAC    1000        CTCATA
                     GTTGATCT   GATTTAG
                     ||||||||   |||||||
                     CAACTAGA   CTAGATC
                            CAA___
GAM149  ZNF83    5'  CTAAATGTGAGATCAAGGA   1813   G    T AGAT
                     TC TTGATCTC CAT  TTAG
                     || |||||||| |||  ||||
```

```
                         AG AACTAGAG GTA    AATC
                          G       T     ___
GAM149  MGC26766 3' TTTACATCATGAGAGATCAA  2509        A   T
                         TTGATCTCTCAT GAT TAGA
                         |||||||||||| ||| ||||
                         AACTAGAGAGTA CTA ATTT
                             _     C
GAM149  SCYB10   3' TCTAAATGTTGAAAGATCAA  836        C  TAG
                         TTGATCT TCA  ATTTAGA
                         ||||||| |||  |||||||
                         AACTAGA AGT  TAAATCT
                            A  TG_
GAM150  EBAF     3' TACAGCTGAGCAATGCA     2721        CG AAATA
                         TGCAT GT   TAGCTGTA
                         ||||| ||   ||||||||
                         ACGTA CG   GTCGACAT
                           A_ A____
GAM150  F7       3' ATACGCAAACACACCGATGCA 706         AAATATA  T
                         TGCATCGGT    GC GTAT
                         |||||||||    || ||||
                         ACGTAGCCA    CG CATA
                            CACAAA_ _
GAM150  F7       3' ATACGCAAACACACCGATGCA 1885        AAATATA  T
                         TGCATCGGT    GC GTAT
                         |||||||||    || ||||
                         ACGTAGCCA    CG CATA
                            CACAAA_ _
GAM150  MGC3771  3' TAGAACATTTACCGATGC    2178          ATAG
                         GCATCGGTAAAT   CTG
                         ||||||||||||   |||
                         CGTAGCCATTTA   GAT
                            CAA_
GAM150  LOC146438 3' TAGAACATTTACCGATGC   3091          ATAG
                         GCATCGGTAAAT   CTG
                         ||||||||||||   |||
                         CGTAGCCATTTA   GAT
                            CAA_
GAM151  BPGM     3' TAAGAAGAAATGCAAAAG    852       CG
                         CTT GCATTTCTTTTTA
                         ||| ||||||||||||
                         GAA CGTAAAGAAGAAT
                          AA
GAM151  HAS2     3' AAATGAAATGCCAAAGGAA   1198      C    T
                         TTCCTT GGCATTTC TTT
                         |||||| ||||||| |||
                         AAGGAA CCGTAAAG AAA
                              A    T
GAM151  HDAC2    3' CATTAAAAAGAAAATATTGAAA 3507       _ CA_
          GGAA                 TTCCTT CGG  TTTCTTTTTAATG
                         |||||| |||  |||||||||||
```

```
                    AAGGAA GTT  AAAGAAAAATTAC
                      A  ATA
GAM151  XRCC2    3' CATTAAAAAGTGGGCAAAGGA 1208      CG ATTT
                    TCCTT GC  CTTTTTAATG
                    ||||| ||  |||||||||
                    AGGAA CG  GAAAAATTAC
                     A_ GGT_
GAM151  APACD    3' CATTAAAAAGAAACCAGGAA 1249     TC CA
                    TTCCT GG  TTTCTTTTTAATG
                    ||||| ||  ||||||||||||
                    AAGGA CC  AAAGAAAAATTAC
                         __  __
GAM151  SCIN     3' CATTAAAATAACCTGAAGGAA 2313         CATTTCT
                    TTCCTTCGG      TTTTAATG
                    |||||||||      ||||||||
                    AAGGAAGTC      AAAATTAC
                        CAAT___
GAM151  USP16    3' CATTAAATACATGCCAGAAG 1303     _  TTCTT
                    CTTC GGCAT    TTTAATG
                    |||| |||||    |||||||
                    GAAG CCGTA    AAATTAC
                     A   CAT__
GAM151  LOC115004 3' AAAAGAAATCCGAAAGAA   2970    C  C
                    TTC TTCGG ATTTCTTTT
                    ||| ||||| |||||||||
                    AAG AAGCC TAAAGAAAA
                      A  _
GAM151  LOC146520 5' GAAGAGAAATGCCATAGGAA 3096      TC
                    TTCCT GGCATTTCTTTTT
                    ||||| |||||||||||||
                    AAGGA CCGTAAAGAGAAG
                       TA
GAM151  LOC219333 3' CATTAAAAAAAAACATGCCG 3607        __ C
                    CGGCAT TT TTTTTAATG
                    |||||| || |||||||||
                    GCCGTA AA AAAAATTAC
                      CA A
GAM152  EIF1A    3' CTTTGTGTTTTTGGTTTACCCT 3442   A_      TCT
                    AG TAAACTAAA  CGCAAAG
                    || |||||||||  |||||||
                    TC ATTTGGTTT  GTGTTTC
                      CC      TT_
GAM152  ENAM     3' TTTGTTTTTAGTTATCTTA 2217        A  TCTC
                    TAAGATAA CTAAA   GCAAA
                    |||||||| |||||   |||||
                    ATTCTATT GATTT   TGTTT
                      _    T___
GAM152  MYCL1    3' TTTGTGGTAGCTTATCTTA 1204        A AATC
                    TAAGATAA CTA   TCGCAAA
                    ||||||| |||   |||||||
```

```
                          ATTCTATT GAT   GGTGTTT
                              C  ____
GAM152  ZNF42    5' CTTTGATGTATTCTAGTTTATC 1018        AATCT _
           T          AGATAAACTA   CG CAAAG
                     |||||||||   || |||||
                      TCTATTTGAT   GT GTTTC
                         CTTAT  A
GAM152  FLJ23604 3' AGAATATAGTTTATCTTA   2134        AA_
                      TAAGATAAACTA  TCT
                     |||||||||||  |||
                      ATTCTATTTGAT  AGA
                          ATA
GAM152  HEY2     3' AGATCTAGTTTTATCTTA   1419        _ A
                      TAAGATAAA CTA ATCT
                     ||||||||| ||| ||||
                      ATTCTATTT GAT TAGA
                         T  C
GAM152  TSC22    3' TGGGACCTAGGCTATCTTA  1265     AA AA
                      TAAGATA CTA TCTCG
                     ||||||| ||| |||||
                      ATTCTAT GAT AGGGT
                         CG  CC
GAM153  FLJ20296 3' ACATTAATAAATTTATTGATTC 1748   A   CAA
           CA           TG AATC  GGATTTATTAATGT
                     || ||||  |||||||||||||
                      AC TTAG   TTTAAATAATTACA
                         C  TTA
GAM153  RAB22A   3' ACATTAATAAATTCTAAGTTTC 2546       CCA
           A            TGAAAT  AGGATTTATTAATGT
                     |||||| |||||||||||||||
                      ACTTTG  TCTTAAATAATTACA
                         AA_
GAM153  UPLC1    3' ACATTTGTTCTCTTGGATCTCA 1740   A    _ TTTATT
                      TGA ATCCAAG GA   AATGT
                     ||| |||||||| ||   |||||
                      ACT TAGGTTC CT   TTACA
                         C   T TGT___
GAM153  LOC122886 3' ACACTGTGTTCCTTGGACCTC 3028   AA    TT TAA
                      GA TCCAAGGA TAT TGT
                     || |||||||| ||| |||
                      CT AGGTTCCT GTG ACA
                         CC     T_  TC_
GAM153  LOC222194 3' ACATCATCTGTTCTTGGACCTC 3637   AA       TTATTA
           A            TGA TCCAAGGAT   ATGT
                     ||| |||||||||   ||||
                      ACT AGGTTCTTG   TACA
                         CC      TCTAC_
GAM154  ITGB1    3' AGTAAATGTCCTGCTA      909        GA
                      TAGCAGGACATT TGCT
                     |||||||||||| ||||
```

```
                    ATCGTCCTGTAA ATGA
                         __
GAM154  RHO     3' TCTAGAGCATGGAGCCTCTA 754      C  ACA G
                    TAG AGG  TT ATGCTCTAGA
                    ||| ||| || ||||||||||
                    ATC TCC  AG TACGAGATCT
                    _  G__ G
GAM154  XPNPEP2 3' CTGGGTCCACATCCTGCTA 1015         CAT AT T
                    TAGCAGGA  TG GC CTAG
                    ||||||||  || || ||||
                    ATCGTCCT  AC TG GGTC
                     AC_ C_ _
GAM154  FLJ12700 3' CTAGAACAGGATGTCCTGC  2110         GA C
                    GCAGGACATT TG TCTAG
                    |||||||||| || |||||
                    CGTCCTGTAG AC AGATC
                       G_ A
GAM154  FLJ13291 3' GTCCAGAGTTAACTGCCCTGCT 2234      A TTGAT   A
          G               TAGCAGG CA   GCTCT GAC
                    |||||||| ||   ||||| |||
                    GTCGTCC GT   TGAGA CTG
                     C CAAT_    C
GAM154  FLJ20811 5' CTAGAGCACAAGTCCTGCTA 2782         A A
                    TAGCAGGAC TTG TGCTCTAG
                    |||||||||| ||| ||||||||
                    ATCGTCCTG AAC ACGAGATC
                      _ _
GAM154  KIAA1643 3' TCCAGAGCCTCTGTCCTGC  2693         TT T   A
                    GCAGGACA GA GCTCT GA
                    |||||||| || ||||| ||
                    CGTCCTGT CT CGAGA CT
                      __ C   C
GAM154  KIAA1755 3' TCCAGAGCATTTATCTGC  2596       ACATT     A
                    GCAGG   GATGCTCT GA
                    |||||   |||||||| ||
                    CGTCT   TTACGAGA CT
                     AT___      C
GAM154  KIAA1762 3' GTCTAGAGCACCACACCGCT 2669     A ACAT A
                    AGC GG   TG TGCTCTAGAC
                    ||| ||   || ||||||||||
                    TCG CC   AC ACGAGATCTG
                     _ AC__ C
GAM154  MGC13033 5' TCCAGAGCATTCCTTCTA 2199      C  CATTG    A
                    TAG AGGA   ATGCTCT GA
                    ||| ||||   ||||||| ||
                    ATC TCCT   TACGAGA CT
                     T ____     C
GAM154  SLC7A3   5' TCTTCTTCAATTCCTGCTA 2281         C  TGCTCT
                    TAGCAGGA ATTGA   AGA
                    ||||||| |||||    |||
```

```
                              ATCGTCCT TAACT    TCT
                            _     TCT___
GAM154   LOC112609 3' GTCTAGAGTGATCCATCC   2960     CATT  _
                            GGA   GAT GCTCTAGAC
                            ||| |   ||| |||||||||
                            CCT   CTA TGAGATCTG
                             AC__   G
GAM154   LOC157349 5' GTCCAAAAGTTTAACTGTCCTG 3201        _  T  CTA_
            C                GCAGGACA TTGA GCT   GAC
                            ||||||||| |||| ||| ||||
                            CGTCCTGT AATT TGA   CTG
                             C  _  AAAC
GAM154   LOC90625 3' TCCAGATGATGCTCCTGCTA  2662       _   ATGC  A
                            TAGCAGGA CATTG   TCT GA
                            ||||||||| |||||   ||| ||
                            ATCGTCCT GTAGT   AGA CT
                              C  ____   C
GAM155   MGAT4B    5' CCGCTACAAGGACAGTG   2360     ATAT  TC
                            CACT   GTT TGTAGCGG
                            ||||   ||| |||||||||
                            GTGA   CAG ACATCGCC
                              ____  GA
GAM155   PRKAR2A 3' GCCACAGAACACATACAG   1091    A  _   A
                            CT TATGT TTCTGT GC
                            || ||||| |||||| ||
                            GA ATACA AAGACA CG
                              C  C   C
GAM155   SCD      3' GCCACGGAAACATACAGAGGA 1177    A A      A
                            TCC CT TATGTTTCTGT GC
                            ||| || |||||||||||| ||
                            AGG GA ATACAAAGGCA CG
                              A C       C
GAM155   DKFZp761H079 3' GCCACCTGAAACATAAAATGGA 2506      CTA     T_ A
                            TCCA   TATGTTTC GT GC
                            ||||   |||||||| || ||
                            AGGT   ATACAAAG CA CG
                             AAA      TC C
GAM155   KIAA0417 3' GCCATGATGGAAACAGATAGTG 2910       A     AGC
                            CACTAT TGTTTCTGT  GGC
                            |||||| |||||||||  |||
                            GTGATA ACAAAGGTA  CCG
                              G     GTA
GAM155   LRBA     3' CCAATTATGGAAACATACAGTG 1327      A       C_
            GA                TCCACT TATGTTTCTGTAG GG
                            |||||| |||||||||||||| ||
                            AGGTGA ATACAAAGGTATT CC
                              C     AA
GAM155   SYAP1   3' GCCACAGAAACATAAGT   2279    A      A
                            ACT TATGTTTCTGT GC
                            ||| |||||||||| ||
```

```
                              TGA ATACAAAGACA CG
                              _            C
GAM155  LOC143188 5' ACAGAAACTATAGCAGA    3264    CA   T
                              TC  CTATA GTTTCTGT
                              || ||||| |||||||||
                              AG  GATAT CAAAGACA
                              AC     _
GAM155  LOC157292 3' GCCTCAGAAACATAAGTG    3378      A      TA
                              CACT TATGTTTCTG GC
                              |||| |||||||||| ||
                              GTGA ATACAAAGAC CG
                              _          TC
GAM156  C18orf1   3' AGTCATTATTGTTGCAGGA   2561    _  T TT
                              TCC GCA AT TAATGACT
                              ||| ||| || ||||||||
                              AGG CGT TG ATTACTGA
                              A   _  TT
GAM156  CRYZ      3' AAGAGTCATCATAGTAGGAA  866      GCA  TTTA
                              TTCC TAT  ATGACTCTT
                              |||| |||  |||||||||
                              AAGG ATA  TACTGAGAA
                              ATG  C___
GAM156  TRPC5     3' GAAGTGTCAAAATATGAGAA  1434    CG    TAA  T
                              TTC CATATTT TGAC CTTC
                              ||| ||||||| |||| ||||
                              AAG GTATAAA ACTG GAAG
                              A_      ___    T
GAM156  DAP13     3' GAAGAACAGTTGAAACATGC  1862     A     GAC
                              GCAT TTTTAAT TCTTC
                              |||| ||||||| |||||
                              CGTA AAAGTTG AGAAG
                              C    ACA
GAM156  DKFZP564O0463 3' GAAGAGCCATTACATGC    1481      ATTT   A
                              GCAT   TAATG CTCTTC
                              ||||   ||||| ||||||
                              CGTA   ATTAC GAGAAG
                              C___   C
GAM156  GRID1     3' AAGAACCATTAGGAGTGGAA  2822      ATA     AC
                              TTCCGC TTTTAATG TCTT
                              |||||| |||||||| ||||
                              AAGGTG AGGATTAC AGAA
                                       CA
GAM156  MGC30052  3' AAGACTTTTTTGAAAATATGCA 2499     C     AAT__ C
          GAA                 TTC GCATATTTT  GA TCTT
                              ||| |||||||||  || ||||
                              AAG CGTATAAAA  TT AGAA
                              A       GTTTT C
GAM156  MGC32104  5' AAGAGTCATGCTGTGATGAA  2494    CG   TTTTA
                              TTC CATA   ATGACTCTT
                              ||| ||||   |||||||||
```

```
                          AAG  GTGT    TACTGAGAA
                           TA  CG___
GAM156  SCN9A     5' GAAGAGGAATTAAAATATACAG 975      GC_        GA
         GA                 TCC  ATATTTTAAT CTCTTC
                            |||  |||||||||| ||||||
                            AGG  TATAAAATTA GAGAAG
                            ACA          AG
GAM156  STK17A    3' AGTCCAATTAAAATATGGAA 1154      GC         __
                            TTCC  ATATTTTAAT GACT
                            ||||  |||||||||| ||||
                            AAGG  TATAAAATTA CTGA
                            __          AC
GAM156  LOC148738 3' AAGAATCATTAAAGGAAGC 2519     ATA       C
                            GC  TTTTAATGA TCTT
                            ||  |||||||||| ||||
                            CG  GAAATTACT AGAA
                            AAG        A
GAM157  BLMH      3' GGTGGCCTAAGAGTTGAGCTC 734         A  CT
                            GAGCTCAAC CTTA  CCGCC
                            ||||||||| |||| |||||
                            CTCGAGTTG GAAT  GGTGG
                            A    CC
GAM157  BLVRB     3' GGCAATAAATGTTGAGCC   768   A      C  CTCC
                            G GCTCAACA TTA   GCC
                            | ||||||||| |||    |||
                            C CGAGTTGT AAT   CGG
                            _      A  AA__
GAM157  DHCR7     3' GGTAGCGTGCACGGTGTTGAAC 821    C      TACTC  C
         T                  AG TCAACACT    CGC ACC
                            || |||||||    ||| |||
                            TC AGTTGTGG    GCG TGG
                            A     CACGT  A
GAM157  FGFR1     3' GGTGACAGAGTGAGTGAGACTC 2032     _ AAC       ___
                            GAG CTC  ACTTACTC  CGCC
                            ||| |||  |||||||| ||||
                            CTC GAG  TGAGTGAG  GTGG
                            A  ___      ACA
GAM157  FGFR1     3' GGTGACAGAGTGAGTGAGACTC 2034     _ AAC       ___
                            GAG CTC  ACTTACTC  CGCC
                            ||| |||  |||||||| ||||
                            CTC GAG  TGAGTGAG  GTGG
                            A  ___        ACA
GAM157  HEM1      3' GGTGACTTGAGCTTGAGCTC 1200         CA  CTC
                            GAGCTCAA  CTTA  CGCC
                            ||||||||| |||| ||||
                            CTCGAGTT  GAGT  GTGG
                            C_   TCA
GAM157  NT5C3     5' GGTGGCGGGGGTGGTGCTGGCT 1689      T  A  TA
         C                  GAGC CA CACT  CTCCGCCACC
                            |||| || |||| ||||||||||
```

```
                          CTCG GT GTGG  GGGGCGGTGG
                            _  C   TG
GAM157  OTOR       3' GCGGGGAAATGTTGAGCTC  1894        C A
                          GAGCTCAACA TT CTCCGC
                          ||||||||| || ||||||
                          CTCGAGTTGT AA GGGGCG
                                    A _
GAM157  PRPSAP2   5' GCAATCAGTAAAACATTGAGCT 954         CAC_    CC__
                    C         GAGCTCAA  TTACT  GC
                              |||||||  |||||  ||
                              CTCGAGTT  AATGA  CG
                                   ACAA    CTAA
GAM157  C14orf4   5' GGTGGCGGAGGCCCCCAGCTC 2788        CAACACTTA
                          GAGCT       CTCCGCCACC
                          |||||       ||||||||||
                          CTCGA       GAGGCGGTGG
                             CCCCCG___
GAM157  CG012     3' GGCGACAGAGTGAGTGAGACTC 3272     _ AAC        ___
                          GAG CTC  ACTTACTC  CGCC
                          ||| |||  ||||||||  ||||
                          CTC GAG  TGAGTGAG  GCGG
                            A  ___        ACA
GAM157  DKFZP434K2235 5' GGTGGCGGGTAACGCCGGACTC 3278    C AACAC  T
                          GAG TC   TTAC CCGCCACC
                          ||| ||   |||| ||||||||
                          CTC AG    AATG GGCGGTGG
                            _ GCCGC  _
GAM157  FLJ20699   3' GGTGCAAGGATTGAGCTC  1766        CA ACTC
                          GAGCTCAA CTT  CGCC
                          |||||||| ||| ||||
                          CTCGAGTT GAA  GTGG
                              AG  C___
GAM157  FLJ23129   3' GGCAACAGGAGAATGTCAAGCC 2088    A CA  C A  ____
                          G GCT ACA TT CTCC  GCC
                          | ||| ||| || ||||  |||
                          C CGA TGT AA GAGG  CGG
                            _ AC  _ _  ACAA
GAM157  HSPC065    3' GTGACGGAGTAGAAGCTT  1482        CAACAC     C
                          GAGCT    TTACTCCG CAC
                          |||||    ||||||||| |||
                          TTCGA    GATGAGGC GTG
                            A_____        A
GAM157  KIAA0960   3' GGTAATTTAAGTGTTGAAGT 3572     _      CTCC
                          GCT CAACACTTA   GCC
                          ||| |||||||||   |||
                          TGA GTTGTGAAT   TGG
                            A     TTAA
GAM157  MGC12466   3' GGTAAAGGAGTGTTGAACTC 3127    C      A CC
                          GAG TCAACACTT CT GCC
                          ||| ||||||||| || |||
```

```
                     CTC AGTTGTGAG GA  TGG
                     A        _  AA
GAM157  MGC12904   3' GCAGTGAGTGCTGAGCTC   2184        A       CC
                     GAGCTCA CACTTACT  GC
                     ||||||| |||||||| ||
                     CTCGAGT GTGAGTGA  CG
                         C       __
GAM157  MSTP028    3' GGCAGTAAGTGTCCAGCTC   2224        CA      CC
                     GAGCT ACACTTACT  GCC
                     ||||| ||||||||| |||
                     CTCGA TGTGAATGA  CGG
                         CC      __
GAM157  RAB24      5' TGACGGAGTAGCGAGCT    2397       AACAC     C
                     AGCTC   TTACTCCG CA
                     |||||   |||||||| ||
                     TCGAG   GATGAGGC GT
                         C____      A
GAM157  LOC113828  5' TGAGGAGACGTTGAGCTC   2439         ACTTA   GC
                     GAGCTCAAC   CTCC CA
                     |||||||||   |||| ||
                     CTCGAGTTG   GAGG GT
                         CA___  A_
GAM157  LOC152300  5' GTGGACAGCATTGAGCTC   3169       CA TAC
                     GAGCTCAA CT TCCGC
                     |||||||| || |||||
                     CTCGAGTT GA AGGTG
                         AC C__
GAM157  LOC197125  3' GGCAGGTAACATTGAGCTC  3420       CAC    CC
                     GAGCTCAA TTACT GCC
                     |||||||| ||||| |||
                     CTCGAGTT AATGG CGG
                         AC_ A_
GAM157  LOC219848  3' GGTGACAGAGTAGGTGCTC  3528       TCAAC    ___
                     GAGC   ACTTACTC CGCC
                     ||||   |||||||| ||||
                     CTCG   TGGATGAG GTGG
                     _____       ACA
GAM157  LOC51157   5' GGTGGCGGGGTTTTGCAGAGCT 1671      AA CTT
                 C           GAGCTC CA ACTCCGCCACC
                     |||||| || ||||||||||
                     CTCGAG GT TGGGGCGGTGG
                         AC TT_
GAM157  LOC92270   5' GGTGACAGAGTGAGTGAGACTC 2828      _ AAC       ___
                     GAG CTC ACTTACTC CGCC
                     ||| ||| |||||||| ||||
                     CTC GAG TGAGTGAG GTGG
                         A ___     ACA
GAM158  B3GALT3    3' GCTGGTGTAAACAAACCTACTA 1057      A    C  G_
             CA            TGTGGTAG TTTGTT TATA AGC
                     ||||||| |||||| |||| |||
```

```
                              ACATCATC AAACAA ATGT  TCG
                                C     _    GG
GAM158 KIAA1985 5' GCTCTGTATTAAAACAAATCCA 2066      A      C___
       CCA                TGGT GATTTGTT   TATAGAGC
                          |||| |||||||   ||||||||
                          ACCA CTAAACAA   ATGTCTCG
                            C      AATT
GAM158 MCM10    3' CTATGCAAATTACCACA    1835      A    TCT
                          TGTGGT GATTTGT  ATAG
                          |||||| ||||||| ||||
                          ACACCA TTAAACG  TATC
                            _      ___
GAM158 LOC149707 5' CTCCACAACATCTACCA    3137       _  TCTATA
                          TGGTAGAT TTGT   GAG
                          |||||||| ||||   |||
                          ACCATCTA AACA   CTC
                            C   C_____
GAM158 LOC200227 5' CTCCACAACATCTACCA    3446       _  TCTATA
                          TGGTAGAT TTGT   GAG
                          |||||||| ||||    |||
                          ACCATCTA AACA    CTC
                            C   C_____
GAM158 LOC255718 5' GCTCTATAGAACATGTCTAC  3741      T
                          GTAGAT TGTTCTATAGAGC
                          |||||| |||||||||||||
                          CATCTG ACAAGATATCTCG
                          T
GAM159 DSG3     3' TTAAATGTTTGGGTTCATAC  873      C_
                          GTAT ATTTAAACATTTAA
                          |||| |||||||||||||
                          CATA TGGGTTTGTAAATT
                          CT
GAM159 LPIN1    3' AAATGATAATGATACTG     2791        TAAA
                          CAGTATCATT  CATTT
                          ||||||||||  |||||
                          GTCATAGTAA  GTAAA
                           TA__
GAM159 TRPM1    3' AAATGAAAGTGATGATACTGT 928          TAAA_
                          ACAGTATCATT  CATTT
                          |||||||||||  |||||
                          TGTCATAGTAG  GTAAA
                           TGAAA
GAM159 DEPP     3' GTTAAATGTTTCTGTCTTCTG 1347     TAT_ TTT
       TT               AACAG  CA  AAACATTTAAC
                          |||||  ||  |||||||||||
                          TTGTC  GT  TTTGTAAATTG
                           TTCT CT_
GAM159 FLJ20668 3' TTAAATGGACCATGATACT   1764       TTAAA
                          AGTATCAT   CATTTAA
                          ||||||||   |||||||
```

```
                        TCATAGTA   GTAAATT
                          CCAG_
GAM159  KIAA1524  5'  TAAATGTTTAGAACCTACTGT  2975        TCA
                        ACAGTA   TTTAAACATTTA
                        ||||||   ||||||||||||
                        TGTCAT   AGATTTGTAAAT
                          CCA
GAM159  PRO1617  5'  AAATCAGTGAATGGTACTG  1850            AAC
                        CAGTATCATTTA  ATTT
                        ||||||||||||  ||||
                        GTCATGGTAAGT  TAAA
                          GAC
GAM159  SDF1    3'  GTTAAATGTGATGAATACTGT  3502        _   TAA
                        ACAGTAT CATT  ACATTTAAC
                        ||||||| ||||  |||||||||
                        TGTCATA GTAG  TGTAAATTG
                          A    ___
GAM159  LOC130074 3'  GTTAGGTGTCAATTGATACT  3043        TTTAA
                        AGTATCA   ACATTTAAC
                        |||||||   |||||||||
                        TCATAGT   TGTGGATTG
                          TAAC_
GAM159  LOC146952 5'  TAAATGTAATTTTATGTACTGT  3287       T  TT  __
                T         AACAGTA CAT  AA  ACATTTA
                          ||||||| ||| ||  |||||||
                          TTGTCAT GTA  TT  TGTAAAT
                          _  TT AA
GAM159  LOC157983 3'  TTGCATGTTAAATGATACT   3208          A  T
                        AGTATCATTTAA CAT TAA
                        |||||||||||| ||| |||
                        TCATAGTAAATT GTA GTT
                          _  C
GAM159  LOC203289 3'  TTGCATGTTAAATGATACT   3463          A  T
                        AGTATCATTTAA CAT TAA
                        |||||||||||| ||| |||
                        TCATAGTAAATT GTA GTT
                          _  C
GAM159  LOC256544 3'  TTGCATGTTAAATGATACT   3695          A  T
                        AGTATCATTTAA CAT TAA
                        |||||||||||| ||| |||
                        TCATAGTAAATT GTA GTT
                            C
GAM160  APPL    3'  AGAACAGAGATTTTACAGT   1405       A      CA
                        ATTG TAAAATCTC  TTCT
                        |||| |||||||||  ||||
                        TGAC ATTTTAGAG  AAGA
                          _       AC
GAM160  F8      3'  AATGGAGAGAATACAATA   708        A  AAA
                        TATTG TA  TCTCCATT
                        ||||| ||  ||||||||
```

```
                      ATAAC AT  AGAGGTAA
                      _ AAG
GAM160  RAB6A    3' AGAATGGAAATAAAACTCAATA 966        TAAA_ C
        TTA              TAATATTGA   AT TCCATTCT
                      |||||||||  || ||||||||
                      ATTATAACT   TA AGGTAAGA
                      CAAAA A
GAM160  RNF14    3' AGAATGGAAATTTATAATAT 1097      ATA  C
                      ATATTG  AAAT TCCATTCT
                      ||||||  ||||  |||||||||
                      TATAAT  TTTA AGGTAAGA
                      A__  A
GAM160  SART2    3' AGAATTGGGTTTTATTAATATT 1443            CC
        A                TAATATTGATAAAATCT ATTCT
                      |||||||||||||||| |||||
                      ATTATAATTATTTTGGG TAAGA
                      T_
GAM160  EEA1     3' AATGGTTTTTGTTTTAACAATA 1035      A   CT___
        TTA              TAATATTG TAAAAT   CCATT
                      |||||||| ||||||   |||||
                      ATTATAAC ATTTTG   GGTAA
                      A    TTTTT
GAM160  FLJ10980 3' AGAATGGAGTGTACCAAATTA 2697    A  A AAAT
                      TAAT TTG TA   CTCCATTCT
                      |||| ||| ||   |||||||||
                      ATTA AAC AT   GAGGTAAGA
                      _ C GT__
GAM160  FLJ22794 3' AATGGTCATCTTATCAATA  3532        A CT
                      TATTGATAA AT CCATT
                      |||||||||| || |||||
                      ATAACTATT TA GGTAA
                      C CT
GAM160  KIAA1328 3' AGAATGGAGCCCACTAATATTA 2601         ATAAAAT
                      TAATATTG    CTCCATTCT
                      ||||||||    |||||||||
                      ATTATAAT    GAGGTAAGA
                      CACCC__
GAM160  PRO0902  3' AATGGAGATCAATTTTA  2357    T  TAAAA
                      TAA ATTGA   TCTCCATT
                      ||| |||||   ||||||||
                      ATT TAACT   AGAGGTAA
                      T   _____
GAM160  RASGRP4  3' AGAACAGGGATTTCTATCAATG 2348          _   CA
        T                ATATTGATA AAATCTC TTCT
                      ||||||||| |||||| ||||
                      TGTAACTAT TTTAGGG AAGA
                      C    AC
GAM160  WBP4     3' AGAATGGAGACTTATACA  1363    _  AA
                      TG ATAA  TCTCCATTCT
                      || |||| |||||||||
```

```
                        AC TATT  AGAGGTAAGA
                         A    C_
GAM160  LOC116150 3' AGAATGGAGCAGTTTAATA  2443        TAAAAT
                        TATTGA     CTCCATTCT
                        ||||||     |||||||||
                        ATAATT     GAGGTAAGA
                         TGAC__
GAM160  LOC164200 5' AATGAGGTTGTTATCAATA  3248          _   C
                        TATTGATAA AATCTC ATT
                        ||||||||| |||||| |||
                        ATAACTATT TTGGAG TAA
                             G     _
GAM160  LOC51320 3' AGAATGATAAATTATCAATAT 1702          AATCTC
                        ATATTGATAA    CATTCT
                        ||||||||||    ||||||
                        TATAACTATT    GTAAGA
                          AAATA_
GAM161  SELPLG   3' CCAAACAGGAAGTGGACATTCT 2539     A   CG   C
                        AGAAT TCCAT  TTTG TTGG
                        ||||| |||||  |||| ||||
                        TCTTA AGGTG  GGAC AACC
                          C     AA    A
GAM161  FLJ21144 3' CCAAAACATAAACAATAAATAT 2007        CC C   C___
        TCTCA              TGAGAATAT AT GTTTG  TTGG
                        |||||||||| || ||||| ||||
                        ACTCTTATA  TA CAAAT   AACC
                          AA  A   ACAA
GAM161  KIAA0676 3' CAAAGTGATGGAACCCTCA   1603      AATA      _
                        TGAG  TCCATCG TTTG
                        ||||  |||||||| ||||
                        ACTC  AGGTAGT AAAC
                         CCA_    G
GAM161  KIAA1393 3' CAAGTGATGAATATGCTCA   2935     A   C  GTTT
                        TGAG ATAT CATC   GCTTG
                        |||| |||| ||||   |||||
                        ACTC TATA GTAG   TGAAC
                          G   A    ____
GAM161  UBN1     3' CCAAGTCACAGATAGACATTCC 1716   A   A C  GTTT
          A              TG GAAT TC ATC   GCTTGG
                        || |||| || |||   ||||||
                        AC CTTA AG TAG   TGAACC
                         _   C  A  ACAC
GAM162  CELSR3   3' AGAACTGAAGACTTTAA     824         TAT
                        TTAAAGTCTTC  TTCT
                        |||||||||||  ||||
                        AATTTCAGAAG  AAGA
                          TC_
GAM162  GPR85    3' TAGAAGTTTGAAGACTTTAA   1868         T_
                        TTAAAGTCTTC ATTTCTA
                        ||||||||||| |||||||
```

```
                      AATTTCAGAAG TGAAGAT
                           TT
GAM162  ITGAV   3' TAGAAATGGAGAGTTTAATA 908        G   T
                      TATTAAA TCT CTATTTCTA
                      ||||||| ||| |||||||||
                      ATAATTT AGA GGTAAAGAT
                           G   _
GAM162  MAPRE2  3' TAGAAGTGAAGACCTTA    1487      A   T
                      TAA GTCTTC ATTTCTA
                      ||| |||||| |||||||
                      ATT CAGAAG TGAAGAT
                           C   _
GAM162  PAX6    5' AGGGGGAAGACTTTAA       837          AT
                      TTAAAGTCTTCT TTCT
                      |||||||||||| ||||
                      AATTTCAGAAGG GGGA

                           __
GAM162  PAX6    5' AGGGGGAAGACTTTAA       726          AT
                      TTAAAGTCTTCT TTCT
                      |||||||||||| ||||
                      AATTTCAGAAGG GGGA

                           __
GAM162  SLC24A1 3' TAGAAATAGAACAGCTTAATA 1150      A C_
                      TATTAA GT TTCTATTTCTA
                      |||||| || |||||||||||
                      ATAATT CG AAGATAAAGAT
                          _ AC
GAM162  SLC31A1 3' TAGAAATAGATATTTTTAA    864        TCT
                      TTAAAG TCTATTTCTA
                      |||||| ||||||||||
                      AATTTT AGATAAAGAT
                           TAT
GAM162  SLC4A7  3' TAGAACAATAGAAACTTTAATA 1043        C       __
                      TATTAAAGT TTCTATT TCTA
                      ||||||||| ||||||| ||||
                      ATAATTTCA AAGATAA AGAT
                           _     CA
GAM162  ZNF22   3' TAGAAATAGAGATGCTTTA   3527      C_
                      TAAAGT TTCTATTTCTA
                      |||||| ||||||||||
                      ATTTCG GAGATAAAGAT
                           TA
GAM162  ARGBP2  5' GGAAAACTGAAGACTTTAATA 1041          TA_
                      TATTAAAGTCTTC TTTCT
                      ||||||||||||| |||||
                      ATAATTTCAGAAG AAAGG
                           TCA
GAM162  C20orf7 3' AGAAATGGATAGCTTTAA    2056      CT
                      TTAAAGT TCTATTTCT
                      ||||||| |||||||||
```

```
                        AATTTCG AGGTAAAGA
                        AT
GAM162  FLJ12704  3' AGAACGCTGGACTTTAATG 2125          TCTAT
                        TATTAAAGTCT    TTCT
                        ||||||||||  ||||
                        GTAATTTCAGG    AAGA
                              TCGC_
GAM162  FLJ13194  3' TAGAAATGTTCTCAGACTTTAA 2141        TC___
                        TTAAAGTCT   TATTTCTA
                        |||||||||   ||||||||
                        AATTTCAGA   GTAAAGAT
                              CTCTT
GAM162  FLJ20005  3' AGAAAAAGACTTTAA     1731       CTA
                        TTAAAGTCTT  TTTCT
                        ||||||||||  |||||
                        AATTTCAGAA  AAAGA

                              ___
GAM162  FLJ20417  5' TAGAAATAAACAAGGCTTTA 1754         C__
                        TAAAGTCTT  TATTTCTA
                        |||||||||  ||||||||
                        ATTTCGGAA  ATAAAGAT
                              CAA
GAM162  KIAA0712  3' AGAAATTAAGACTTTAA     1529       CT
                        TTAAAGTCTT ATTTCT
                        ||||||||||  ||||||
                        AATTTCAGAA  TAAAGA
                              T_
GAM162  KIAA0750  5' AGAAAGAGAAGACTTTAA    1510        A
                        TTAAAGTCTTCT TTTCT
                        ||||||||||||| |||||
                        AATTTCAGAAGA AAAGA
                              G
GAM162  KIAA1128  3' TAGAGTATTCAGACTTTGATA 2821        TCTAT
                        TATTAAAGTCT    TTCTA
                        |||||||||||    |||||
                        ATAGTTTCAGA    GAGAT
                              CTTAT
GAM162  KIAA1281  3' TAGAAGAGAGAGACTTTAA 3461          _  A
                        TTAAAGTCT TCT TTTCTA
                        ||||||||| ||| ||||||
                        AATTTCAGA AGA GAAGAT
                              G  _
GAM162  KIAA1841  3' AGAGAACAGACTTTAATA  3151          TCTA
                        TATTAAAGTCT    TTTCT
                        |||||||||||    |||||
                        ATAATTTCAGA    AGAGA
                              CA__
GAM162  Rab11-FIP2 3' AGATGTAGAACTTTAATA  1580        CT   T
                        TATTAAAGT  TCTAT TCT
                        |||||||||  ||||| |||
```

```
                       ATAATTTCA AGATG AGA
                          __      T
GAM162  RABEX5   3' TAGTCGATGGAAGACTTTAA 1504          T_
                   TTAAAGTCTTCTATT CTA
                   ||||||||||||| |||
                   AATTTCAGAAGGTAG GAT
                          CT
GAM162  SGKL     3' TAGAGGTAAGACTTTAATA 1438          TC
                   TATTAAAGTCT TATTTCTA
                   |||||||||| ||||||||
                   ATAATTCAGA ATGGAGAT

                          __
GAM162  SYTL3    3' TAGAAAATGGCCAGATTTTAAT 3183       T_    _
            A              TATTAAAGTCT CTATTT CTA
                   ||||||||||| |||||| |||
                   ATAATTTTAGA GGTAAA GAT
                          CC    A
GAM162  TTY7     3' GAAAAAGACTTTGATA     2220        CTA
                   TATTAAAGTCTT TTTC
                   |||||||||||| ||||
                   ATAGTTTCAGAA AAAG

                          ___
GAM162  LOC113612 3' TAGAAATAGTTGACTTAATA 2968    A TT
                   TATTAA GTC CTATTTCTA
                   |||||| ||| |||||||||
                   ATAATT CAG GATAAAGAT
                        _ TT
GAM162  LOC121457 3' TAGAAATAGTTCTTTAA     2993    TCTT
                   TTAAAG CTATTTCTA
                   |||||| |||||||||
                   AATTTC GATAAAGAT
                        TT__
GAM162  LOC133491 3' TAGAATTGGGACTTTAGTA 3015       TT T
                   TATTAAAGTC CTA TTCTA
                   |||||||||| ||| |||||
                   ATGATTTCAG GGT AAGAT
                          __ T
GAM162  LOC143282 3' AGAAATAGGCGTACTTTAA 3054       CT_
                   TTAAAGT TCTATTTCT
                   ||||||| |||||||||
                   AATTTCA GGATAAAGA
                          TGC
GAM162  LOC143524 3' TAGAGAAGGGAAAGACTTTA 3059       _ A_
                   TAAAGTCTT CT TTTCTA
                   ||||||||| || ||||||
                   ATTTCAGAA GG AGAGAT
                          A GA
GAM162  LOC144559 5' TAGAGAAGGGAAAGACTTTA 3066       _ A_
                   TAAAGTCTT CT TTTCTA
                   ||||||||| || ||||||
```

```
                      ATTTCAGAA GG  AGAGAT
                        A  GA
GAM162  LOC153222 3'  TAGAAATGGTTGTACTTTAATG 3180          CTT_
                      TATTAAAGT    CTATTTCTA
                      |||||||||    |||||||||
                      GTAATTTCA   GGTAAAGAT
                        TGTT
GAM162  LOC219623 5'  AGAAAAGAAGACTTCAAT    3525      A      A
                      ATT AAGTCTTCT TTTCT
                      ||| ||||||||| |||||
                      TAA TTCAGAAGA AAAGA
                          C        _
GAM162  LOC219918 5'  TAGAGAAGGGAAAGACTTTA 3530          _ A_
                      TAAAGTCTT CT TTTCTA
                      ||||||||| || ||||||
                      ATTTCAGAA GG  AGAGAT
                        A GA
GAM162  LOC220071 5'  TAGAGAAGGGAAAGACTTTA 3602          _ A_
                      TAAAGTCTT CT TTTCTA
                      ||||||||| || ||||||
                      ATTTCAGAA GG  AGAGAT
                        A GA
GAM162  LOC254431 3'  AGGTAAAGACTTTAGTA     3717        C
                      TATTAAAGTCTT TATTT
                      |||||||||||| |||||
                      ATGATTTCAGAA ATGGA
                              _
GAM162  LOC255515 3'  TAGAGAAGGGAAAGACTTTA 3688          _ A_
                      TAAAGTCTT CT TTTCTA
                      ||||||||| || ||||||
                      ATTTCAGAA GG  AGAGAT
                        A GA
GAM162  LOC56959  5'  ATAGAAACAGAGGACGTGACTT 3219        _____  A    |||
                TGATA            TAAAGTC   TTCT TTTCTA  T
                      |||||||    |||| |||||| |
                      GTTTCAG    GAGA AAAGAT  A
                        TGCAG   C     |||
GAM162  LOC90906  3'  TAGAGAAGGGAAAGACTTTA 2685          _ A_
                      TAAAGTCTT CT TTTCTA
                      ||||||||| || ||||||
                      ATTTCAGAA GG  AGAGAT
                        A GA
GAM163  ENAM     5'  TATAGACCATTAAGAATA    2216      TC  C  C
                      TATTCTTA ATG GTC ATA
                      |||||||| ||| ||| |||
                      ATAAGAAT TAC CAG TAT
                        __  _  A
GAM163  EFNA5    3'  CTATGGACAAGGAAGAATAGT 876        ATCATGC
                      ATTATTCTT    GTCCATAG
                      |||||||||    ||||||||
```

```
                        TGATAAGAA      CAGGTATC
                          GGAA___
GAM163  LOC159199 5' CTATGGACAAGCCAAGAA  3236      ATCAT __
                      TTCTT   GC GTCCATAG
                      |||||   || ||||||||
                      AAGAA   CG CAGGTATC
                        C____  AA
GAM163  LOC90321  3' ATGGAGGTGGACAGAGAATAA 2630       ATCA  G
                      TTATTCTT  TGC TCCAT
                      ||||||||  ||| |||||
                      AATAAGAG  GTG AGGTA
                        ACAG  G
GAM164  KRAS2     3' AATATTATATTTTTTCTATAAA 1166      GAT
             AA             TTTTTA  AAAAAATATAATATT
                            ||||||  |||||||||||||
                            AAAAAT  TTTTTATATTATAA
                              ATC
GAM164  KRAS2     3' AATATTATATTTTTTCTATAAA 2331      GAT
             AA             TTTTTA  AAAAAATATAATATT
                            ||||||  |||||||||||||
                            AAAAAT  TTTTTATATTATAA
                              ATC
GAM165  APXL      3' AGGACTTTCTCTTCTACAC  843       TATA
                      GTGTGGGA  AAAGTCCT
                      ||||||||  ||||||||
                      CACATCTT  TTTCAGGA
                        CTC_
GAM165  ASTN      3' AGGTGCTTATATCCCACCAAC 2852   __      AA _
                      GT GTGGGATATA AGT CCT
                      || |||||||||| ||| |||
                      CA CACCCTATAT TCG GGA
                        AC        __  T
GAM165  GALK2     3' AGGACTTTCTGTGCCACA  891      G TA
                      TGTGG ATA  AAAGTCCT
                      ||||| |||  ||||||||
                      ACACC TGT  TTTCAGGA
                        G C_
GAM165  MCL1      3' AGGACTTTTATACCTGT   1970   TG A
                      G GG TATAAAAGTCCT
                      | || ||||||||||||
                      T CC ATATTTCAGGA
                      GT _
GAM165  PACE4     5' AGGACTTTTACTACCATGGTA 2434      TG ATA
                      TACCGTG GG  TAAAAGTCCT
                      ||||||| ||  |||||||||
                      ATGGTAC TC  ATTTTCAGGA
                        CA ___
GAM165  PODXL     3' AGGACTTTTATGGGCTCGGC 1206     G  A_
                      GT TGGG  TATAAAAGTCCT
                      || |||| |||||||||||
```

```
                           CG GCTC GTATTTTCAGGA
                           _   GG
GAM165  TNFSF8       3' GGACTCTCTCACACAGG     811      _         TATAAA
                           CC GTGTGGGA     AGTCC
                           || |||||||   |||||
                           GG CACACTCT     TCAGG
                             A    C_____
GAM165  ATP1B4       3' GACCTCTATATCCTGGTG   1401      GTGT       AAA
                           TACC  GGGATATA GTC
                           ||||  |||||||| |||
                           GTGG  TCCTATAT CAG
                           ____       CTC
GAM165  CDC14A       3' AGGACCCTTATAGGTACTCACA 1047        A___     AA
                           TGTGGG  TATAA GTCCT
                           ||||||  ||||| |||||
                           ACACTC  ATATT CAGGA
                             ATGG    CC
GAM165  DKFZP434C171 3' GGACTCTTATGTCACTGCA  1641      TG _     A
                           TG G GATATAA AGTCC
                           || | ||||||| |||||
                           AC C CTGTATT TCAGG
                             GT A     C
GAM165  EMR2         3' AGGACTTTCATACCGACAAC  1453      _ G A A
                           GT GT GG TAT AAAGTCCT
                           || || || ||| ||||||||
                           CA CA CC ATA TTTCAGGA
                             A  G  _  C
GAM165  FYCO1        3' AGGACTTTGTGGGGCCACAAG  2063      CG    GA_
          TA               TAC TGTGG  TATAAAGTCCT
                           ||| |||||  |||||||||||
                           ATG ACACC  GTGTTTCAGGA
                             A_    GGG
GAM165  GGA2         3' AGGACTTTCCCGTCCACACAC  2448       _ ATA
                           GTGTG GGAT  AAAGTCCT
                           ||||| ||||  ||||||||
                           CACAC CCTG  TTTCAGGA
                             A    CCC
GAM165  GGA2         3' AGGACTTTCCCGTCCACACAC  1604       _ ATA
                           GTGTG GGAT  AAAGTCCT
                           ||||| ||||  ||||||||
                           CACAC CCTG  TTTCAGGA
                             A    CCC
GAM165  ICT1         3' AGGACTTTCACACCATAAGG   834      G    GATATA
                           CC TGTGG     AAAGTCCT
                           || |||||     ||||||||
                           GG ATACC     TTTCAGGA
                             A   ACAC__
GAM165  ZFP100       3' AGGACTCCCTATCCCACA     2877         TAAA
                           TGTGGGATA  AGTCCT
                           |||||||||  ||||||
```

```
                         ACACCCTAT  TCAGGA
                         CCC_
GAM165  LOC64744 3' GACTTTATGAAGATCCCACAC 2607          ATA___
                         GTGTGGGAT    AAAGTC
                         ||||||||    ||||||
                         CACACCCTA    TTTCAG
                         GAAGTA
GAM166  MEF-2    3' TGCTATTAAATAGTAAAC  2688         T ATAAC
                         GTTTACTATTTA TG   GCA
                         |||||||||||| ||   |||
                         CAAATGATAAAT AT   CGT
                         T _____
GAM166  LOC146184 5' TATCAATAAATAGCAAAC  3281      A
                         GTTT CTATTTATTGATA
                         |||| |||||||||||||
                         CAAA GATAAATAACTAT
                         C
GAM167  CDH5     3' CAGTGATGACTATTCTCAAATG 858      G  A     ATTC
                         CAT TGA AATAGTCAT   CTG
                         ||| ||| |||||||||   |||
                         GTA ACT TTATCAGTA   GAC
                         A   C      GT__
GAM167  LNK     3' CAGAGAACACTATTTTTACAT 1216          CATA _
                         ATGTGAAAATAGT  TTC CTG
                         |||||||||||||  ||| |||
                         TACATTTTTATCA  AAG GAC
                         C___ A
GAM167  NPR2    3' CAGAAATGGACATTTTCATATG 786        A  A   C
                         CATGTGAAAAT GTC TATT CTG
                         |||||||||||| ||| |||| |||
                         GTATACTTTTA CAG GTAA GAC
                         _ _ A
GAM167  CLLD8   3' GCAGGAACACAATTAGGATATT 2219     G  A  _____    |||
          TTCATA          AAATA TC TA    TTCCTG  C
                         ||||| || ||    ||||||  |
                         TTTAT AG AT    AAGGAC  G
                         _ G TAACAC    |||
GAM167  FLJ22301 3' CAGGTGAGGACCATTTTCAC 2094       A ATATT
                         GTGAAAAT GTC   CCTG
                         |||||||| |||    ||||
                         CACTTTTA CAG    GGAC
                         C GAGT_
GAM167  FLJ22833 3' AGGGAACACCAGTTTTCACATG 2016               AGTCATA
                         CATGTGAAAAT    TTCCT
                         ||||||||||     |||||
                         GTACACTTTTG    AGGGA
                         ACCACA_
GAM167  KIAA0125 3' GAAATGACATTCACATG    1548         AATA   A
                         CATGTGAA  GTCAT TTC
                         ||||||||  ||||| |||
```

```
                      GTACACTT  CAGTA AAG
                      A___    _
GAM167  KIAA0125 3' GAAATGACATTCACATG   1549       AATA   A
                      CATGTGAA  GTCAT TTC
                      |||||||| |||||| |||
                      GTACACTT  CAGTA AAG
                      A___    _
GAM167  KIAA0125 3' GAAATGACATTCACATG   1550       AATA   A
                      CATGTGAA  GTCAT TTC
                      |||||||| |||||| |||
                      GTACACTT  CAGTA AAG
                      A___    _
GAM167  KIAA0125 3' GAAATGACATTCACATG   1551       AATA   A
                      CATGTGAA  GTCAT TTC
                      |||||||| |||||| |||
                      GTACACTT  CAGTA AAG
                      A___    _
GAM167  KIAA0125 3' GAAATGACATTCACATG   1552       AATA   A
                      CATGTGAA  GTCAT TTC
                      |||||||| |||||| |||
                      GTACACTT  CAGTA AAG
                      A___    _
GAM167  KIAA1199 3' CAGAAATCTGCTGCATTTCACA 2951        A_  T T C
         TG             CATGTGAAA TAG CA ATT CTG
                      |||||||||| ||| || ||| |||
                      GTACACTTT GTC GT TAA GAC
                      AC  _ C  A
GAM167  LANCL2   3' ATATGACTTCTTCACAT   1860       AAT
                      ATGTGAA  AGTCATAT
                      ||||||| ||||||||
                      TACACTT  TCAGTATA
                      CT_
GAM167  SEZ6     3' CAGGAGTACCTTTCTCCACATG 2997       AAAAT TCA
                      CATGTG  AG TATTCCTG
                      |||||| || |||||||||
                      GTACAC  TC ATGAGGAC
                      CTCTT C__
GAM167  SNX10    3' AGGAAGATATTTTCAGAT   1442    G     GTCATA
                      AT TGAAAATA    TTCCT
                      || ||||||||    |||||
                      TA ACTTTTAT    AAGGA
                      G    AG____
GAM167  TNFRSF21 3' AGTGTGACTTTTCCCACA   1502     AA T
                      TGTG AA AGTCATATT
                      |||| || |||||||||
                      ACAC  TT TCAGTGTGA
                      CC T
GAM167  TTTY11   5' CAGGAATAGTCAGCATTTCACA 2221         ATAGTCA
         T             ATGTGAAA   TATTCCTG
                      ||||||     |||||||||
```

```
                          TACACTTT     ATAAGGAC
                          ACGACTG
GAM167  LOC143879 3' GAATACTTAGTATTTTCACATG 3063              GTCA_
                          CATGTGAAAATA    TATTC
                          |||||||||||    |||||
                          GTACACTTTTAT    ATAAG
                          GATTC
GAM167  LOC145439 5' CAGGAATACAGAGATTCGCAT 3078           ATAGTCA
             G              CATGTGAAA    TATTCCTG
                          |||||||||    ||||||||
                          GTACGCTT    ATAAGGAC
                          AGAGAC_
GAM167  LOC147353 3' CAGGAATAGAACTTGCACATG 3293          AAAAT  CA
                          CATGTG    AGT TATTCCTG
                          ||||||    ||| ||||||||
                          GTACAC    TCA ATAAGGAC
                          GT___ AG
GAM167  LOC221584 5' GAATATGGGCTACTTCATATG 3620            AA    _
                          CATGTGAA TAGTC ATATTC
                          ||||||||| ||||| |||||
                          GTATACTT ATCGG TATAAG
                          C_   G
GAM167  LOC257054 3' CAGGAATGTGTCATTTCCCACA 3682       A_  AGT
                          TGTG AAAT  CATATTCCTG
                          |||| ||||  |||||||||
                          ACAC TTTA  GTGTAAGGAC
                          CC   CT_
GAM167  LOC91145  5' CAGGAATGTACACTTTACAT 2713          AATA  C
                          ATGTGAA   GT ATATTCCTG
                          |||||||   || |||||||||
                          TACATTT   CA TGTAAGGAC
                          CA__  _
GAM167  LOC93297  3' GAATATGTTTGTGTATGTTCAC 2929        A____  T
      ATG               CATGTGAA   ATAG CATATTC
                          |||||||||   |||| |||||||
                          GTACACTT   TGTT GTATAAG
                          GTATG   T
GAM168  BACH2    3' AAGCTGTTCGTTGTATCA 1961     A       _
                          TGA TACAACGAATA CTT
                          ||| ||||||||||| |||
                          ACT ATGTTGCTTGT GAA
                          _       C
GAM168  GAN      3' TGAAGTATAGGGATGTATTTA 1974           ACGA_
                          TGAATACA   ATACTTCA
                          ||||||||   ||||||||
                          ATTTATGT   TATGAAGT
                          AGGGA
GAM168  MHC2TA   3' TGAAGCATTTACTTTGTGTTCA 720          C__  A
                          TGAATACAA  GAAT CTTCA
                          |||||||||  |||| |||||
```

```
                        ACTTGTGTT  TTTA GAAGT
                           TCA   C
GAM168  MTM1      3' TGAAGTATTGTGTTTA    723         ACGA
                        TGAATACA  ATACTTCA
                        |||||||  |||||||
                        ATTTGTGT  TATGAAGT
                           ____

GAM168  AWP1      3' TGAAGTAATTGTGCTGTATTTA 1872        __   A
                        TGAATACA ACGA TACTTCA
                        |||||||| |||| |||||||
                        ATTTATGT TGTT ATGAAGT
                            CG   A
GAM168  BLCAP     3' TGAAGTATGGTGTGTTCA    1324        ACGA
                        TGAATACA  ATACTTCA
                        |||||||  |||||||
                        ACTTGTGT  TATGAAGT
                            GG__
GAM168  C5orf3    3' TGAAGTATTCAGGTTCTCA   1859    AT AAC
                        TGA AC  GAATACTTCA
                        ||| ||  ||||||||||
                        ACT TG  CTTATGAAGT
                         CT GA_
GAM168  CRK7      3' AAGCTGTCCGTTGTATTC    1690        A  _
                        GAATACAACG ATA CTT
                        |||||||||| ||| |||
                        CTTATGTTGC TGT GAA
                            C  C
GAM168  FLJ11101  3' TGAAGTTTTGATTGTATTTA  1814        _  T
                        TGAATACAA CGAA ACTTCA
                        ||||||||| |||| ||||||
                        ATTTATGTT GTTT TGAAGT
                            A   _
GAM168  FLJ12876  3' TGAAGTGTAGATCATTGTATTC 2004        C ___
              A             TGAATACAA GA  ATACTTCA
                        ||||||||| ||  |||||||
                        ACTTATGTT CT  TGTGAAGT
                          A AGA
GAM168  KLF12     3' TGAAGTGTAGATTTGTATTTA  1374        CGA_
                        TGAATACAA  ATACTTCA
                        |||||||||  |||||||
                        ATTTATGTT  TGTGAAGT
                          TAGA
GAM168  MGC4734   3' AAGTGTTCTGTATTCA      2513      AC
                        TGAATACA GAATACTT
                        |||||||| ||||||||
                        ACTTATGT CTTGTGAA
                           __
GAM168  PRO2000   3' GAGTATTCTTTATATTCA    1469     C C
                        TGAATA AA GAATACTT
                        |||||| || ||||||||
```

```
                          ACTTAT TT CTTATGAG
                           A   T
GAM168  RAB33B   3' TGAAGTGTTCACATTCA    2191      ACAAC
                          TGAAT    GAATACTTCA
                          |||||    ||||||||||
                          ACTTA    CTTGTGAAGT
                           CA___
GAM168  RGS12    3' TGAAGCCCGCTGTGTTCA    972        A AATA
                          TGAATACA CG   CTTCA
                          |||||||| ||   |||||
                          ACTTGTGT GC   GAAGT
                            C CC__
GAM168  ZNF387   3' TGAAGTATGTTTGTATTTA   1522       CGA
                          TGAATACAA  ATACTTCA
                          |||||||||  ||||||||
                          ATTTATGTT  TATGAAGT
                             TG_
GAM168  LOC158381 3' TGAAGTAATTGTGCTGTATTTA 2905        __  A
                          TGAATACA  ACGA TACTTCA
                          ||||||||  |||| |||||||
                          ATTTATGT  TGTT ATGAAGT
                             CG   A
GAM168  LOC196411 3' AAGTTTCTTTGTGTTCA    3412      C  T
                          TGAATACAA GAA ACTT
                          ||||||||| ||| ||||
                          ACTTGTGTT CTT TGAA
                              T  _
GAM168  LOC51186  5' GAAGTCATTGTATTCA     1680      C ATA
                          TGAATACAA GA   CTTC
                          ||||||||| ||   ||||
                          ACTTATGTT CT   GAAG
                             A  ___
GAM169  RDX      3' TAGAGATTAAACCAATTA    971        G
                          TAATTGGTTTAATC TTTA
                          |||||||||||||| ||||
                          ATTAACCAAATTAG AGAT
                                _
GAM169  TRPC3    3' AATAAATGTTGAAACCAACTGA 1010     A    AAT
                          TTA TTGGTTT  CGTTTATT
                          ||| |||||||  ||||||||
                          AGT AACCAAA  GTAAATAA
                             C     GTT
GAM169  LOC131000 3' TAATAAACGATTTAATGAA   3038     G  T
                          TT GTT AATCGTTTATTA
                          || ||| |||||||||||
                          AA TAA TTAGCAAATAAT
                             G   T
GAM170  ACTA2    3' TGTGAATGTCCTGTGGAA    839        AG CTAAT  _
                          TTCCACAG CA    TTC CA
                          |||||||| ||    ||| ||
```

```
                        AAGGTGTC GT   AAG GT
                          CT _____    T
GAM170  ASPH    3' GAAATAATTGCTCTGTTGAA 2251      C      CTA
                        TTC ACAGAGCA  ATTTC
                        ||| ||||||||  |||||
                        AAG TGTCTCGT  TAAAG
                          T    TAA
GAM170  ASPH    3' GAAATAATTGCTCTGTTGAA 2253      C      CTA
                        TTC ACAGAGCA  ATTTC
                        ||| ||||||||  |||||
                        AAG TGTCTCGT  TAAAG
                          T    TAA
GAM170  BRCA1   3' TGGAAGTTAGCACTCTAGGGAA 1392     AC   CA
                        TTCC AGAG  CTAATTTCCA
                        |||| ||||  ||||||||||
                        AAGG TCTC  GATTGAAGGT
                          GA   AC
GAM170  CDC42   3' GAAGACAGACATCTGTGGAA 856         GCA AA
                        TTCCACAGA  CT TTTC
                        |||||||||  || ||||
                        AAGGTGTCT  GA GAAG
                          ACA  CA
GAM170  CLASP1  3' TTGGAAATAAAGAAGTGCTCTG 2718           A____
                        CAGAGCACT   ATTTCCAA
                        |||||||||   ||||||||
                        GTCTCGTGA   TAAAGGTT
                          AGAAA
GAM170  CPNE3   3' GAAATTAGTGTGGGGAA    1069     ACAGA
                        TTCC   GCACTAATTTC
                        ||||   |||||||||||
                        AAGG   TGTGATTAAAG
                          GG___
GAM170  DACH    3' TTGGAAATTTTTCTATGG   2388    C  CACT
                        CCA AGAG   AATTTCCAA
                        ||| ||||   |||||||||
                        GGT TCTT   TTAAAGGTT
                          A  T___
GAM170  ECM2    5' GAAATTGGCTGGTGGAA    823       AG  AC
                        TTCCAC AGC TAATTTC
                        |||||| ||| |||||||
                        AAGGTG TCG GTTAAAG
                          G_  __
GAM170  EDNRA   3' TAGACTGTCTCTGTGGAA   2681          _ __
                        TTCCACAGAG CA CTA
                        |||||||||| || |||
                        AAGGTGTCTC GT GAT
                          T CA
GAM170  ENC1    3' TTGGAAATCAGTTGTG     1045    GAGC  A
                        CACA   ACT ATTTCCAA
                        ||||   ||| |||||||||
```

```
                        GTGT   TGA TAAAGGTT
                        ____       C
GAM170  FANCF   3' TTGGTGGCTGCCCTGTGGAA 1999      A _ ATTT
                        TTCCACAG GCA CTA   CCAA
                        |||||||| ||| |||   ||||
                        AAGGTGTC CGT GGT   GGTT
                               C  C   ____
GAM170  FCAR    3' GAAAACTTAGTCTGTGGAG 2405        GCA  __
                        TTCCACAGA  CTAA TTTC
                        |||||||||  |||| ||||
                        GAGGTGTCT  GATT AAAG
                             ___   CA
GAM170  FCAR    3' GAAAACTTAGTCTGTGGAG 2407        GCA  __
                        TTCCACAGA  CTAA TTTC
                        |||||||||  |||| ||||
                        GAGGTGTCT  GATT AAAG
                             ___   CA
GAM170  GAS7    3' TTGGAAATATACAGCTCTGTG 1259        ACTA_
                        CACAGAGC   ATTTCCAA
                        ||||||||   |||||||||
                        GTGTCTCG   TAAAGGTT
                          ACATA
GAM170  KCNJ5   5' GAAATTAATCTCTGGGGAA 784      A   CAC
                        TTCC CAGAG  TAATTTC
                        |||| |||||  |||||||
                        AAGG GTCTC  ATTAAAG
                           G   TA_
GAM170  MEF2A   3' GAGAAAATGCTTTGTAGAA 1228     C     CTAA
                        TTC ACAGAGCA   TTTC
                        ||| ||||||||   ||||
                        AAG TGTTTCGT   AGAG
                          A     AAA_
GAM170  MIR16   3' GGAAACTAAACTCTGTGGAA 1704       CAC A
                        TTCCACAGAG  TA TTTCC
                        ||||||||||  || |||||
                        AAGGTGTCTC  AT AAAGG
                            AA_ C
GAM170  P4HB    3' TTGAAAATTCCGTCTGTGGGA 787       G ACT   C
                        TTCCACAGA C  AATTT CAA
                        |||||||||| |  ||||| |||
                        AGGGTGTCT G   TTAAA GTT
                            _CC_    A
GAM170  RAF1    3' TTGGAAATCAGCTTCTGGAGGA 3168     A_   CA A
            A                TTCC CAGAG  CT ATTTCCAA
                        |||| |||||  || ||||||||
                        AAGG GTCTT  GA TAAAGGTT
                          AG   C_ C
GAM170  RPS6KA5 3' TTGGAAATTTTTCTGTTGAA 1153     C     CACT
                        TTC ACAGAG   AATTTCCAA
                        ||| ||||||   |||||||||
```

```
                    AAG TGTCTT   TTAAAGGTT
                      T    T___
GAM170  TBL1X    3' GAAATGGCCTGTGGAA      1233        A  ACTA
                    TTCCACAG GC   ATTTC
                    |||||||| ||   |||||
                    AAGGTGTC CG   TAAAG
                           _  G___
GAM170  ARHGAP10 5' GGAGCCTGCTTGTGGAA      1926       G   CTAAT
                    TTCCACA AGCA    TTCC
                    ||||||| ||||    ||||
                    AAGGTGT TCGT    GAGG
                          _   CC___
GAM170  ATP9A    3' TTGGAAATCAGTCTGT      2619      GCA  A
                    ACAGA  CT ATTTCCAA
                    |||||  || ||||||||
                    TGTCT  GA TAAAGGTT
                        ___  C
GAM170  Di-Ras2  3' TTGGAAATATGTTCCTGGAA  1725      CA    CTA
                    TTCCA GAGCA  ATTTCCAA
                    ||||| |||||  ||||||||
                    AAGGT CTTGT  TAAAGGTT
                        C_   A__
GAM170  FHOD2    3' GAGAACGATGCTCTGTGAGA 2981     _       CTAA
                    TC CACAGAGCA    TTTC
                    || |||||||||    ||||
                    AG GTGTCTCGT    AGAG
                     A       AGCA
GAM170  FLJ10704 3' TTGGAAATTAGTGTTATCTGGA 1795       CAG
             A                TTCCA  AGCACTAATTTCCAA
                    |||||  |||||||||||||||
                    AAGGT  TTGTGATTAAAGGTT
                      CTA
GAM170  FLJ12085 3' TTGGAAATTATGCACTTTG   2006    C  A  C
                    CA AG GCA TAATTTCCAA
                    || || ||| ||||||||||
                    GT TC CGT ATTAAAGGTT
                     T  A   _
GAM170  FLJ20209 3' AGATTGGTTGCTCTGGAA    3351       CA    _
                    TTCCA GAGCA CTAATTT
                    ||||| ||||| |||||||
                    AAGGT CTCGT GGTTAGA
                       __       T
GAM170  FLJ22174 5' TTGGAAATTGAAGCTGTAGAG 1969     C  AGCAC
                    TTC ACAG    TAATTTCCAA
                    ||| ||||    ||||||||||
                    GAG TGTC    GTTAAAGGTT
                      A  GAA__
GAM170  HSPC129  3' TTGGAAATTAAAGGTGGA    1685        AGAGCAC
                    TCCAC    TAATTTCCAA
                    |||||    ||||||||||
```

```
                    AGGTG     ATTAAAGGTT
                     GAA____
GAM170  KIAA0632 3' GGCCCCCAGTGCTCTGTGGGA 1634              AATTT
                    TTCCACAGAGCACT    CC
                    |||||||||||||    ||
                    AGGGTGTCTCGTGA    GG
                        CCCCC
GAM170  KIAA1184 3' TTGGAAATCAGAAGTCTGTGAG 1994        _    GCA A
            A           TC CACAGA  CT ATTTCCAA
                    || |||||| || ||||||||
                    AG GTGTCT  GA TAAAGGTT
                     A   GAA C
GAM170  KIAA1671 3' GAAATCAGTGTTGTGGAG  2725          GA   A
                    TTCCACA GCACT ATTTC
                    ||||||| ||||| |||||
                    GAGGTGT TGTGA TAAAG
                        __   C
GAM170  KIAA1728 3' TGGTAGTGCTCCTGGAA  2818     CA      ATTT
                    TTCCA GAGCACTA   CCA
                    ||||| ||||||||   |||
                    AAGGT CTCGTGAT   GGT
                     C_       ____
GAM170  KIAA1737 3' TTGGAAAAACCCTCTGTGGAG 2789         CACTAA
                    TTCCACAGAG    TTTCCAA
                    ||||||||||    |||||||
                    GAGGTGTCTC    AAAGGTT
                        CCAA__
GAM170  KIAA1750 3' ATTGGAAATTGTTGCTGTGTTC 2811        _____      |||
            TGTG        CAGAGCAC   TAATTTCCAA  T
                    |||||||   ||||||||||  |
                    GTCTTGTG   GTTAAAGGTT  A
                      TCGTT       |||
GAM170  KIAA1900 3' TGGAAACATGTTGTGGAA  2972      GA CTAA
                    TTCCACA GCA   TTTCCA
                    ||||||| |||   ||||||
                    AAGGTGT TGT   AAAGGT
                      __  AC__
GAM170  KIAA1946 3' AAGTTAGTGCTCTGCTGAA  3246     CA
                    TTC CAGAGCACTAATTT
                    ||| |||||||||||||
                    AAG GTCTCGTGATTGAA
                      TC
GAM170  LALP1    3' AAATGAATGGTCTGTGGAA  1915       G CTA
                    TTCCACAGA CA  ATTT
                    |||||||| || ||||
                    AAGGTGTCT GT  TAAA
                      G AAG
GAM170  LRRFIP2  3' TTGGAAATCTGCCTGCAGA  1743    CA A CTA
                    TC CAG GCA  ATTTCCAA
                    || ||| |||  ||||||||
```

```
                        AG  GTC CGT   TAAAGGTT
                        AC  _   C__
GAM170  MGC1842  3' TGGCAGCAGTGCTCTGGGAA 2724      A     AATTT
                        TTCC CAGAGCACT    CCA
                        |||| |||||||||    |||
                        AAGG GTCTCGTGA    GGT
                            _   CGAC_
GAM170  MGC9753  5' TGGCCTGGTGCCTGTGGAA 2333      A    ATTT
                        TTCCACAG GCACTA    CCA
                        |||||||| ||||||    |||
                        AAGGTGTC CGTGGT    GGT
                            _    CC__
GAM170  PEG10    3' GAATTGGTCTGTGGAA      1606        GCA
                        TTCCACAGA CTAATTT
                        ||||||||| |||||||
                        AAGGTGTCT GGTTAAG

                            ___
GAM170  PGRMC2   3' TTGGAAATTAGGAGAAGGAA 1287      ACAGAGCA
                        TTCC     CTAATTCCAA
                        ||||     ||||||||||
                        AAGG     GATTAAAGGTT
                        AAGAG___
GAM170  PPP4R1L  5' GGAAAGCCCTGTGGAA      3139      A ACTAA
                        TTCCACAG GC    TTTCC
                        |||||||| ||    |||||
                        AAGGTGTC CG    AAAGG
                            C  _____
GAM170  PRO0386  5' GAACTAATGTTCTGTGGAA  1843      C A
                        TTCCACAGAGCA TA TTT
                        |||||||||||| || |||
                        AAGGTGTCTTGT AT AAG
                            A  C
GAM170  PRO0456  3' TGGAATTCATACTCTGTGGAA 1476        CACTAAT
                        TTCCACAGAG     TTCCA
                        ||||||||||     |||||
                        AAGGTGTCTC     AAGGT
                            ATACTT_
GAM170  SLC26A8  5' AGTCAGTATCTGTGGAA    2455      GC  A
                        TTCCACAGA ACT ATT
                        ||||||||| ||| |||
                        AAGGTGTCT TGA TGA
                        A_   C
GAM170  SNTG1    5' TTGGAAATAGCTTTGTG    1867      ACTA
                        CACAGAGC  ATTTCCAA
                        ||||||||  ||||||||
                        GTGTTTCG  TAAAGGTT
                            A___
GAM170  ZNF396   3' TTGGAAATAAGTCAATGGAA 3034      CA GCA A
                        TTCCA GA  CT ATTTCCAA
                        ||||| ||  || ||||||||
```

```
                          AAGGT  CT  GA TAAAGGTT
                          AA ___   A
GAM170  LOC145098 5' TTGGAAATATCTTCTGTG   3074        CACTA
                         CACAGAG   ATTTCCAA
                         ||||||| ||||||||
                         GTGTCTT   TAAAGGTT
                          CTA__
GAM170  LOC146136 5' GAAAAGGCCTCTGTGGAG   2964        CA  AA
                         TTCCACAGAG CT TTTC
                         |||||||||| || ||||
                         GAGGTGTCTC GA AAAG
                           CG __
GAM170  LOC148195 3' GGAAGGCATCCTGTGGAA   3298        A__ A AATT
                         TTCCACAG GC CT   TCC
                         |||||||| || ||   |||
                         AAGGTGTC CG GA   AGG
                           CTA _ ____
GAM170  LOC149086 5' TGGAGATGATCCGTGGAA   3306        A GCACTA
                         TTCCAC GA    ATTTCCA
                         |||||| ||    |||||||
                         AAGGTG CT    TAGAGGT
                          C AG____
GAM170  LOC149420 3' TTGGAAATTAGAGGTGGAA   3133       AGAGCA
                         TTCCAC    CTAATTTCCAA
                         ||||||    |||||||||||
                         AAGGTG    GATTAAAGGTT
                          GA____
GAM170  LOC149912 5' TGGAAAGTGCTCTGTGG   3317        AAT
                         CCACAGAGCACT TTCCA
                         |||||||||||| |||||
                         GGTGTCTCGTGA AAGGT
                           ___
GAM170  LOC151816 5' GGAGTGTGCTCTGGGAA   3350     A     TAAT
                         TTCC CAGAGCAC   TTCC
                         |||| ||||||||   ||||
                         AAGG GTCTCGTG   GAGG
                          _    T___
GAM170  LOC152991 5' GAAATGGGTCATACTCTGTGGA 3365        C___  A
                         TCCACAGAG   ACT ATTTC
                         ||||||||| ||| |||||
                         AGGTGTCTC   TGG TAAAG
                          ATAC  G
GAM170  LOC157556 3' TGGAGGGGTGCTCTGTGGAA   3382          AA
                         TTCCACAGAGCACT TTTCCA
                         |||||||||||||| ||||||
                         AAGGTGTCTCGTGG GGAGGT
                           ___
GAM170  LOC157697 5' AAATCTTGTGCTCTGCGAA   3204     CA    TA_
                         TTC CAGAGCAC  ATTT
                         ||| ||||||||  ||||
```

```
                              AAG  GTCTCGTG  TAAA
                              C_         TTC
GAM170  LOC158431 3' TGGAAATTGTTTCTGTAGAA 3390    C    C T
                              TTC ACAGAG AC AATTTCCA
                              ||| |||||| || |||||||
                              AAG TGTCTT TG TTAAAGGT
                              A         _ _
GAM170  LOC200488 5' GAAATGAGTCTGTGGGA   3478       GCA  A
                              TTCCACAGA  CT ATTTC
                              ||||||||| || |||||
                              AGGGTGTCT  GA TAAAG
                                  ___ G
GAM170  LOC220565 3' GAAAAGGCCTCTGTGGAG  3494        CA AA
                              TTCCACAGAG CT TTTC
                              |||||||||| || ||||
                              GAGGTGTCTC GA AAAG
                                  CG __
GAM170  LOC221751 5' TTGGAAATTGAAGCTGTAGAG 3552    C  AGCAC
                              TTC ACAG   TAATTTCCAA
                              ||| ||||   ||||||||||
                              GAG TGTC   GTTAAAGGTT
                              A   GAA__
GAM170  LOC253978 5' TTGGAATCTGTGCTTTGCAGAA 3743    CA     TAAT
                              TTC CAGAGCAC  TTCCAA
                              ||| ||||||||  ||||||
                              AAG GTTTCGTG  AAGGTT
                              AC      TCT_
GAM170  LOC257319 3' GAAATTAATCCTTTGTGG   3683       CAC
                              CCACAGAG  TAATTTC
                              ||||||||  |||||||
                              GGTGTTTC  ATTAAAG
                              CTA
GAM170  LOC92162 5' GGAGGCGCCTGTGGAA      2816     A  A AATT
                              TTCCACAG GC CT   TCC
                              |||||||| || ||   |||
                              AAGGTGTC CG GG   AGG
                              _  C  ____
GAM170  LOC92391 3' GGAACAGCTCTGTGGAA     2842        ACTAAT
                              TTCCACAGAGC   TTCC
                              |||||||||||   ||||
                              AAGGTGTCTCG   AAGG
                              AC____
GAM171  BACH2   3' CCGTGTTGGCCCCAGCCACG  1963    CA ACAA AA_
                              CG GC  TG  CCAACACGG
                              || ||  ||  |||||||||
                              GC CG  AC  GGTTGTGCC
                              AC ____ CCC
GAM171  NCL     3' CGTGTTGGTTTTGACTG     2552     _ CAAT
                              CAG CA  GAACCAACACG
                              ||| ||  |||||||||||
```

```
                                 GTC GT    TTTGGTTGTGC
                                  A  ____
GAM171   NEO1     3' CGTGTCTTTGTGCTGTG    932           T ACCAA
                      CGCAGCACAA GA    CACG
                      ||||||||| ||    ||||
                      GTGTCGTGTT CT    GTGC
                                  T  _____
GAM171   SLC21A3  3' CTGTTGGTGTGCTGC     1183          AATGA    C
                      GCAGCAC    ACCAACA G
                      |||||||    ||||||| |
                      CGTCGTG    TGGTTGT C
                                 _____       A
GAM171   UGCG     5' CCGTGTTGGCGGCCGCAGCGG 1012     A ACAA  AA
                      CCGC GC   TG CCAACACGG
                      |||| ||   || |||||||||
                      GGCG CG   GC GGTTGTGCC
                           A CCG_  __
GAM171   MGC3101  3' CCGCGTTTTCCTGTGCTGC  2047        AT  CC  A
                      GCAGCACA GAA  AAC CGG
                      |||||||| |||  ||| |||
                      CGTCGTGT CTT  TTG GCC
                                 C_  __   C
GAM171   MGC3413  3' CCATGTTAGTGCTACATTGTGC 2269      A___  C  C
                      GCACAATG   AC AACA GG
                      ||||||||   || |||| ||
                      CGTGTTAC   TG TTGT CC
                                ATCG  A   A
GAM171   LOC151568 5' CCGTGTTGGCCTTGGCTAGG  2444     GC  A  TGAA
                      CC AGC CAA   CCAACACGG
                      || ||| |||   |||||||||
                      GG TCG GTT   GGTTGTGCC
                                A_  _  CC__
GAM171   LOC152765 5' GTGTGTCTTGTGCTGC      3175       T ACCA
                      GCAGCACAA GA   ACAC
                      ||||||||| ||   ||||
                      CGTCGTGTT CT   TGTG
                                 _  G___
GAM171   LOC158314 5' CCACCCTTCACTGTGCTGCGG 3387         A  CCAACAC
                      CCGCAGCACA TGAA    GG
                      |||||||||| ||||     ||
                      GGCGTCGTGT ACTT     CC
                                C  CCCA___
GAM171   LOC57086  3' CTGTTGGTGTGCTGC      1914       AATGA    C
                      GCAGCAC    ACCAACA G
                      |||||||    ||||||| |
                      CGTCGTG    TGGTTGT C
                                 _____       A
GAM172   ABCE1     3' TTGACATTTGATAAATAAACAT 2533   A   A    CATC
              CA                C ATGT TATTTATC  GTCAA
                      | |||| |||||||    |||||
```

```
                        A TACA ATAAATAG   CAGTT
                         C  A       TTTA
GAM172  DMC1      3' TGATTTATGATAACTATACATT 1356        T    CATC
     G                      CAATGTATA TTATC   GTCA
                        ||||||||| |||||   ||||
                        GTTACATAT AATAG    TAGT
                            C    TATT
GAM172  PHEMX    3' GTGGTCAAATATACATCA     2467    A        AT
                        C ATGTATATTT CCAT
                        | |||||||||| ||||
                        A TACATATAAA GGTG
                          C        CT
GAM172  PHEMX    3' GTGGTCAAATATACATCA     2468    A        AT
                        C ATGTATATTT CCAT
                        | |||||||||| ||||
                        A TACATATAAA GGTG
                          C        CT
GAM172  PHEMX    3' GTGGTCAAATATACATCA     2469    A        AT
                        C ATGTATATTT CCAT
                        | |||||||||| ||||
                        A TACATATAAA GGTG
                          C        CT
GAM172  PHEMX    3' GTGGTCAAATATACATCA     1237    A        AT
                        C ATGTATATTT CCAT
                        | |||||||||| ||||
                        A TACATATAAA GGTG
                          C        CT
GAM172  H-L(3)MBT 3' ACGATGGGGATACATT       1632        ATTTA
                        AATGTAT    TCCATCGT
                        |||||||    ||||||||
                        TTACATA    GGGTAGCA
                            G____
GAM172  KIAA0979 3' GGTGGGATCAACATACATTG 1602         A  T   _
                        CAATGTAT TT ATCC ATC
                        |||||||| || |||| |||
                        GTTACATA AA TAGG TGG
                           C  C  G
GAM172  LOC220672 3' TTGACATTTGATAAATAAACAT 2566   A   A      CATC
     CA                     C ATGT TATTTATC   GTCAA
                        | |||| |||||||||   |||||
                        A TACA ATAAATAG   CAGTT
                          C  A       TTTA
GAM172  LOC257336 5' TTGAAAAAAATAAATGTACATT 3694             CCATCG
                        AATGTATATTTAT   TCAA
                        |||||||||||||    ||||
                        TTACATGTAAATA    AGTT
                            AAAAA_
GAM173  MGC16169 3' AGCACCAACAGCACAGTTCTTC 2312         C__ _  TAACAA
     A                      TGAAGAGC GC GTT   TGCT
                        ||||||| || |||    ||||
```

```
                      ACTTCTTG  CG CAA     ACGA
                      ACA  A   CC____
GAM173  LOC151414 3'  AGCATTAAAAACCAGCAGCTCT 3156      C __   AAC
     TCA               TGAAGAGC GC  GTTT  AATGCT
                      ||||||| || |||| ||||||
                      ACTTCTCG CG  CAAA  TTACGA
                      A  AC   AA_
GAM173  LOC153817 5'  AGCATTGTTAAAGTCTCTCTTC 2591      CC  G
     A                TGAAGAG  GC TTTAACAATGCT
                      ||||||| || |||||||||||
                      ACTTCTC  TG AAATTGTTACGA
                      TC  _
GAM173  LOC51145  3'  AGCTGCAAAAACGAGCTCTTCA 1665      CG    AACAAT
                      TGAAGAGC CGTTT    GCT
                      |||||||| |||||    |||
                      ACTTCTCG GCAAA    CGA
                      A_  AACGT_
GAM174  ENAM     5'  CAAAGGCAAGCTAACAAAGTTC 2215      ACTAAT    C
     AA               TTGAATTT    CTTGCC TTG
                      ||||||||    |||||| |||
                      AACTTGAA    GAACGG AAC
                      ACAATC    A
GAM174  DOCK3    3'  CAAGGACAAGGAGAATGAATTC 2750      CTAA   C
     AA               TTGAATTTA   TCTTG CCTTG
                      ||||||||| ||||| |||||
                      AACTTAAGT   GGAAC GGAAC
                      AAGA    A
GAM174  GAPCENA  3'  AAGGGATCAGAAATTCAA      1412      A AATCTTG
                      TTGAATTT CT     CCCTT
                      |||||||| ||     |||||
                      AACTTAAA GA     GGGAA
                      _  CTA____
GAM175  HNRPA2B1 3'  ATTTTGTGAATGGATTGGA   902       G  AGC
                      TCCAATC CAT  TATAAAAT
                      ||||||| ||| ||||||||
                      AGGTTAG GTA  GTGTTTTA
                      _  A__
GAM175  HNRPA2B1 3'  ATTTTGTGAATGGATTGGA   2186      G  AGC
                      TCCAATC CAT  TATAAAAT
                      ||||||| ||| ||||||||
                      AGGTTAG GTA  GTGTTTTA
                      _  A__
GAM175  bA430M15.1 3'  TATTTTATTACAGATTGGA   3073      GCATAGCT
                      TCCAATC     ATAAAATA
                      |||||||     ||||||||
                      AGGTTAG     TATTTTAT
                      ACAT____
GAM175  LOC146481 3'  CTATTTTATAGCCACCCAGGTA 3092    A  GCATA_
     GG               CC ATC    GCTATAAAATAG
                      || ||    ||||||||||||
```

```
                          GG TGG    CGATATTTTATC
                          A  ACCCAC
GAM176  LOC146229 3' ACAGCAATCAAAACATCAA  3087         GC   T
                          TTGATGTTTTG TGCT GT
                          |||||||||| |||| ||
                          AACTACAAAC ACGA CA
                             TA    _
GAM177  FLJ20413 3' ATAGACGAAAATCAACT    1753      AT
                          AGTT ATTTTCGTCTAT
                          |||| |||||||||||
                          TCAA TAAAAGCAGATA
                             C_
GAM178  CRP     3' AGAAAACTAACACCCAGAAAGG 2920      GAA_ ATAC
           AG              CTCT  TGG  TAGTTTCT
                          |||| ||| |||||||||
                          GAGG  ACC  ATCAAAGA
                             AAAG  CACA
GAM178  DBY     3' AAAACAGCAGCCCTATTCAGA 1140        ATA__ A
                          TCTGAATGG  CT GTTTT
                          ||||||||| || |||||
                          AGACTTATC   GA CAAAA
                             CCGAC _
GAM178  ERBB2   3' AAAGCGACCCATTCAGAGA  1115         ATACTA
                          TCTCTGAATGG   GTTTT
                          |||||||||||   |||||
                          AGAGACTTACC   CGAAA
                             CAG___
GAM178  ITGA1   3' AGAACATGTATTCATCCAGA 2660      A   TA
                          TCTG ATGGATAC GTTTT
                          |||| |||||||| |||||
                          AGAC TACTTATG CAAGA
                             C   TA
GAM178  MS4A1   3' AGAAAATAAGTATCCATCAGAG 710       A    A
           A              TCTCTGA TGGATACT GTTTTCT
                          |||||||| |||||||| |||||||
                          AGAGACT ACCTATGA TAAAAGA
                             _    A
GAM178  ARSDR1  3' AAAACAATTCTTCATTCAGA 1656         TACTA
                          TCTGAATGGA   GTTTT
                          ||||||||||   |||||
                          AGACTTACTT   CAAAA
                             CTTAA
GAM178  ATP1B4  3' AAAACTAGTATGTGGAAAG 1400     GAA G
                          CT  TG ATACTAGTTTT
                          ||  || |||||||||||
                          GA  GT TATGATCAAAA
                             AAG  G
GAM178  FLJ00024 3' AGAAAACCGTCCATTTAGA 2665         ACTA
                          TCTGAATGGAT  GTTTTCT
                          ||||||||||   ||||||
```

```
                            AGATTTACCTG   CAAAAGA
                              C___
GAM178 FLJ10493 3' AAAGCATATCCGTTCA      1782         CTA
                   TGAATGGATA GTTTT
                   |||||||||| |||||
                   ACTTGCCTAT CGAAA
                            A__
GAM178 FLJ11175 3' AGACTAACATCCATTCTGA   1816    T     AC
                   TC GAATGGAT TAGTTT
                   || |||||||| ||||||
                   AG CTTACCTA ATCAGA
                     T    CA
GAM178 KIAA0977 3' AGAAAACTAGTGATACCA    1578        A__
                   TGG  TACTAGTTTCT
                   |||  |||||||||||
                   ACC  GTGATCAAAGA
                     ATA
GAM178 TRIP3   3' AGAAAACTTGACATTCAGATGA 3102     _     GATACT
                   TC TCTGAATG   AGTTTCT
                   || ||||||||   |||||||
                   AG AGACTTAC   TCAAAGA
                    T    AGT___
GAM178 LOC149117 3' AAAACTTTATCCATTGAGA  3307     G     CT
                   TCT AATGGATA AGTTT
                   ||| |||||||| ||||||
                   AGA TTACCTAT TCAAAA
                     G    T_
GAM178 LOC196993 5' AGAAAACTTTCCATTC     3471          TACT
                   GAATGGA  AGTTTCT
                   |||||||  |||||||
                   CTTACCT  TCAAAGA
                      T___
GAM178 LOC56965 5' AGAACTCTGTATCCATCAGAGA 1900      A    T TT
                   TCTCTGA TGGATAC AG  TTCT
                   ||||||| ||||||| || ||||
                   AGAGACT ACCTATG TC  AAGA
                    _     _ TC
GAM179 NUMA1   3' AGTCACTTCTCCATCACA     3604        A A
                   TGTGATGGA AA TGACT
                   ||||||||| || |||||
                   ACACTACCT TT ACTGA
                        C C
GAM179 SLC15A1 3' ATTGGTCATCTTCCCTATCACA 1182       A_ A
                   TGTGATGG AA ATGACTAAT
                   |||||||| || |||||||||
                   ACACTATC TT TACTGGTTA
                      CC C
GAM179 CNOT3   5' AAAATTCAGTTCCTCCATTACA 1505         AAAAT  _
                   TGTGATGGA   GACT AATTTT
                   |||||||||   |||| ||||||
```

```
                             ACATTACCT    TTGA TTAAAA
                               CC___     C
GAM179  FLJ10898  5'  AGTCATTTCTCCATCACA   2527          A
                            TGTGATGGA AAATGACT
                            ||||||||| ||||||||
                            ACACTACCT TTTACTGA
                                 C
GAM179  FLJ14686  3'  AAAATTAGTTGTTACCTCCTCA 2286       T  AA_ TG
          CA                TGTGA GGA   AA  ACTAATTTT
                            ||||| |||  ||  |||||||||
                            ACACT CCT   TT  TGATTAAAA
                             _  CCA  GT
GAM179  HDAC9-PENDING 3'  AAAATTGTATATTTTTTCCATC 1526    T       TG__ T
          TCA                TG GATGGAAAAA   AC AATTTT
                            || |||||||||    || ||||||
                            AC CTACCTTTTT   TG TTAAAA
                            T       TATA _
GAM179  ZAK     3'  GGTCACTTTCCCATTACA   2427         A  A
                            TGTGATGG AAA TGACT
                            |||||||| ||| |||||
                            ACATTACC TTT ACTGG
                              C  C
GAM179  LOC119548 5'  TGGGCCATTTTTCCACAACA  2984      GA       A_
                            TGT TGGAAAAATG CTA
                            ||| |||||||||| |||
                            ACA ACCTTTTTAC GGT
                              AC       CG
GAM179  LOC153937 5'  AAAATGCAGTTTTTCCTTCACA 3185      T     GACTA
                            TGTGA GGAAAAAT   ATTTT
                            ||||| ||||||||   |||||
                            ACACT CCTTTTTG   TAAAA
                               T    ACG__
GAM179  LOC221895 3'  GGTACTTTTCTCATCACA   3568         _   ATG
                            TGTGATG GAAAA  ACT
                            ||||||| |||||  |||
                            ACACTAC CTTTT  TGG
                              T   CA_
GAM180  BLNK    5'  GACGTGACCACTGGACAGTTAT 1441         ATTTTTAA
          T                 GATAACTGT    TCACGTC
                            |||||||||     |||||||
                            TTATTGACA    AGTGCAG
                              GGTCACC_
GAM180  FLJ20152 3'  GACAGGAAGAAAAATACAGTTA 1870          AA AC
                            TAACTGTATTTTT TC GTC
                            ||||||||||||| || |||
                            ATTGACATAAAAA AG CAG
                              GA GA
GAM181  BTG2    3'  GAAAAGACAAAGGTTAC     1330      AA   C
                            GTGA CTTTGTC TTTC
                            |||| ||||||| ||||
```

```
                                CATT GAAACAG AAAG
                                G_       A
GAM181   CELSR2   3' GGAAAGGACAAAGCCACA   826        AAA
                                TGTG CTTTGTCCTTTCC
                                |||| ||||||||||||
                                ACAC GAAACAGGAAAGG
                                C__
GAM181   GAB2     3' AAAGGACAAGGACATGAG   1424        GAAA
                                TTCATGT CTTTGTCCTTT
                                ||||||| ||||||||||
                                GAGTACA GGAACAGGAAA

                                ____
GAM181   GAB2     3' AAAGGACAAGGACATGAG   2375        GAAA
                                TTCATGT CTTTGTCCTTT
                                ||||||| ||||||||||
                                GAGTACA GGAACAGGAAA

                                ____
GAM181   GOLGA4   5' AGAGTTTGAAATCTTCACATGA 2553         AC_ TC
          A                     TTCATGTGAA TTTG CTTT
                                |||||||||| |||| ||||
                                AAGTACACTT AAGT GAGA
                                CTA  TT
GAM181   MEF2D    3' GAAAAGACAAAGTCCTCG   3721     A_      C
                                TGA ACTTTGTC TTTC
                                ||| |||||||| ||||
                                GCT TGAAACAG AAAG
                                CC       A
GAM181   NEBL     5' AAAGGACGCCACATGAG   1294        AAACTT
                                TTCATGTG TGTCCTTT
                                |||||||| ||||||||
                                GAGTACAC GCAGGAAA
                                C_____
GAM181   PCSK1    3' GAAAATATGATGTTTCACAT  743        T TG CC
                                ATGTGAAAC T T TTTC
                                ||||||||| | | ||||
                                TACACTTTG A A AAAG
                                 T GT TA
GAM181   PRKAR2B  3' GGAAAAGAGAGCTCTCTACATG 951        AAACT G C
          AA                    TTCATGTG TT TC TTTCC
                                |||||||| || || |||||
                                AAGTACAT GA AG AAAGG
                                CTCTC G A
GAM181   SCGB3A2  3' AAAGGACAAATAAAGCAATGAA 2361        _ GAAAC
                                TTCAT GT TTTGTCCTTT
                                ||||| || ||||||||||
                                AAGTA CG AAACAGGAAA
                                A AAAT_
GAM181   SMP1     3' AGAGGAAACTTTCACATGAA  1490        CTTTG
                                TTCATGTGAAA TCCTTT
                                ||||||||||| ||||||
```

```
                        AAGTACACTTT  AGGAGA
                         CAA__
GAM181  SYNGR1   3' GGAAAAAAGGTTTCACAT  1147          G__
                    ATGTGAAACTTT  TCC
                    ||||||||||| |||
                    TACACTTTGGAA  AGG
                         AAA
GAM181  TGFA     3' GGAAACTGTTTAATATCACATG 1001         _____  TTTG
            AA          TTCATGTGA  AAC  TCC
                        ||||||||  |||  |||
                        AAGTACACT  TTG  AGG
                         ATAAT  TCAA
GAM181  ACAA2    5' GGCAAAGTCTCACCTGAA    3540     T   A
                    TTCA GTGA ACTTTGTC
                    |||| |||| ||||||||
                    AAGT CACT TGAAACGG
                      C   C
GAM181  C1orf34  3' AAAGGACAAAGCCTCAGGGAA  2576    ATG  AA
                    TTC  TGA CTTTGTCCTTT
                    |||  ||| |||||||||||
                    AAG  ACT GAAACAGGAAA
                     GG_  CC
GAM181  CAMKK2   3' GGAAAGGACCTGCCCCACATGA 1310        AAACTTT
            A           TTCATGTG   GTCCTTTCC
                        ||||||||   |||||||||
                        AAGTACAC   CAGGAAAGG
                         CCCGTC_
GAM181  FLJ10849 3' GAAAGGATAACATTTCTCATGA 1803     T   CT
            A           TTCATG GAAA TTGTCCTTTC
                        |||||| |||| ||||||||||
                        AAGTAC CTTT AATAGGAAAG
                         T  AC
GAM181  FLJ13262 3' GGAATAAATTTCACATGAA    2112        C   _
                    TTCATGTGAAA TTTGT CC
                    ||||||||||| ||||| ||
                    AAGTACACTTT AAATA GG
                     _   A
GAM181  FLJ21977 5' GGACAAAGCTCACATGAA     2237        AA
                    TTCATGTGA CTTTGTCC
                    ||||||||| ||||||||
                    AAGTACACT GAAACAGG
                         C_
GAM181  FLJ22301 3' GAAAGCTCACTTCCATGAA    2095    T ACTT TC
                    TTCATG GAA  TG CTTTC
                    |||||| |||  || |||||
                    AAGTAC CTT  AC GAAAG
                     _  C___  TC
GAM181  HERC1    3' GAAAGGACAGTTTACATGAA   1071          TT
                    TTCATGTGAAACT GTCCTTTC
                    ||||||||||||| ||||||||
```

```
                       AAGTACATTTTGA CAGGAAAG
                                __
GAM181  KIAA0280 3' AAAGGAATCACATGAA    3536        AACTTTG
                       TTCATGTGA    TCCTTT
                       |||||||||    ||||||
                       AAGTACACT    AGGAAA
                            A_____
GAM181  KIAA0391 3' GAAAAGATAATTACTTACATGA 1517       AACT   C
            A              TTCATGTGA   TTGTC TTTC
                       ||||||||| ||||| ||||
                       AAGTACATT  AATAG AAAG
                            CATT    A
GAM181  PRO1386  3' GAAAAAACAAAGTTCTGCATGA 2188      GA     CC
            G              TTCATGT AACTTTGT TTTC
                       ||||||| |||||||| ||||
                       GAGTACG TTGAAACA AAAG
                          TC     AA
GAM181  RBMS1    3' GAAAGGTGTTCTTACATGAA 1711      _ TTTGT
                       TTCATGTGA AAC   CCTTTC
                       ||||||||| |||   ||||||
                       AAGTACATT TTG   GGAAAG
                            C  T____
GAM181  RBMS1    3' GAAAGGTGTTCTTACATGAA 1712      _ TTTGT
                       TTCATGTGA AAC   CCTTTC
                       ||||||||| |||   ||||||
                       AAGTACATT TTG   GGAAAG
                            C  T____
GAM181  RBMS1    3' GAAAGGTGTTCTTACATGAA 1713      _ TTTGT
                       TTCATGTGA AAC   CCTTTC
                       ||||||||| |||   ||||||
                       AAGTACATT TTG   GGAAAG
                            C  T____
GAM181  RBMS1    3' GAAAGGTGTTCTTACATGAA 970       _ TTTGT
                       TTCATGTGA AAC   CCTTTC
                       ||||||||| |||   ||||||
                       AAGTACATT TTG   GGAAAG
                            C  T____
GAM181  ROBO2    5' AAAAGACAAAGTTCGAATTGA 2635   TG_ A    C
                       TCA  TGAA CTTTGTC TTT
                       |||  |||| ||||||| |||
                       AGT  GCTT GAAACAG AAA
                          TAA  _    A
GAM181  SGP28    3' AAAGAACAATATAATTTTCACA 1270      CT____ C
            TGAA            TTCATGTGAAA  TTGT CTTT
                       ||||||||||  |||| ||||
                       AAGTACACTTT   AACA GAAA
                          TAATAT  A
GAM181  ST7L     3' AAAGGACAACTGTAGATGAA 1746     G AAACT
                       TTCAT TG  TTGTCCTTT
                       ||||| ||  |||||||||
```

```
                        AAGTA AT    AACAGGAAA
                          G GTC__
GAM181   ST7L      3' AAAGGACAACTGTAGATGAA 2456      G AAACT
                        TTCAT TG   TTGTCCTTT
                        ||||| ||   |||||||||
                        AAGTA AT    AACAGGAAA
                          G GTC__
GAM181   ST7L      3' AAAGGACAACTGTAGATGAA 2475      G AAACT
                        TTCAT TG   TTGTCCTTT
                        ||||| ||   |||||||||
                        AAGTA AT    AACAGGAAA
                          G GTC__
GAM181   LOC152263 3' GAAAGGACAAAATAAACACA 3356        AAAC_
                        TGTG    TTTGTCCTTTC
                        ||||    ||||||||||
                        ACAC    AAACAGGAAAG
                         AAATA
GAM181   LOC157507 5' ACAAAGCTATCACATGAA   3202          AA_
                        TTCATGTGA  CTTTGT
                        |||||||||  ||||||
                        AAGTACACT  GAAACA
                         ATC
GAM181   LOC158158 3' GAAAGGACATCTACACCGAA 3211     AT  AAACTT
                        TTC GTG    TGTCCTTTC
                        ||| |||    |||||||||
                        AAG CAC    ACAGGAAAG
                         C_  ATCT__
GAM181   LOC219730 3' GGAAAGGACAAAATGGAGAGTG 3588       GTGAAAC
         A                   TCAT    TTTGTCCTTTCC
                        ||||    ||||||||||||
                        AGTG    AAACAGGAAAGG
                         AGAGGTA
GAM181   LOC255158 3' GAAAAAACAAAAAGTTATATAT 3693       A   __  CC
         GAA                 TTCATGTG AACTT TGT TTTC
                        |||||||| ||||| ||| ||||
                        AAGTATAT TTGAA ACA AAAG
                          A   AA AA
GAM182   PTPRM     3' ATGCAAAACTCAACGATC   963      G _  C
                        GAT CGT GAGT TTGCAT
                        ||| ||| |||| ||||||
                        CTA GCA CTCA AACGTA
                         _  A   A
GAM182   HCA4      3' AATGCAAGAAGGAACACATAAG 2450       CG  C GAG_
         TA                  TACT ATG GT   TCTTGCATT
                        |||| ||| ||   |||||||||
                        ATGA TAC CA   AGAACGTAA
                          A_  A AGGA
GAM182   HCA4      3' AATGCAAGAAGGAACACATAAG 3086       CG  C GAG_
         TA                  TACT ATG GT   TCTTGCATT
                        |||| ||| ||   |||||||||
```

```
                        ATGA  TAC CA   AGAACGTAA
                        A_   A AGGA
GAM183  FLJ13154 3' ACCAGAATCTCCACTGTAGT  2070          ___        A
                        ACTGCA  GAGATTCT GT
                        ||||||  |||||||| ||
                        TGATGT  CTCTAAGA CA
                         CAC        C
GAM183  HDAC9-PENDING 3' ACTAGAATCTCTTAAGTAT  1527        GC
                        ATACT AGAGATTCTAGT
                        ||||| ||||||||||||
                        TATGA TCTCTAAGATCA
                         AT
GAM183  KIAA0232 3' TTACTAGCATTGCAGTGTC  2958            AGATT
                        GATACTGCAG   CTAGTAA
                        ||||||||||   |||||||
                        CTGTGACGTT   GATCATT
                         AC___
GAM183  KIAA1010 3' ACTAGAATCTCTAGAATTTGA  2933     TACTGC
                        TCGA   AGAGATTCTAGT
                        ||||   ||||||||||||
                        AGTT   TCTCTAAGATCA
                        TAAGA_
GAM183  LOC219894 3' TGCTGTCTCTGCAGTACTGA  3596    A       TCT
                        TCG TACTGCAGAGAT  AGTA
                        ||| |||||||||||| ||||
                        AGT ATGACGTCTCTG  TCGT
                        C        ___
GAM184  PABPC4  3' AATAAAGAAAAAAAATCTCCA 1064      A      AG
                        TGGAGA TTTTTTTC TTGTT
                        |||||| |||||||| |||||
                        ACCTCT AAAAAAG AATAA
                         A      A_
GAM184  SH3GL2  3' GACTGAAAAGAAATTCTCCA 983            _
                        TGGAGAATTTTTTT CAGTT
                        |||||||||||||| |||||
                        ACCTCTTAAAGAAA GTCAG
                          A
GAM184  IMP-2   3' CAAACAAAGAAAAAATTCCACA 1309   GA      CAG
                        TG GAATTTTTTT TTGTTTG
                        || ||||||||| |||||||
                        AC CTTAAAAAAG AACAAAC
                         AC       A__
GAM184  KIAA0872 3' CAAAAGAAAAAAAATTCTCC  1593         _ AG
                        GGAGAATTTTTTT C TTG
                        ||||||||||||| | |||
                        CCTCTTAAAAAAA G AAC
                         A AA
GAM184  MGC19570 5' CAAACAACCGACTCCTTTCCA  2514       ATTTTTT A
                        TGGAGA    TC GTTGTTTG
                        ||||||    || ||||||||
```

```
                          ACCTTT    AG CAACAAAC
                          CCTC___  C
GAM184  PTPN4    3' CAAACAAGGCTCAAAATTCTC 961          TTTCAG
                        GAGAATTTT    TTGTTTG
                        ||||||||    ||||||
                        CTCTTAAAA    AACAAAC
                          CTCGG_
GAM184  TIX1     5' CAAACAACTGAAAAAGCTGCA 2604     G AAT
                        TG AG  TTTTTTCAGTTGTTTG
                        || ||  ||||||||||||||
                        AC TC  GAAAAAGTCAACAAAC
                          G ___
GAM185  PSG5     3' AAAAAACTCCATGTTATTGGAC 955         TC_    AC
          TAA              TTAGTTCA ATATGGA TTTTT
                        ||||||||  |||||||  |||||
                        AATCAGGT  TGTACCT AAAAA
                          TAT    CA
GAM185  FAPP2    3' AAAAAGCTGGTGGTGAAC  2267        ATGGAA
                        GTTCATCAT    CTTTTT
                        |||||||||    ||||||
                        CAAGTGGTG    GAAAAA
                          GTC___
GAM185  LOC145820 3' AAGTGCCACAAAATGAACTAA 3084        CATA  A
                        TTAGTTCAT    TGG ACTT
                        |||||||||    ||| ||||
                        AATCAAGTA    ACC TGAA
                          AAAC  G
GAM185  LOC83690 3' AAAAAGTTGAACAAAGATGAAC 2202        ATATGG_
          TAA              TTAGTTCATC    AACTTTTT
                        ||||||||||    ||||||||
                        AATCAAGTAG    TTGAAAAA
                          AAACAAG
GAM186  IGF1     3' TATACTACAGCAGAATGACT 762        A ACG  C
                        AGTTATTC TG  GTAG ATA
                        |||||||| ||  |||| |||
                        TCAGTAAG AC  CATC TAT
                        _ GA_  A
GAM186  FLJ20035 3' ATGTTCTGTCATGAATACT 1733     T      T
                        AGT ATTCATGACGG AGCAT
                        ||| ||||||||||| |||||
                        TCA TAAGTACTGTC TTGTA
                        _       _
GAM186  FXYD3    3' TATGCTACCCTTAATAAC  1966     TCA C
                        GTTAT TGA GGTAGCATA
                        ||||| ||| |||||||||
                        CAATA ATT CCATCGTAT
                          ___  C
GAM186  FXYD3    3' TATGCTACCCTTAATAAC  1263     TCA C
                        GTTAT TGA GGTAGCATA
                        ||||| ||| |||||||||
```

```
                            CAATA  ATT CCATCGTAT
                            ___     C
GAM186  GMFB    3' TATTGAGCCATGAATAATTTA 1090            A__
                            TAAGTTATTCATG  CGGTA
                            |||||||||||| |||||
                            ATTTAATAAGTAC  GTTAT
                                 CGA
GAM187  ADCY2   3' ATGTTGAATGTATCTAGTG 2710        TT G
                            CACTAG TA ATTCAACAT
                            |||||| || |||||||||
                            GTGATC AT TAAGTTGTA
                                T_  G
GAM187  CCNA1   3' GTTGGATCAACTAATG     1070    C    TA
                            CA TAGTT  GATTCAAC
                            || |||||  ||||||||
                            GT ATCAA  CTAGGTTG
                               A    __
GAM187  COG6    3' ATGTTGACCTGAGCTAGT   2961        AT
                            ACTAGTTTAG TCAACAT
                            |||||||||| |||||||
                            TGATCGAGTC AGTTGTA
                               C_
GAM187  DACH    3' GTATATTGAACCCTAGGCTAGT 2387      A_   C
            G              CACTAGTTTAG TTCAA ATAC
                            |||||||||| ||||| ||||
                            GTGATCGGATC AAGTT TATG
                               CC    A
GAM187  FKBP1A  3' GTGTGTTTACCTAAACTA    775         ATTC
                            TAGTTTAG   AACATAC
                            ||||||||   |||||||
                            ATCAAATC   TTGTGTG
                               CAT_
GAM187  HSPD1   3' ATGTTCTAACTCCTAGACTAGT 2559          ATTC___
            G              CACTAGTTTAG    AACAT
                            |||||||||||    |||||
                            GTGATCAGATC    TTGTA
                               CTCAATC
GAM187  JJAZ1   3' TATGTTGAATTGATCTAG    1622    TTTA
                            CTAG   GATTCAACATA
                            ||||   |||||||||||
                            GATC   TTAAGTTGTAT
                               TAG_
GAM187  MAN1A1  3' GTATGTCAAAGAATAAATTAGT 3543       GA_ CA
                            ACTAGTTTA TT ACATAC
                            ||||||||| || ||||||
                            TGATTAAAT AA TGTATG
                               AAG AC
GAM187  PKIB    3' ATGTTGAAAGACTTAGTG    2254       _  AGA
                            CACTA GTTT TTCAACAT
                            ||||| |||| ||||||||
```

```
                          GTGAT CAGA  AAGTTGTA
                          T    ___
GAM187  RRM2B    3' GTATGTTGAAATAAACTA  2799       GA
                    TAGTTTA TTCAACATAC
                    ||||||| ||||||||||
                    ATCAAAT AAGTTGTATG
                          A_
GAM187  SWAP70   3' GTATGTGCTGTTAAACTAG  2917           ATTCA
                    CTAGTTTAG  ACATAC
                    |||||||||  ||||||
                    GATCAAATT  TGTATG
                          GTCG_
GAM187  ABHD3    3' GTTTTAATTTAAACTAGT  2436              C_
                    ACTAGTTTAGATT AAC
                    ||||||||||||| |||
                    TGATCAAATTTAA TTG
                          TT
GAM187  ATIP1    3' ATGTTCTTTTAAATTAGTG  1924           TTC
                    CACTAGTTTAGA  AACAT
                    ||||||||||||  |||||
                    GTGATTAAATTT  TTGTA
                          TC_
GAM187  DKFZP564F013 3' TATGTTGAATTATGTCAGTG  3640     AG TTA
                    CACT T  GATTCAACATA
                    |||| |  |||||||||||
                    GTGA G  TTAAGTTGTAT
                          CT TA_
GAM187  FN5      3' TATGTTGAATCAAAGTG  1898      AGT A
                    CACT  TT GATTCAACATA
                    ||||  || |||||||||||
                    GTGA  AA CTAAGTTGTAT
                          ___ _
GAM187  KIAA0416 3' TATGCTGAAGACTGGT    1637        TAGA  A
                    ACTAGTT  TTCA CATA
                    |||||||  |||| ||||
                    TGGTCAG  AAGT GTAT
                          ____  C
GAM187  KIAA0455 3' TATGTTGATTCTACCTGTG  2948    T TT  T
                    CAC AG  TAGA TCAACATA
                    ||| ||  |||| |||||||||
                    GTG TC  ATCT AGTTGTAT
                          _ C_  T
GAM187  KIAA0912 3' GTATGTTTTACTTAAACTAG  2689          ATTC
                    CTAGTTTAG  AACATAC
                    |||||||||  |||||||
                    GATCAAATT  TTGTATG
                          CATT
GAM187  KIAA0981 3' ATGTTGAATTTTAAACTAG  2597             _
                    CTAGTTTAGA TTCAACAT
                    |||||||||| |||||||
```

```
                    GATCAAATTT AAGTTGTA
                         T
GAM187  KIAA1911  3'  TATGTTGAAAAACTGCTGTG  2976      T  TTAGA
                      CAC AGT    TTCAACATA
                      ||| |||    |||||||||
                      GTG TCG    AAGTTGTAT
                       _   TCAAA
GAM187  KRTHB2    3'  GTATGTTGAACCCAAACTGTG  2310      T   AGA
                      CAC AGTTT  TTCAACATAC
                      ||| |||||  ||||||||||
                      GTG TCAAA  AAGTTGTATG
                       _   CCC
GAM187  RPS6KC1   3'  GTATGTTGAATGTGGTCCCAG  1429     AGT_  G
                      CT  TTA ATTCAACATAC
                      ||  ||| |||||||||||
                      GA  GGT TAAGTTGTATG
                      CCCT  G
GAM187  TOMM70A   3'  ATGTTGATTTTTAAATTA    1558          T_
                      TAGTTTAGA TCAACAT
                      ||||||||| |||||||
                      ATTAAATTT AGTTGTA
                          TT
GAM188  CDC23     3'  TGCACAGTAGATGCTATGGA  1141             AAC
                      TCTATAGCATCTACT TGTA
                      ||||||||||||||| ||||
                      AGGTATCGTAGATGA ACGT
                          C__
GAM188  EGLN3     3'  TGGAGGTGGTAGATGCCACAGA  2330     ATA     A G
                      TCT GCATCTACTA CT TA
                      ||| |||||||||| || ||
                      AGA CGTAGATGGT GA GT
                       CAC        G G
GAM188  EGLN3     3'  TGGAGGTGGTAGATGCCACAGA  1976     ATA     A G
                      TCT GCATCTACTA CT TA
                      ||| |||||||||| || ||
                      AGA CGTAGATGGT GA GT
                       CAC        G G
GAM188  JAM3      3'  GTACACAGATGCTACAGA   2280    A    ACTAAC
                      TCT TAGCATCT    TGTAC
                      ||| ||||||||    |||||
                      AGA ATCGTAGA    ACATG
                       C     C_____
GAM188  RNF7      3'  ACAGCTTAGAAGTGCTATA  1485       T A  _
                      TATAGCA CT CTAA CTGT
                      ||||||| || |||| ||||
                      ATATCGT GA GATT GACA
                       _  A   C
GAM188  WBSCR5    3'  GTACAGTTAACTTATAGA   1973        CATCTAC
                      TCTATAG   TAACTGTAC
                      |||||||   |||||||||
```

```
                        AGATATT    ATTGACATG
                        CA_____
GAM188  WBSCR5   3' GTACAGTTAACTTATAGA  2250       CATCTAC
                        TCTATAG    TAACTGTAC
                        |||||||    |||||||||
                        AGATATT    ATTGACATG
                        CA_____
GAM188  WBSCR5   3' GTACAGTTAACTTATAGA  1479       CATCTAC
                        TCTATAG    TAACTGTAC
                        |||||||    |||||||||
                        AGATATT    ATTGACATG
                        CA_____
GAM188  C8orf13  3' TGCACAGCTGTTTAGGCTATAG 3206        ATCT TAA   A
              A            TCTATAGC  AC  CTGT CA
                        ||||||||  ||  |||| ||
                        AGATATCG  TG  GACA GT
                         GATT TC_   C
GAM188  CDT6     3' TATAGTTAATAATAAATGCTGT 1945       C C___
              A            TATAGCAT TA   TAACTGTA
                        ||||||| ||   ||||||||
                        ATGTCGTA AT   ATTGATAT
                         A AATA
GAM188  DKFZp566D234 3' TGCAGCATGCTATAGA    2613         CTACTAA
                        TCTATAGCAT    CTGTA
                        ||||||||||    |||||
                        AGATATCGTA    GACGT
                           C_____
GAM188  FLJ10525 3' GTACAGTTTTAGTATAGA  1786      GCAT  CT
                        TCTATA  CTA AACTGTAC
                        ||||||  ||| ||||||||
                        AGATAT  GAT TTGACATG
                        ____  T_
GAM188  FLJ12078 5' TGCTAGAGTAATGCTATA    2121       C   AACT
                        TATAGCAT TACT   GTA
                        |||||||| ||||   |||
                        ATATCGTA ATGA   CGT
                        _   GAT_
GAM188  KIAA0007 3' TGTACAGTTATATTTGTCTATA 3154       _ TC C
                        TATAG CA  TA TAACTGTACA
                        |||||| ||  || ||||||||||
                        ATATC GT  AT ATTGACATGT
                         T TT _
GAM188  KIAA1728 3' TGTACAATTAGTACTTTATAG 2819       CATC    C
                        CTATAG   TACTAA TGTACA
                        ||||||   |||||| |||||
                        GATATT   ATGATT ACATGT
                           TC__    A
GAM188  MGC4643  3' TGTACAGTCTAAAGCTACAGA 2272     A   ATCTACTA
                        TCT TAGC    ACTGTACA
                        ||| ||||    |||||||||
```

```
                              AGA ATCG     TGACATGT
                               C  AAATC___
GAM188  MPPE1     3' TGTACAGTATGTAAATGCTAT 2029      C  TA
                              ATAGCAT TAC  ACTGTACA
                              |||||||| ||| ||||||||
                              TATCGTA ATG  TGACATGT
                                 A  TA
GAM188  RNPS1     3' TGTACAGTCAGTACTATA   2376     CATC   A
                              TATAG   TACT ACTGTACA
                              |||||   |||| ||||||||
                              ATATC   ATGA TGACATGT
                               ____    C
GAM188  RNPS1     3' TGTACAGTCAGTACTATA   1326     CATC   A
                              TATAG   TACT ACTGTACA
                              |||||   |||| ||||||||
                              ATATC   ATGA TGACATGT
                               ____    C
GAM188  TUSP      3' AGTAGAAGATGCTACAGA   1907     A    A  A
                              TCT TAGCATCT CTA CT
                              ||| |||||||| ||| ||
                              AGA ATCGTAGA GAT GA
                               C       A  _
GAM188  LOC153027 3' TGTACAGTCAGTTCTATA   2792     CATCT  A
                              TATAG    ACT ACTGTACA
                              |||||    ||| ||||||||
                              ATATC    TGA TGACATGT
                              T____    C
GAM188  LOC153114 5' GTGAGCAGACTGCTATAGA  3367        _  A  A
                              TCTATAGCA TCT CT AC
                              ||||||||| ||| || ||
                              AGATATCGT AGA GA TG
                                C   C  G
GAM189  SORT1     3' CATCAAAGCCAAAAGGACCTAC 974     A C    AAA
                 A            TGTA G TCTTTTTG  TTGATG
                              |||| | ||||||||  ||||||
                              ACAT C AGGAAAAC  AACTAC
                              _  C      CGA
GAM189  ATP9A     3' CATCAATCTGGAAAGAACTTAC 2618    C    GAA
                 A            TGTAAG TCTTTTT  ATTGATG
                              |||||| |||||||  |||||||
                              ACATTC AGAAAGG  TAACTAC
                                A    TC_
GAM189  DKFZP434K1772 3' TTTCAAAAAGAGGTTACA 2797     G
                              TGTAA CTCTTTTTGAAA
                              ||||| |||||||||||
                              ACATT GAGAAAACTTT
                                 G
GAM189  UNC5D     3' CAATTTCAAAGAGAACCCACA 2392     AAGC
                              TGT  TCTTTTTGAAATTG
                              |||  |||||||||||||
```

```
                        ACA   AGAGAAACTTTAAC
                        CCCA
GAM190  SCD      3' AGCCAGACAAAATTTGAGAATA 1176      CA TG CCA
                        TAT  T  A  TTTGTCTGGCT
                        ||| | |  ||||||||||
                        ATA  A  T  AAACAGACCGA
                        AG GT TA_
GAM190  SOS2     3' AGCCATATGTAGTCATTGA  2824      T  CATT  C
                        TCA TGAC   TGT TGGCT
                        ||| ||||   ||| |||||
                        AGT ACTG   GTA ACCGA
                         T  AT__  T
GAM190  BANP     3' CCAGACAAGTGCCCAACGA  2744      A  AC
                        TC TTG  CATTTGTCTGG
                        || ||| ||||||||||
                        AG AAC  GTGAACAGACC
                         C  CC
GAM190  KIAA0446 5' AGCCAGACAAAAAGAATGATTC 2831     T    GACCA
                        A ATCATT   TTTGTCTGGCT
                        | ||||||   ||||||||||
                        C TAGTAA   AAACAGACCGA
                         T    GAA__
GAM190  LOC115110 3' GGCTGAAATGGTCAAT      2924        GTC
                        ATTGACCATTT TGGCT
                        ||||||||||| |||||
                        TAACTGGTAAA GTCGG
                            ___
GAM190  LOC148443 3' AGCCAACACATATGGTCAATGA 3118        T C_
                        TCATTGACCAT TGT TGGCT
                        ||||||||||| ||| |||||
                        AGTAACTGGTA ACA ACCGA
                             T  CA
GAM190  LOC151826 3' TTATTCAAAGGCCAATGATA  3161        A A  TC
                        TATCATTG CC TTTG  TGG
                        |||||||| || |||| |||
                        ATAGTAAC GG AAAC  ATT
                          C  _  TT
GAM190  LOC200609 5' CCACCACCAATGGTCAAGATAT 3479     A     T C_
                        ATATC TTGACCATT GT  TGG
                        ||||| ||||||||| || |||
                        TATAG AACTGGTAA CA  ACC
                          _     C  CC
GAM191  BHLHB3   3' TCAAGTGCATCTATTCCCA  2163          AAATAC  GT
                        TGGGAATA   TACT TGA
                        ||||||||   |||| |||
                        ACCCTTAT   GTGA ACT
                          CTAC__  __
GAM191  ITK      3' CATGAGGTAATATTATTATTCC 1223      _  C  GT_
          CA              TGGGAATAA AATA TACT  TG
                        ||||||||| |||| ||||  ||
```

```
                          ACCCTTATT TTAT ATGG  AC
                            A    A   AGT
GAM191  MPV17     3' CTTGATAATAGTCTTATTCCCA 2888        AAT   C  TG
                          TGGGAATAA  ACTA TGT AG
                          ||||||||| |||| ||| ||
                          ACCCTTATT  TGAT ATA  TC
                            C__    A  GT
GAM191  MSR1      3' TCAGCATTTTTATTCCCA   930         TACTAC
                          TGGGAATAAAA   TGTTGA
                          |||||||||||   ||||||
                          ACCCTTATTTT   ACGACT
                                 T_____
GAM191  RNMT      3' TCAGCACCATTATTCCCA   1061        AATACTAC
                          TGGGAATAA   TGTTGA
                          |||||||||   ||||||
                          ACCCTTATT   ACGACT
                               ACC_____
GAM191  SCP2      3' CAGAAACAGTATTTTCTTCCCA 976      T     ACTG
                          TGGGAA AAAATACT  TTG
                          |||||| ||||||||  |||
                          ACCCTT TTTTATGA  GAC
                               C    CAAA
GAM191  DKFZP564K0822 3' CTCAACAATTTTGTATTCCCA 3630       AAATACTAC
                          TGGGAATA   TGTTGAG
                          ||||||||   |||||||
                          ACCCTTAT   ACAACTC
                               GTTTTA___
GAM191  KIAA0564  3' CAAAATGTACCTTATTCCCA 2742       AA  TACTG
                          TGGGAATAA TAC   TTG
                          ||||||||| |||   |||
                          ACCCTTATT ATG   AAC
                               CC  TAA__
GAM191  KIAA0769  3' CGGCATTATTTTATTCCCA  1560           CTAC
                          TGGGAATAAAATA  TGTTG
                          |||||||||||||  |||||
                          ACCCTTATTTTAT  ACGGC
                               T___
GAM191  KIAA1163  3' CTTGGTTAGTATTTGATTCCCA 3122       A    CTG TG
                          TGGGAAT AAATACTA  T AG
                          ||||||| ||||||||  | ||
                          ACCCTTA TTTATGAT  G TC
                            G     T__ GT
GAM191  KIAA1332  3' CAACAAAGGATTTTATTCC  2909        A AC
                          GGAATAAAAT CT TGTTG
                          |||||||||| || |||||
                          CCTTATTTTA GG ACAAC
                               _ AA
GAM191  SFRS11    3' AGTAATAATTTATTCCCA   1155        A C
                          TGGGAATAAA TA TACT
                          |||||||||| || ||||
```

```
                         ACCCTTATTT AT ATGA
                            A  A
GAM191  ZNF387    3' CTCAACAGTAATTCCACTCCCA 1521      ATAAAATAC
                         TGGGA      TACTGTTGAG
                         |||||      ||||||||||
                         ACCCT      ATGACAACTC
                            CACCTTA__
GAM191  LOC138639 3' CTCAACACACCAAGCCTTATTC 3020         AATACTAC_
            CCA           TGGGAATAA      TGTTGAG
                          ||||||||       |||||||
                          ACCCTTATT      ACAACTC
                             CCGAACCAC
GAM191  LOC147299 3' CAACATTTTATTTCCA     3107        TACTAC
                          TGGGAATAAAA    TGTTG
                          |||||||||||    |||||
                          ACCTTTATTTT    ACAAC

                               _____
GAM191  LOC90019  5' CTCAACAGCTGCTTATTCCCG 2445        AATACTA
                          TGGGAATAA     CTGTTGAG
                          |||||||||     ||||||||
                          GCCCTTATT     GACAACTC
                             CGTC___
GAM192  B3GALT5   5' AGATCAGAGACTGTAAAAAGT 2320     C_      C
                         GCTT TACAGTCTTT GTTT
                         |||| |||||||||| ||||
                         TGAA ATGTCAGAGA TAGA
                             AA      C
GAM192  BTEB1     3' GAAACGAAAGAAAGCAAAGC  808        CTACAG
                         GCTT    TCTTTCGTTTC
                         ||||    |||||||||||
                         CGAA    AGAAAGCAAAG
                             ACGAA_
GAM192  RP2       3' GCTAAAACTGTAGAAGC     1340       C  C
                         GCTTCTACAGT TTT GT
                         ||||||||||| ||| ||
                         CGAAGATGTCA AAA CG
                             _    T
GAM192  C12orf22  3' AAACAAAACTGTAGAAGC    2169       C  C
                         GCTTCTACAGT TTT GTTT
                         ||||||||||| ||| ||||
                         CGAAGATGTCA AAA CAAA

                             _  _
GAM192  C20orf26  3' GGAAACGCGCTCTGTAGAA   2879        TCTTT
                          TTCTACAG   CGTTTCC
                          ||||||||   |||||||
                          AAGATGTC   GCAAAGG
                             TCGC_
GAM192  FLJ14627  5' GAACTTGAAGACTGCAGAGC  2283     T  A    C_
                         GCT CT CAGTCTTT GTTT
                         ||| || |||||||| ||||
```

```
                          CGA GA GTCAGAAG  CAAG
                          _  C         TT
GAM192  GPR72     3' GGAAACACACTCCTGCAGAAGC 2867        A  TCTTTC
         TG              TAGCTTCT CAG     GTTTCC
                        ||||||| |||    ||||||
                        GTCGAAGA GTC    CAAAGG
                          C  CTCACA
GAM192  GPT2      3' GAAAAGGTTAAATCGTAGAAGC 2418        A  CTT_ G
         TA              TAGCTTCTAC GT   TC TTTC
                        ||||||||| ||   || ||||
                        ATCGAAGATG TA   GG AAAG
                          C  AATT  A
GAM192  KIAA0470 5' GCCAAAGACTTAGAAGCTA 1556        C    C
                        TAGCTTCTA AGTCTTT GT
                        ||||||||| |||||| ||
                        ATCGAAGAT TCAGAAA CG
                          _        C
GAM192  KIAA1328 5' GAAATCATACCTGCAGAAGCTA 2602        A  TCTTTC
                        TAGCTTCT CAG     GTTTC
                        ||||||| |||    |||||
                        ATCGAAGA GTC     TAAAG
                          C  CATAC_
GAM192  KIAA1981 3' AGATGAAACCATGGAAGC 3430        CA CT
                        GCTTCTA GT TTCGTTT
                        ||||||| || |||||||
                        CGAAGGT CA AAGTAGA
                          AC __
GAM192  MGC17330 3' GGAAACGAGTTTGTACAGAAGT 2342        __  TCT
                        GCTTCT ACAG  TTCGTTTCC
                        |||||| ||||  |||||||||
                        TGAAGA TGTT  GAGCAAAGG
                          CA  T__
GAM192  MRPL35   3' GAAACGAAAAAGTTAAGC 1701     CT AGTC
                        GCTT AC  TTTCGTTTC
                        |||| ||  |||||||||
                        CGAA TG   AAAGCAAAG
                          T_ AA__
GAM192  LOC205011 5' GAAAACAAGAGTAGAGGC 3492        AG  TCG
                        GCTTCTAC TCTT  TTTC
                        |||||||| ||||  ||||
                        CGGAGATG AGAA  AAAG
                          __  CA_
GAM193  KIAA1228 3' CGGAACACACCCTCTCA 2712     AAA
                        TGAGA  GTGTGTTCTG
                        |||||  ||||||||||
                        ACTCT  CACACAAGGC
                          CC_
GAM193  KIAA1655 5' GCGACTCGGGGCACTGCTCCTC 2754        AAA _     A
         A              TGAG  AGT GTGTTCTGA TCGC
                        ||||  ||| |||||||| ||||
```

```
                        ACTC  TCG CACGGGGCT AGCG
                        C__    T      C
GAM193  NDST3     3' TAGAACACACCTTTTCCA  1157    A     _
                        TG GAAAAG TGTGTTCTG
                        || |||||| |||||||||
                        AC CTTTTC ACACAAGAT
                        _        C
GAM193  PP1057    3' GCAATTACACACTTGTCTCA 2189      A     TCT   C
                        TGAGA AAGTGTGT  GAAT GC
                        ||||| ||||||||  |||| ||
                        ACTCT TTCACACA  TTTA CG
                            G    ___    A
GAM193  RNP24     3' CGACTCAGCATACATTTCCCA 1333    A    G   T   A
                        TG GAAAA TGTGT CTGA TCG
                        || ||||| ||||| |||| |||
                        AC CTTTT ACATA GACT AGC
                        C    _    C  C
GAM193  LOC150142 5' CAGAACACCACCTCTCA   3142       AAA   _
                        TGAGA  GTG TGTTCTG
                        |||||  ||| |||||||
                        ACTCT  CAC ACAAGAC
                        C__   C
GAM193  LOC199899 5' ATTCAAAACACACATTC   3473      AA    C
                        GAA  GTGTGTT TGAAT
                        |||  ||||||| |||||
                        CTT  CACACAA ACTTA
                        A_     A
GAM193  LOC222068 3' ATTTTAATACACTTCCCTCA 3573      AA     CT
                        TGAG AAGTGTGTT GAAT
                        |||| ||||||||| ||||
                        ACTC TTCACATAA TTTA
                        CC      T_
GAM194  HUS1      3' TTCCTATTATAATTACATCT 3509     A    TC
                        GGAT TAGTT ATAATAGGAA
                        |||| ||||| ||||||||||
                        TCTA ATTAA TATTATCCTT
                        C    __
GAM194  TRPM8     3' TCCTATTGAAGGAACCACCCCC 2052    ATATA   A_
                        GG   GTTTC TAATAGGA
                        ||   ||||| ||||||||
                        CC   CAAGG GTTATCCT
                        CCCAC    AA
GAM194  LOC148936 3' CCTACCTGATATTACATCCTA 3304       A   T  TAA
                        TAGGAT TAGT TCA  TAGG
                        |||||| |||| |||  ||||
                        ATCCTA ATTA AGT  ATCC
                        C    T  CC_
GAM194  LOC148938 3' CCTACCTGATATTACATCCTA 3303       A   T  TAA
                        TAGGAT TAGT TCA  TAGG
                        |||||| |||| |||  ||||
```

```
                          ATCCTA ATTA AGT  ATCC
                              C   T   CC_
GAM194  LOC200803 3' TTCCTATTATATGGTATCC  3452        AGTTTC
                          GGATAT    ATAATAGGAA
                          ||||||    ||||||||||
                          CCTATG    TATTATCCTT
                             GTA___
GAM194  LOC255332 5' TTCCTATTACTCTGCATATCTT 3696        A TTCA
             A               TAGGATAT GT  TAATAGGAA
                             |||||||| ||  |||||||||
                             ATTCTATA CG  ATTATCCTT
                               _ TCTC
GAM194  LOC90459  3' CTAGATGAAACCATATCTTA  2641        A    AA
                          TAGGATAT GTTTCAT  TAG
                          |||||||| |||||||  |||
                          ATTCTATA CAAAGTA  ATC
                             C    G_
GAM195  DKFZp434E0519 5' TGGAAATCCGTGTGTAA    2241          ACG
                          TTACACACGGA  TTTA
                          |||||||||||  ||||
                          AATGTGTGCCT  AGGT
                              AA_
GAM195  HSU84971  3' GTTATAAACATTCTTATGTGTA 1439     C_   C
             AT              ATTACACA  GGAA GTTTATAAC
                             |||||||| |||| |||||||||
                             TAATGTGT  TCTT CAAATATTG
                               AT   A
GAM195  LOC157663 3' AGCTTCCCATTGTGTAATA  3203     C__   C
                          TATTACACA   GGAA GTT
                          |||||||||   |||| |||
                          ATAATGTGT   CCTT CGA
                             TAC   _
GAM196  EXT2     3' GAGAAGAGAAGCGTGTTA   737        G
                          TAACACGCTTCT TTCTC
                          |||||||||||| |||||
                          ATTGTGCGAAGA AAGAG
                              G
GAM196  MBNL    3' ATAGATGAGAGCGTGCATGC  1936    TTC__
                          GC   TGTTCTCATCTAT
                          ||   |||||||||||||
                          CG   GCGAGAGTAGATA
                             TACGT
GAM196  PLN     3' AGATGAGAACTGGTGGTTA  946     A  TCT
                          TAAC CGCT  GTTCTCATCT
                          |||| ||||  ||||||||||
                          ATTG GTGG  CAAGAGTAGA
                             _  T__
GAM196  SLC12A2 3' AGCAATAAAAGCGTGTTA   796        C  _
                          TAACACGCTT TGTT CT
                          |||||||||| |||| ||
```

```
                      ATTGTGCGAA ATAA GA
                       A    C
GAM196  SLC1A3   3' AGATGAGAAGACTAGCAGC 1092      T ___
                      GCT CTG  TTCTCATCT
                      ||| |||  |||||||||
                      CGA GAT  AAGAGTAGA
                       C  CAG
GAM196  BTBD3    3' ATAGATGATGAAAAGCTGTTA 1600    C  CTG _
                      TAACA GCTT  TTC TCATCTAT
                      ||||| ||||  ||| ||||||||
                      ATTGT CGAA  AAG AGTAGATA
                       _   ___   T
GAM196  KIAA1237 3' AGATGAGGATGAGCGT      3166      CT
                      ACGCTT GTTCTCATCT
                      |||||| ||||||||||
                      TGCGAG TAGGAGTAGA

                        __
GAM196  NAALAD2  3' ATAGATGAGAATTTTCCGT 1215      CTTCT
                      ACG   GTTCTCATCTAT
                      |||   |||||||||||
                      TGC   TAAGAGTAGATA
                      CTTT_
GAM196  PEG10    3' ATAGATGAATTAGTAAGC  1605    _  TTC
                      GCTT CTG  TCATCTAT
                      |||| |||  ||||||||
                      CGAA GAT  AGTAGATA
                       T  TA_
GAM197  RAI2     5' AGAATTAGGCTTAAAAAATGCC 1959      CG  TATGAT
           T            AGGCATTT TAA    ATTCT
                        |||||||| |||    |||||
                        TCCGTAAA ATT    TAAGA
                         AA  CGGAT_
GAM197  UMPK     3' CATGGAGATGAAATGCCT   1436         AA_
                      AGGCATTTCGT TATG
                      ||||||||||| ||||
                      TCCGTAAAGTA GTAC
                        GAG
GAM197  ZNF134   3' GAAAATCATGAAATGCCT   1021      GTAAT   A
                      AGGCATTTC   ATGAT TTC
                      |||||||||   ||||| |||
                      TCCGTAAAG   TACTA AAG
                        _____    A
GAM197  ARL8     3' AGAATATCACATTATTCAATGC 3594    TC   A
                      GCATT GTAAT TGATATTCT
                      ||||| ||||| |||||||||
                      CGTAA TATTA ACTATAAGA
                        CT   C
GAM197  KIAA0546 3' AATGTTAATTATGAAACACCT 2911    CA     A
                      AGG TTTCGTAAT TGATATT
                      ||| ||||||||| ||||||
```

```
                          TCC AAAGTATTA ATTGTAA
                          AC         _
GAM197  KIAA0644  3' AGAACATCACTGAAAATGCCT 1557         _ TAATA   A
                          AGGCATTT CG   TGAT TTCT
                          ||||||| ||   |||| ||||
                          TCCGTAAA GT   ACTA AAGA
                          A C____   C
GAM197  KIAA1508  3' GGATATCACATAATGCC  2614       TCGTA A
                          GGCATT   AT TGATATTC
                          ||||||   || ||||||||
                          CCGTAA   TA ACTATAGG
                          _____  C
GAM197  MTHFS    3' ATTGTAATTATGAAATACCT 1302      C      _ TG
                          AGG ATTTCGTAAT A AT
                          ||| ||||||||| | ||
                          TCC TAAAGTATTA T TA
                          A       A GT
GAM197  SUCLA2   3' GTCATATTAAGAAACACCT 1066    CA  G
                          AGG TTTC TAATATGAT
                          ||| |||| |||||||||
                          TCC AAAG ATTATACTG
                          AC   A
GAM197  LOC149910 3' AGAACTTTATTTACCATGAAAT 3140         AAT__  TA
          GCCT                AGGCATTTCGT   ATGA TTCT
                          |||||||||||   |||| ||||
                          TCCGTAAAGTA   TATT AAGA
                          CCATT  TC
GAM197  LOC222171 3' GAATATTTACACAATGCCT 3575       TC ATAT
                          AGGCATT GTA   GATATTC
                          ||||||| |||   |||||||
                          TCCGTAA CAT   TTATAAG
                          CA  ____
GAM198  ZNF24    3' GACAAATACATTATTTCTG 1342        _ AA
                          TAGAAATAATG AT GTC
                          ||||||||||| || |||
                          GTCTTTATTAC TA CAG
                          A AA
GAM198  ALS2CR12 3' GATGGTTGGCACACCATTTCTG 2471      AA ATAAGT
          TA              TATAGAAAT TG   CCATC
                          |||||||||| ||   |||||
                          ATGTCTTTA AC    GGTAG
                          CC ACGGTT
GAM198  FLJ10508 3' GATGGCTCTTATCATCATCTTT 1783      A A     T_
          ATA              TATAGA AT ATGATAAG CCATC
                          |||||| || |||||||| ||||
                          ATATTT TA TACTATTC GGTAG
                          C C   TC
GAM198  FLJ13197 3' GATTCATCATTATTCCTA 2072      A     A
                          TAG AATAATGAT AGTC
                          ||| ||||||||| ||||
```

```
                              ATC TTATTACTA TTAG
                               C        C
GAM198  FLJ21934  3' GATGATGTCATTACTTCTATA 2085        A     A_
                     TATAGAA TAATGATA GTC
                     ||||||| |||||||| |||
                     ATATCTT ATTACTGT TAG
                               C        AG
GAM198  FLJ23132  3' ATGGACTTAATCTCTG      3691     AATAAT _
                     TAGA    GAT AAGTCCAT
                     ||||    ||| ||||||||
                     GTCT    CTA TTCAGGTA
                     _____        A
GAM198  KIAA0470  3' ATGGACTTCTTCATCTGTA   1555      AATAA  T_
                     TATAGA   TGA AAGTCCAT
                     ||||||   ||| ||||||||
                     ATGTCT   ACT TTCAGGTA
                     _____      TC
GAM198  LEPROTL1  3' GCTGCGTATTATTTCTATA   1620            ATA
                     TATAGAAATAATG  AGT
                     |||||||||||||  |||
                     ATATCTTTATTAT  TCG
                               GCG
GAM198  LYSAL1    5' GACCCCAGCATTATTTCTATA 1164            ATAA_
                     TATAGAAATAATG   GTC
                     |||||||||||||   |||
                     ATATCTTTATTAC   CAG
                               GACCC
GAM198  RAB40A    5' GATGGATGCATGCATTATTTC 3229          ATAA_
                     GAAATAATG   GTCCATC
                     |||||||||   |||||||
                     CTTTATTAC   TAGGTAG
                               GTACG
GAM198  STK38L    3' GATAGGGTTTCATTTATTTCTA 2845       _ TA GT _
            TA        TATAGAAATAA TGA A CC ATC
                     ||||||||||| ||| | || |||
                     ATATCTTTATT ACT T GG TAG
                       T __TG A
GAM198  ZNF363    3' GATAGACTTATCATAGCTCTAT 2974     AA A      C
            A            TATAGA TA TGATAAGTC ATC
                     |||||| || ||||||||| |||
                     ATATCT AT ACTATTCAG TAG
                       CG _      A
GAM198  LOC146481 3' GACAGTCATGCATTTCTATA   3093        A_  AA
                     TATAGAAAT ATGAT GTC
                     ||||||||| ||||| |||
                     ATATCTTTA TACTG CAG
                       CG  A_
GAM198  LOC152008 3' ATGGAGGCATTATTTCTA    3165          ATAAG
                     TAGAAATAATG   TCCAT
                     |||||||||||   |||||
```

```
                    ATCTTTATTAC   AGGTA
                       GG___
GAM198  LOC153020 3' GATGGACCCTTCAAGCAATTTC 3178       AA__  TAA
         TATA              TATAGAAAT  TGA GTCCATC
                    |||||||||  |||  |||||||
                    ATATCTTTA  ACT  CAGGTAG
                        ACGA   TCC
GAM198  LOC199786 3' GCTTAAGCCATTATTTCTG 3433       A__
                    TAGAAATAATG  TAAGT
                    ||||||||||  |||||
                    GTCTTTATTAC  ATTCG
                       CGA
GAM198  LOC220766 3' ATGGACTTCTTCATCTGTA 3498     AATAA  T_
                    TATAGA   TGA AAGTCCAT
                    ||||||  |||  ||||||||
                    ATGTCT   ACT  TTCAGGTA
                    _____   TC
GAM199  ADAM12   3' CTAGAGCACTGCCACCAGTA 1029   A  A  AAT  _
                    TACT GGT GCA  TG TCTAG
                    |||| ||| |||  || |||||
                    ATGA CCA CGT  AC AGATC
                     _   C   C__  G
GAM199  HOXC13   3' CTAGATGTAGATGCTGCCTA 2538       AAT_
                    TAGGTAGCA  TGTCTAG
                    |||||||||  |||||||
                    ATCCGTCGT  GTAGATC
                        AGAT
GAM199  NRIP1    3' CTAGACAATTTCTTCTA  2549     T  C
                    TAGG AG AAATTGTCTAG
                    |||| || ||||||||||
                    ATCT TC TTTAACAGATC
                       _  _
GAM199  RRM2B    3' CTAAACAATTTGCATTTA  2798     A      C
                    TAGGT GCAAATTGT TAG
                    ||||| ||||||||| |||
                    ATTTA CGTTTAACA ATC
                       _       A
GAM199  BIRC4    3' TTAGCATTTGCTACCAAGTA 806     A      T T
                    TACT GGTAGCAAAT G CTAG
                    |||| |||||||||| | ||||
                    ATGA CCATCGTTTA C GATT
                      A       __
GAM199  FLJ11301 3' GCGGTATTTACTACCTAG  1822     C   __
                    CTAGGTAG AAAT TGT
                    |||||||| |||| |||
                    GATCCATC TTTA GCG
                        A  TG
GAM199  LAP1B    5' AGGCAGGTTTGCTACACAG 2696   AG      _
                    CT GTAGCAAAT TGTCT
                    || ||||||||| |||||
```

```
                          GA  CATCGTTTG ACGGA
                          CA        G
GAM199  MGC11324 3' TAGATCTGTACCTAGTA    2273        G AATT
                          TACTAGGTA CA   GTCTA
                          |||||||| || |||||
                          ATGATCCAT GT   TAGAT
                            _   C___
GAM199  PRO2958  3' ACACCTTTGCTACCAGTA    1841      A      T_
                          TACT GGTAGCAAA  TGT
                          |||| ||||||||| |||
                          ATGA CCATCGTTT ACA
                            _        CC
GAM199  SH3BGRL2 3' CTAGACAAAGCTACCCAG    2208    A   AAA
                          CT GGTAGC  TTGTCTAG
                          || ||||||  ||||||||
                          GA CCATCG  AACAGATC
                           C    A__
GAM199  LOC144997 3' CTAGACAGATATCCACTTAGTA 3271         AGCAAA
                          TACTAGGT    TTGTCTAG
                          ||||||||    ||||||||
                          ATGATTCA    GACAGATC
                              CCTATA
GAM199  LOC148809 3' CTAGACAACATGACCCTACC   3125      ___ AA
                          GGTAG  CA TTGTCTAG
                          |||||  || ||||||||
                          CCATC  GT AACAGATC
                            CCA AC
GAM199  LOC219540 3' CTAGACAATTTTTTTTAG   3612      TAGC
                          CTAGG   AAATTGTCTAG
                          |||||   |||||||||||
                          GATTT   TTTAACAGATC
                             TT__
GAM200  PTGER3  3' CTATAGAGTATTCCATAATTTG 790      T  AC  _
        AA               TTCAA TTAT  GGAT TTCTATAG
                          ||||| |||| |||| ||||||||
                          AAGTT AATA  CTTA GAGATATC
                            T   C_   T
GAM200  SIRT1    3' CTATAGATGATATTTTAAATTG 1416         TACGGATT
        AA               TTCAATTTA    TCTATAG
                          |||||||||    |||||||
                          AAGTTAAAT    AGATATC
                            TTTATAGT
GAM200  FLJ10898 3' AGAAACTGTTAAATTGAA    2526      T   A
                          TTCAATTTA ACGG TTTCT
                          ||||||||| |||| |||||
                          AAGTTAAAT TGTC AAAGA
                             _  _
GAM201  FLJ10511 3' ATGCCTATAATACCATAATGCC 1784   C _   ACACC
        AG               CT GT TTATG   ATAGGCAT
                          || || |||||   ||||||||
```

```
                    GA CG AATAC    TATCCGTA
                       C T    CATAA
GAM201 KIAA1462  3' ATGCCTATAATTAGGAAGGAGT 3521     G  A  CACC
                    ACTC TTT TGA   ATAGGCAT
                    |||| ||| |||   ||||||||
                    TGAG AAG ATT   TATCCGTA
                       G  G  AA__
GAM201 MESDC2   3' CCCTGGTGGCATAAACGAGT 2950        A   TA
                    ACTCGTTTATG CACCA GG
                    |||||||||| ||||| ||
                    TGAGCAAATAC GTGGT CC
                         G   C_
GAM201 LOC149620 5' ATGCCTACAAAGGAAATGAGT 3135         ATGACACCA
                    ACTCGTTT     TAGGCAT
                    ||||||||     |||||||
                    TGAGTAAA     ATCCGTA
                       GGAAAC___
GAM201 LOC219988 5' ATGCCTACAGTGTCTGTATTAG 3534   GTT  _   CA
          A           TC  TAT GACAC  TAGGCAT
                    || ||| ||||| |||||||
                    AG  ATG CTGTG  ATCCGTA
                    ATT  T   AC
GAM202 BHMT2    3' CTGAAATAATCGAACAGGAAA 1730      A  TA
                    TTTCT GTTC  ATTATTTCAG
                    ||||| ||||  |||||||||
                    AAAGG CAAG  TAATAAAGTC
                        A   C_
GAM202 COL15A1  3' AAATAATCTGAAACTAGAAA 862          _ TA
                    TTTCTAGTT C ATTATTT
                    ||||||||| | |||||||
                    AAAGATCAA G TAATAAA
                       A TC
GAM202 PDGFRA   3' TCTGAAATAATGGGATTAGAAA 1280         A
                    TTTCTAGTTCTA TTATTTCAGA
                    |||||||||||| ||||||||||
                    AAAGATTAGGGT AATAAAGTCT
                          _
GAM202 DORFIN   5' TTCTGGCCTCCAGAACTAGA 1631          AATTATT
                    TCTAGTTCT    TCAGAA
                    |||||||||    ||||||
                    AGATCAAGA    GGTCTT
                       CCTCC__
GAM202 FLJ20034 5' TCTGTGATAAGCAGAACTAGAA 1732         AA   T
          A          TTTCTAGTTCT TTATT CAGA
                    |||||||||| ||||| ||||
                    AAAGATCAAGA AATAG GTCT
                         CG   T
GAM202 KIAA0831 5' TCTGCATTGAACTAGAAA    1589      T TATTT
                    TTTCTAGTTC AAT   CAGA
                    |||||||||| |||    ||||
```

```
                        AAAGATCAAG TTA    GTCT
                        _   C____
GAM202  MBLL39    3' TTCTGAAATAATCAGCAGAAA 1243      A   CTA
                        TTTCT GTT  ATTATTTCAGAA
                        ||||| |||  |||||||||||
                        AAAGA CGA   TAATAAAGTCTT
                        _   C__
GAM202  TSP-NY    3' CTGGGAGCAGAACTAGAAA 2261           AATTA TT
                        TTTCTAGTTCT   T  CAG
                        ||||||||||   |  |||
                        AAAGATCAAGA    A GTC
                            CG___GG
GAM202  LOC112840 3' CTGAAAGTAGAACTGAAA    2384      T    ATTA
                        TTTC AGTTCTA  TTTCAG
                        |||| |||||||  ||||||
                        AAAG TCAAGAT   AAAGTC
                        _   G___
GAM202  LOC136895 3' AAATATTAGAACTAGAAA    2458           T
                        TTTCTAGTTCTAAT ATTT
                        ||||||||||||||| ||||
                        AAAGATCAAGATTA TAAA

                            _
GAM202  LOC145790 5' TTCTGAAATAATCTCTGGAGG 3083       TTCTA
                        TTTCTAG    ATTATTTCAGAA
                        |||||||    |||||||||||
                        GGAGGTC    TAATAAAGTCTT
                            TC___
GAM202  LOC151040 3' TCAGGGATCTAGAACTAGAAA 3153           ATT TT A
                        TTTCTAGTTCTA  AT  C GA
                        |||||||||||  || | ||
                        AAAGATCAAGAT   TA G CT
                            C__ GG A
GAM202  LOC157869 3' TTCTGAAATAATTTCAAGC   3207      CT_
                        GTT  AATTATTTCAGAA
                        |||  |||||||||||
                        CGA  TTAATAAAGTCTT
                            ACT
GAM202  LOC222028 3' TTCTAAGTAGTTAAAATTAGAA 3631          C     C
            A               TTTCTAGTT TAATTATTT AGAA
                        |||||||||| ||||||||| ||||
                        AAAGATTAA ATTGATGAA TCTT
                            A      _
GAM202  LOC222252 3' TCAGGGATCTAGAACTAGAAA 3652           ATT TT A
                        TTTCTAGTTCTA  AT  C GA
                        |||||||||||  || | ||
                        AAAGATCAAGAT   TA G CT
                            C__ GG A
GAM203  FLJ20485  3' TGTGATGGAGTATAC       1875      CGA   T
                        GTATACT  CCATC ACG
                        |||||||  ||||| |||
```

```
                    CATATGA  GGTAG TGT
                    ‾‾‾     ‾
GAM203  LOC132617 3' CGTAGATGATGTGAATGA  3040     A  TCGAC
                    TCGT TAC   CATCTACG
                    |||| |||   ||||||||
                    AGTA GTG   GTAGATGC
                       A  TA___
GAM204  PER2    3' AGATATGTAAATAAGCTCTCA 2013   A T AC
                    A AG GC  GTTTACATATCT
                    | || ||  |||||||||||
                    A TC CG  TAAATGTATAGA
                    C  T AA
GAM204  SLC14A2  3' AGATATGTTTAGTTTAGACTTT 1360      GC__ GTTT
         ATA           TATAAAGT  AC  ACATATCT
                    ||||||||  ||  ||||||||
                    ATATTTCA  TG  TGTATAGA
                      GATT ATT_
GAM204  C20orf82 3' ATGTAAACGCCCACCTTA  3316    A  CA
                    TAA GTG  CGTTTACAT
                    ||| |||  |||||||||
                    ATT CAC  GCAAATGTA
                      C  CC
GAM204  DKFZp566D234 3' ATATGTAAATTATGCTTTA  2610      CAC
                    TAAAGTG  GTTTACATAT
                    |||||||  ||||||||||
                    ATTTCGT  TAAATGTATA
                           AT_
GAM204  EFS2   3' AGACATGGGTGTGCACCTTA 1257   A    TTTA A
                    TAA GTGCACG   CAT TCT
                    ||| |||||||   ||| |||
                    ATT CACGTGT   GTA AGA
                      C   GG__  C
GAM204  FLJ13194 3' ATGTTTATGCACACTTTATA 2140      CA TT
                    TATAAAGTG CGT ACAT
                    ||||||||| ||| ||||
                    ATATTTCAC GTA TGTA
                        AC  TT
GAM204  ZNF291  3' AGATATGGCATGTACTTTA 1930      C TTA
                    TAAAGTGCA GT  CATATCT
                    ||||||||| ||  ||||||||
                    ATTTCATGT CG  GTATAGA
                          A ___
GAM204  LOC157503 3' ATGAAACCATGCACTTTGTA 3380     C_ A
                    TATAAAGTGCA GTTT CAT
                    ||||||||||| |||| |||
                    ATGTTTCACGT CAAA GTA
                         AC  _
GAM204  LOC254431 3' AGATATGTAAACACTGGTAC 3716     AC__
                    GTGC  GTTTACATATCT
                    ||||  |||||||||||
```

```
                                CATG   CAAATGTATAGA
                                GTCA
GAM205  BRCA1    3' CTAATGAAGTGGGCTCCA   1390      A   A    T
                                TG GA GTCT TTTCATTAG
                                || || |||| |||||||||
                                AC CT CGGG GAAGTAATC
                                _  _     T
GAM205  C18orf1  3' AGTGAAGGACCTCTCA      2562       A   TT
                                TGAGA GTCT  TTCATT
                                ||||| ||||  ||||||
                                ACTCT CAGG  AAGTGA
                                   C      __
GAM205  CENTD1   3' GCTAATGATGACATCTCA   1614       A   TTTT
                                TGAGA GTC   TCATTAGC
                                ||||| |||   ||||||||
                                ACTCT CAG   AGTAATCG
                                     A   T___
GAM205  CENTD1   3' GCTAATGATGACATCTCA   2473       A   TTTT
                                TGAGA GTC   TCATTAGC
                                ||||| |||   ||||||||
                                ACTCT CAG   AGTAATCG
                                     A   T___
GAM205  CPNE3    3' CTAATGAAAAACTGCTTA   1068      A   CT
                                TGAG AGT  TTTTCATTAG
                                |||| |||  ||||||||||
                                ATTC TCA  AAAAGTAATC
                                   G     __
GAM205  EPB72    3' CTAATGAAAAACATTACTC  1086     A   C
                                GAG AGT TTTTTCATTAG
                                ||| ||| |||||||||||
                                CTC TTA AAAAAGTAATC
                                  A   C
GAM205  GBP1     3' GCTAATGAAGAAAACTTCTC 894          C
                                GAGAAGT TTTTTCATTAGC
                                ||||||| |||||||||||
                                CTCTTCA AAGAAGTAATCG
                                     A
GAM205  MMP2     3' GCCAATGGAGACTGTCTCA  1124      _      TTT   A
                                TGAGA AGTCTT  CATT GC
                                ||||| ||||||  |||| ||
                                ACTCT TCAGAG  GTAA CG
                                     G    ___     C
GAM205  PSCD4    3' CTAACAGGAAACACTTCTCA 1447         C   CA
                                TGAGAAGT TTTTT  TTAG
                                |||||||| |||||  ||||
                                ACTCTTCA AAAGG  AATC
                                      C   AC
GAM205  SLC7A6   3' GCTAATGAAATGGGAACCTC 1077      AAG  T
                                GAG  TCT TTTCATTAGC
                                |||  ||| |||||||||
```

```
                          CTC  GGG AAAGTAATCG
                          CAA  T
GAM205  XKRY    5' CTAATGAAAATTATTCTC  1142      GTCT
                          GAGAA   TTTTCATTAG
                          |||||   ||||||||||
                          CTCTT   AAAAGTAATC
                          ATT_
GAM205  XKRY    5' CTAATGAAAATTATTCTC  2551      GTCT
                          GAGAA   TTTTCATTAG
                          |||||   ||||||||||
                          CTCTT   AAAAGTAATC
                          ATT_
GAM205  C1orf16 3' GCCAATGGGAACTTCTCA   1568        CTT TT  A
                          TGAGAAGT  T CATT GC
                          ||||||||  | |||| ||
                          ACTCTTCA  A GTAA CG
                          ___GG  C
GAM205  C3orf4  3' GCTAATGTCTGTTAGACTTTC 1890         TTTT__
            A             TGAGAAGTCT   CATTAGC
                          ||||||||||   |||||||
                          ACTTTTCAGA   GTAATCG
                          TTGTCT
GAM205  FLJ10483 3' GCCAATGAAAATGTGCTTC  1781     CT_      A
                          GAAGT  TTTTCATT GC
                          |||||  |||||||| ||
                          CTTCG  AAAAGTAA CG
                          TGT      C
GAM205  FLJ12568 3' GCTAATGAAAATGTTTTCT  2122      TCT
                          AGAAG  TTTTCATTAGC
                          |||||  |||||||||||
                          TCTTT  AAAAGTAATCG
                          TGT
GAM205  FLJ20340 3' GCTTTGAAAAACTTTTCA   1750      CT    TT
                          TGAGAAGT TTTTCA AGC
                          |||||||| |||||| |||
                          ACTTTTCA AAAAGT TCG
                          __      T_
GAM205  FLJ20727 5' GCTAATGGACTTGACTCTCA 1769      A  TTT
                          TGAGA GTC  TTCATTAGC
                          ||||| |||  |||||||||
                          ACTCT CAG  AGGTAATCG
                          _ TTC
GAM205  FLJ20736 3' CTAATGGACATCTTCTCA   1770        TCTTT
                          TGAGAAG   TTCATTAG
                          |||||||   |||||||||
                          ACTCTTC   AGGTAATC
                          TAC__
GAM205  PDE1C   3' GCTAATGACCTGGCTTTCA   1172      A  TTTT
                          TGAGA GTC  TCATTAGC
                          ||||| |||  ||||||||
```

```
                       ACTTT CGG    AGTAATCG
                       _   TCC_
GAM205  TOB2    5' GCTAAGGGTGAAACTTTTCA 3680      C  T  A
                       TGAGAAGT TT TTC TTAGC
                       ||||||||| || ||| |||||
                       ACTTTTCA AG GGG AATCG
                         A  T  _
GAM205  TSC22   3' CTAATGAAATGGATTTCCCA 1264    A     T
                       TG GAAGTCT TTTCATTAG
                       || |||||||| |||||||||
                       AC CTTTAGG AAAGTAATC
                          C    T
GAM205  TSP-NY  3' GCTAAGAATGAAAAAGACTTCT 2262              ___
         C                GAGAAGTCTTTTTCAT  TAGC
                       |||||||||||||||  ||||
                       CTCTTCAGAAAAAGTA  ATCG
                               AGA
GAM205  TUCAN   3' GCTAACAAAAGCTTCTCA  1598      T  TCA
                       TGAGAAG CTTTT  TTAGC
                       ||||||| |||||  |||||
                       ACTCTTC GAAAA  AATCG
                         _    C__
GAM205  LOC138241 5' GCCAATGGGGGAATTCTCA 3019      GTC TT  A
                       TGAGAA  TTT  CATT GC
                       ||||||  |||  |||| ||
                       ACTCTT  AGG  GTAA CG
                         A__   GG    C
GAM205  LOC152345 3' AATGGAGAGACTTCCG    3170    A      T
                       TG GAAGTCTTTT CATT
                       || |||||||||| ||||
                       GC CTTCAGAGAG GTAA
                         _      _
GAM205  LOC154214 5' CTAATGAAAAGGACCTTA  3189     AA
                       TGAG  GTCTTTTTCATTAG
                       ||||  |||||||||||||
                       ATTC  CAGGAAAAGTAATC
                            __
GAM205  LOC154790 5' AATGAAAAGAACTTCCCA  3192    A   CT
                       TG GAAGT TTTTCATT
                       || ||||| |||||||||
                       AC CTTCA AAAAGTAA
                          C    AG
GAM205  LOC158427 3' CTAATGAAAATAACTCCCA 2478    A A CT
                       TG GA GT TTTTCATTAG
                       || || || |||||||||
                       AC CT CA AAAAGTAATC
                          C _ AT
GAM205  LOC161003 5' AGTATAAAAGCTTCTCA   2520      T  TC
                       TGAGAAG CTTTT ATT
                       ||||||| ||||| |||
```

```
                          ACTCTTC GAAAA  TGA
                           _      TA
GAM205  LOC200830 3' GCTAATGGGCTGACTACTCA 3480      A   TTT
                     TGAG AGTC   TTCATTAGC
                     |||| ||||  |||||||||
                     ACTC TCAG   GGGTAATCG
                        A   TC_
GAM205  LOC221421 3' GCTAATGAAAGAGATTCT   3558      G
                     AGAA TCTTTTTCATTAGC
                     |||| ||||||||||||||
                     TCTT AGAGAAAGTAATCG
                        _
GAM205  LOC257017 5' CTAAGTTAAGACTTTTCA   3736            TTTCA
                     TGAGAAGTCTT   TTAG
                     |||||||||||   ||||
                     ACTTTTCAGAA   AATC
                               TTG__
GAM205  LOC257353 5' GCTAATAATGATGGCCTCTCA 3738     A  T TTC
                     TGAGA GTC TT  ATTAGC
                     ||||| ||| ||  ||||||
                     ACTCT CGG AG  TAATCG
                         C   T TAA
GAM205  LOC90459   3' GCCAATGAATTTCTGCTTTTCA 2642          CTTT_   A
                     TGAGAAGT   TTCATT GC
                     ||||||||   |||||| ||
                     ACTTTTCG   AAGTAA CG
                       TCTTT     C
GAM206  CXADR     3' TATTGAGATGACACTAGGTGC 820       _ CA CCC
                     GCAC TAG TC  TTTCAATA
                     |||| ||| ||  ||||||||
                     CGTG ATC AG  AGAGTTAT
                        G  AC T__
GAM206  EPB72     3' TATTGAGGATTGAGCCAGTGC 1087      A A CCC
                     GCACT GC TC  TTTCAATA
                     ||||| || ||  ||||||||
                     CGTGA CG AG  GGAGTTAT
                         C _ TTA
GAM206  FCAR      5' ATTGAAAGGAGAGCAACGG  880     CACTA A C
                     CCG   GC TC CCTTTCAAT
                     |||   || || |||||||||
                     GGC   CG AG GGAAAGTTA
                       AA___ _ A
GAM206  FCAR      5' ATTGAAAGGAGAGCAACGG  2400    CACTA A C
                     CCG   GC TC CCTTTCAAT
                     |||   || || |||||||||
                     GGC   CG AG GGAAAGTTA
                       AA___ _ A
GAM206  FCAR      5' ATTGAAAGGAGAGCAACGG  2401    CACTA A C
                     CCG   GC TC CCTTTCAAT
                     |||   || || |||||||||
```

```
                          GGC    CG AG GGAAAGTTA
                          AA___ _ A
GAM206  FCAR    5' ATTGAAAGGAGAGCAACGG  2402    CACTA A C
                          CCG    GC TC CCTTTCAAT
                          III    II II IIIIIIIII
                          GGC    CG AG GGAAAGTTA
                          AA___ _ A
GAM206  FCAR    5' ATTGAAAGGAGAGCAACGG  2403    CACTA A C
                          CCG    GC TC CCTTTCAAT
                          III    II II IIIIIIIII
                          GGC    CG AG GGAAAGTTA
                          AA___ _ A
GAM206  FCAR    5' ATTGAAAGGAGAGCAACGG  2404    CACTA A C
                          CCG    GC TC CCTTTCAAT
                          III    II II IIIIIIIII
                          GGC    CG AG GGAAAGTTA
                          AA___ _ A
GAM206  FCAR    5' ATTGAAAGGAGAGCAACGG  2406    CACTA A C
                          CCG    GC TC CCTTTCAAT
                          III    II II IIIIIIIII
                          GGC    CG AG GGAAAGTTA
                          AA___ _ A
GAM206  KCNAB1  3' TGAAAATGCTAGTGGG     2585    G      CCCC
                          CC CACTAGCAT    TTTCA
                          II IIIIIIIII    IIIII
                          GG GTGATCGTA    AAAGT
                          _      ____
GAM206  NCOA6   3' TATTGAAAGGAGCTAATGC  1468    C    ATCC
                          GCA TAGC   CCTTTCAATA
                          III IIII   IIIIIIIIII
                          CGT ATCG   GGAAAGTTAT
                          A   A___
GAM206  SDHC    3' TATTGAAAGAAGAGAGGTGGGG 2856    G   AGCA CC
                          CC CACT   TC CTTTCAATA
                          II IIII   II IIIIIIIII
                          GG GTGG   AG GAAAGTTAT
                          G   AG__  AA
GAM206  CBLN1   5' GGAGGGGACGCTAGTCGCGG  1101    _    A
                          CCGC ACTAGC TCCCCTTT
                          IIII IIIIII IIIIIIII
                          GGCG TGATCG AGGGGAGG
                          C    C
GAM206  CSTF2   3' TATTGAAAAAAGATGACCTGC  819    CTAG   CCC
                          GCA   CATC  TTTCAATA
                          III   IIII  IIIIIIII
                          CGT   GTAG  AAAGTTAT
                          CCA_  AAA
GAM206  GS3955  5' AAAGGGGGTGCAGCGCGG    1953    A A
                          CCGC CT GCATCCCCTTT
                          IIII II IIIIIIIIIII
```

```
                      GGCG GA CGTGGGGGAAA
                        C _
GAM206 KIAA0184 3' ATTGAAAGAGGTGTGCTGG  2715      TC _
                      CTAGCA CC CTTTCAAT
                      |||||| || ||||||||
                      GGTCGT GG GAAAGTTA
                        GT A
GAM206 MGC14697 5' GTTGAAGGACACCAGCTGCGG 2276       CTA ATCCC_
                      CCGCA GC   CTTTCAAT
                      ||||| || ||||||||
                      GGCGT CG   GGAAGTTG
                        ___ ACCACA
GAM206 RRN3    3' AGGTGGAAGTTGCTAGTGC  1827        ___ _
                      GCACTAGCA TCC CCT
                      ||||||||| ||| |||
                      CGTGATCGT AGG GGA
                        TGA  T
GAM206 WDR13   5' AAGGAATGCTAGGCGG   1759     A    CC
                      CCGC CTAGCAT CCTT
                      |||| ||||||| ||||
                      GGCG GATCGTA GGAA
                        _      A_
GAM206 LOC219287 3' GAAAGAGGGATGCTACACGG  3609    CAC       _
                      CCG  TAGCATCCC CTTTC
                      |||  |||||||||| |||||
                      GGC  ATCGTAGGG GAAAG
                      AC_       A
GAM206 LOC221979 5' ATTGAAACTGCTAGTG    3571       TCCCC
                      CACTAGCA   TTTCAAT
                      ||||||||   |||||||
                      GTGATCGT   AAAGTTA
                        C____
GAM206 LOC255328 3' TATTGAAAGGGCTGCACCATGC 3710      CTA_ TC
                      GCA   GCA CCCTTTCAATA
                      |||   ||| |||||||||||
                      CGT   CGT GGGAAAGTTAT
                      ACCA  C_
GAM206 LOC257115 3' TATTGAAAGGAAAGTGCTATCG 3709     CAC     CC_
                      CG TAGCAT CCTTTCAATA
                      || |||||| |||||||||||
                      GC ATCGTG GGAAAGTTAT
                      T__     AAA
GAM206 LOC51145 3' ATTGAAAGGGGAAATGTGTCA 1666    C  TAGCA
                      C GCAC   TCCCCTTTCAAT
                      | ||||   ||||||||||||
                      A TGTG   AGGGGAAAGTTA
                      C  TAA__
GAM207 BCL11A  3' AAACTAGAACAGGTATAT   2018       TA
                      ATATACCTGTTTT TTT
                      ||||||||||||| |||
```

```
                              TATATGGACAAGA  AAA
                                 TC
GAM207  C8orf1   3' GAAACCTTGACAGGTACTTCA 1099      TA      TTTA
                       TGA TACCTGTT   TTTC
                       ||| |||||||   ||||
                       ACT ATGGACAG   AAAG
                        TC      TTCC
GAM207  KPNA1    3' AAATAAAAACAGTATC   3159     TAC
                       GATA CTGTTTTTATTT
                       |||| ||||||||||||
                       CTAT GACAAAATAAA
                              ___
GAM207  NRXN1    3' AAATAAAAACAAGTATCTCA 2457     T  C
                       TGA ATAC TGTTTTTATTT
                       ||| |||| |||||||||||
                       ACT TATG ACAAAAATAAA
                        C  A
GAM207  NRXN1    3' AAATAAAAACAAGTATCTCA 1158     T  C
                       TGA ATAC TGTTTTTATTT
                       ||| |||| |||||||||||
                       ACT TATG ACAAAAATAAA
                        C  A
GAM207  PCDHGA8  3' AAATAATTTTTAAGGTGTATCA 1459          GTTT__
                       TGATATACCT    TTATTT
                       ||||||||||    ||||||
                       ACTATGTGGA    AATAAA
                              ATTTT
GAM207  SNX5     3' GAAATATCTACAGGTATAT  1500         TTT
                       ATATACCTGT  TATTTC
                       ||||||||||  ||||||
                       TATATGGACA  ATAAAG
                         TCT
GAM207  BNIP2    3' GAAATATGCAGGTATAT    2762         TTT
                       ATATACCTGT  TATTTC
                       ||||||||||  ||||||
                       TATATGGACG  ATAAAG
                         T__
GAM207  DRIL2    3' AAATGAAAACAGATCA     1305     ATAC
                       TGAT  CTGTTTTTATTT
                       ||||  |||||||||||
                       ACTA  GACAAAAGTAAA
                              ____
GAM207  DVS27    3' AAATAAAAGCAGAATGTATATC 2335        ___
          A            TGATATAC CTGTTTTTATTT
                       |||||||| ||||||||||||
                       ACTATATG GACGAAAATAAA
                         TAA
GAM207  FLJ12960 3' GAAGGGGGAGCAGGCACATCA 2074     ATA     TA
                       TGAT CCTGTTTT TTTC
                       |||| |||||||| ||||
```

```
                    ACTA  GGACGAGG GAAG
                       CAC       GG
GAM207 FLJ20793  3' GAATACTAACAGGTATTTCA  3542      T      TT
                    TGA ATACCTGTT TATTT
                    ||| ||||||||| |||||
                    ACT TATGGACAA ATAAG
                      T       TC
GAM207 KIAA0040  3' GAAATAAAATTAAAGGTATA  1515          GT__
                    TATACCT  TTTTATTTC
                    |||||||  |||||||||
                    ATATGGA  AAAATAAAG
                       AATT
GAM207 KIAA1349  3' GAAATAAAAGCAGCATCA    2893      ATAC
                    TGAT  CTGTTTTTATTTC
                    ||||  |||||||||||||
                    ACTA  GACGAAAATAAAG
                       C___
GAM207 KIAA1373  3' AAATATTAACAGGTATAT    2903          TT
                    ATATACCTGTT TATTT
                    ||||||||||| |||||
                    TATATGGACAA ATAAA
                       TT
GAM207 SCDGF-B   3' AAGTAGAAAGGTATATCA    2147          GT
                    TGATATACCT TTTTATTT
                    |||||||||| ||||||||
                    ACTATATGGA AAGATGAA
                          __
GAM207 SCDGF-B   3' AAGTAGAAAGGTATATCA    2314          GT
                    TGATATACCT TTTTATTT
                    |||||||||| ||||||||
                    ACTATATGGA AAGATGAA
                          __
GAM207 LOC121441 3' AAATAAAAACAGGAATATTA  2991        A
                    TGATAT CCTGTTTTTATTT
                    |||||| |||||||||||||
                    ATTATA GGACAAAAATAAA
                       A
GAM207 LOC157729 3' AAATAAAGATAGCATGTCA   3205        AC
                    TGATAT CTGTTTTTATTT
                    |||||| |||||||||||
                    ACTGTA GATAGAAATAAA
                       C_
GAM207 LOC200339 3' GAAGTTCACAGGTATATC    3475          TTTT
                    GATATACCTGT ATTTC
                    ||||||||||| |||||
                    CTATATGGACA TGAAG
                          CT__
GAM207 LOC221300 3' AAATGGCAAACAGGTATAT   3545             _
                    ATATACCTGTTT TTATTT
                    |||||||||||| ||||||
```

```
                    TATATGGACAAA GGTAAA
                              C
GAM207  LOC257235 5' GAAACCATTGCAGGTATTTCA 3728    T     TTTTA
                    TGA ATACCTGT    TTTC
                    ||| ||||||||    ||||
                    ACT TATGGACG    AAAG
                      T     TTACC
GAM207  LOC93333 5' AAATGGTTAAGGGTATATCA 2932        GTTT
                    TGATATACCT  TTATTT
                    ||||||||||  ||||||
                    ACTATATGGG  GGTAAA
                         AATT
GAM208  PCDH7    3' AAACAGTATTAATGCAGAAATG 938    A _
                    CGT TC GCATTAATACTGTTT
                    ||| || ||||||||||||||
                    GTA AG CGTAATTATGACAAA
                      A A
GAM208  TRC8     3' AAACAGTATCAATGTTGA 1365    _   A
                    TCG CATT ATACTGTTT
                    ||| |||| |||||||||
                    AGT GTAA TATGACAAA
                      T   C
GAM208  LOC145225 3' AAACAGTATTAACCCTGC   3275     ___
                    GCA  TTAATACTGTTT
                    |||  |||||||||||
                    CGT  AATTATGACAAA
                      CCC
GAM209  BHMT2    3' AGCATTATTGAAATAAATGTTT 1729      C__ TGG
                A        TAGACATTTA  CA  GATGCT
                    |||||||||| ||  ||||||
                    ATTTGTAAAT  GT  TTACGA
                      AAA  TA_
GAM209  CANX     3' AGCATCCTGATTAAATGTCTG 3409       CCA
                    TAGACATTTA  TGGGATGCT
                    ||||||||||  |||||||||
                    GTCTGTAAAT  GTCCTACGA
                       TA_
GAM209  COPG2    3' AGCAGATCAAGCAAATGTCTA 3194       ACCA GA
                    TAGACATTT  TGG  TGCT
                    |||||||||  |||  ||||
                    ATCTGTAAA  ACT  ACGA
                      CGA_ AG
GAM209  MS4A1    3' CATTTCACAAATGTTTAGT 711       ACCA GG
                    ACTAGACATTT  TG ATG
                    ||||||||||| ||  |||
                    TGATTTGTAAA  AC TAC
                       C___ TT
GAM209  SEL1L    3' CATGTGTATTAATGTCTA   1180      __  _
                    TAGACATT TAC CATG
                    |||||||| ||| ||||
```

```
                         ATCTGTAA ATG GTAC
                         TT  T
GAM209  TPK1    3' CATCCTTAAATGTCTA    1988        CCAT
                         TAGACATTTA  GGGATG
                         |||||||||| |||||
                         ATCTGTAAAT  TCCTAC

                            ____
GAM209  CYorf14 3' CTGTGGGCAATAAATGTCTG 1839            ____
                         TAGACATTTA  CCATGG
                         |||||||||  ||||||
                         GTCTGTAAAT  GGTGTC
                            AACG
GAM209  HSPC228 3' AGCATTTCATAAATGTTTAGT 1688          CCA GG
                         ACTAGACATTTA  TG ATGCT
                         |||||||||||| || |||||
                         TGATTTGTAAAT  AC TACGA
                            ___ TT
GAM209  MGC1127 3' AGCTGGGTAATAAATGTCTA 2336      ___ ATGGGAT
                         TAGACATT TACC    GCT
                         |||||||| ||||    |||
                         ATCTGTAA ATGG    CGA
                         ATA  GT_____
GAM209  SLC16A4 3' AGCATTCTGAGAAATGTCTA 1144        ACCA
                         TAGACATTT  TGGGATGCT
                         |||||||||  |||||||||
                         ATCTGTAAA  GTCTTACGA
                         GA__
GAM209  LOC147180 5' CACCTGTTTAAATGTCTG   3292      CC   A
                         TAGACATTTA ATGGG TG
                         |||||||||| ||||| ||
                         GTCTGTAAAT TGTCC AC
                         T_    _
GAM209  LOC148195 5' GCATCCCATTGGTGTCAGT  3297    A ATTT  _
                         ACT GAC   ACCA TGGGATGC
                         ||| |||   |||| ||||||||
                         TGA CTG   TGGT ACCCTACG
                         _  ____   T
GAM209  LOC158572 3' AGCATCCTTTCAATAAATGCCT 3221     A    CCAT_
          G                 TAG CATTTA   GGGATGCT
                         ||| ||||||   ||||||||
                         GTC GTAAAT   TCCTACGA
                         C     AACTT
GAM209  LOC201595 3' AGCACTGCTGTAAATGTCTAG 3453          CATG A
                         CTAGACATTTAC  GG TGCT
                         |||||||||||  || ||||
                         GATCTGTAAATG  TC ACGA
                         TCG_ _
GAM209  LOC203427 5' CATTTAGGAAGCAAGATGTCTA 3464          ACCATG__
          G                 CTAGACATTT  GGATG
                         |||||||||     |||||
```

```
                         GATCTGTAGA     TTTAC
                             ACGAAGGA
GAM210  PDE1A     3' ATCAGCATGAAAACATCCTA 1171     AT     _ GA
                       TAG TGTTTTCA GT GAT
                       ||| |||||||| || |||
                       ATC ACAAAAGT CG CTA
                         CT     A A_
GAM210  ELAC1     3' AATCATCTCACCCCGAAATGCA 3506    _   A__
                       TGT TTTC  GTGAGATGATT
                       ||| ||||  ||||||||||
                       ACG AAAG  CACTCTACTAA
                         T   CCC
GAM210  LOC154790 5' AATCAGATCATATGAAAACAAT 3191          _   GA
             CTA           TAGATTGTTTTCA GTGA TGATT
                       |||||||||||| |||| |||||
                       ATCTAACAAAAGT TACT ACTAA
                             A   AG
GAM210  LOC158434 3' CAGTCACTAAAAACAATC  3389      C   GA
                       GATTGTTTT AGTGA TG
                       ||||||||| ||||| ||
                       CTAACAAAA TCACT AC
                             A   G_
GAM211  MAP3K5   3' TCTGAGTAGAAATGCGT  1261     A     TT
                       ACGCAT TTCTACTC GGA
                       |||||| |||||||| |||
                       TGCGTA AAGATGAG TCT

                            _     __
GAM211  DKFZP564F0522 3' TAATTCCACAGTCAGAACATGC 2825     A _ CT
                       GCAT TTCT ACT TGGAATTA
                       |||| |||| ||| ||||||||
                       CGTA AAGA TGA ACCTTAAT
                         C   C   C_
GAM211  GPCR150  3' TAATTCCAAGAAGTTTTTATAG 1496    GC  TTCT _
           T              AC ATA   ACT CTTGGAATTA
                       || |||   ||| ||||||||||
                       TG TAT   TGA GAACCTTAAT
                       A_  TTT_  A
GAM211  SLC26A7  3' TAATTCAGTATAGAATATGC 2340          CT TG
                       GCATATTCTA CT GAATTA
                       |||||||||| || ||||||
                       CGTATAAGAT GA CTTAAT
                             AT __
GAM211  SLC6A14  3' TAATTTCAAATAGAATATG 1369          CTC
                       CATATTCTA TTGGAATTA
                       ||||||||| |||||||||
                       GTATAAGAT AACTTTAAT
                             A__
GAM211  LOC116228 3' TAGTTCTGAATTAAAATATGC 2980      C CTC TG
                       GCATATT TA T GAATTA
                       ||||||| || | ||||||
```

```
                          CGTATAA AT  A  CTTGAT
                            A TA_ GT
GAM212  CCNC     3' ATAATGTCTTCAGTGGAACAC 1192          A_____        III
                          GTGTTCCA    ACATTA  T
                          ||||||||    ||||||  |
                          CACAAGGT    TGTAAT  A
                            GACTTC       III
GAM212  MSL3L1   5' TAATGGTTGGAACAGAA    1331       G      A
                          TTC TGTTCCAA CATTA
                          ||| |||||||| |||||
                          AAG ACAAGGTT GTAAT
                            _        G
GAM212  THBS1    3' TAATGTTTGCACACTGAA   1004       _  TC
                          TTC GTGT  CAAACATTA
                          ||| ||||  |||||||||
                          AAG CACA  GTTTGTAAT
                            T   C_
GAM212  CSRP3    3' TAATGCTTGGAATGGGAG   1031       G      A
                          TTC TGTTCCAA CATTA
                          ||| |||||||| |||||
                          GAG GTAAGGTT GTAAT
                            G       C
GAM212  FLJ11181 5' TAATGTTCGGCAAACATGAA 1817          __  A
                          TTCGTGTT CC AACATTA
                          |||||||| || |||||||
                          AAGTACAA GG TTGTAAT
                            AC C
GAM212  FLJ23132 3' TAATGTTTCCAACATGAA   3692        CC
                          TTCGTGTT AAACATTA
                          |||||||| ||||||||
                          AAGTACAA TTTGTAAT
                            CC
GAM212  GAB3     3' TAATGTTTGTTACAGAA    2378    G  TC
                          TTC TGT  CAAACATTA
                          ||| |||  |||||||||
                          AAG ACA  GTTTGTAAT
                            _  TT
GAM212  MGC13033 3' TAATGTTTGGAATGGAG    2198    G
                          TTC TGTTCCAAACATTA
                          ||| |||||||||||||
                          GAG GTAAGGTTTGTAAT
                            _
GAM212  PRO0386  5' TAATGTTCTGTGGAACAT   1844          ___
                          GTGTTCCA AACATTA
                          |||||||| |||||||
                          TACAAGGT TTGTAAT
                            GTC
GAM212  LOC149351 5' TAATGTGAGGAAAAACACGGA 3132       ___  AA
                          TTCGTGT TCC ACATTA
                          |||||| ||| ||||||
```

```
                              AGGCACA  AGG  TGTAAT
                               AAA  AG
GAM212  LOC163590 3'  TAATGTTTGGACTTGGA    2512      T  T
                      TTCG GT CCAAACATTA
                      |||| || ||||||||||
                      AGGT CA GGTTTGTAAT
                       T  _
GAM212  LOC256307 3'  TAATGCTACATGGAACATGAA 3726          AA___
                      TTCGTGTTCCA    CATTA
                      |||||||||||    |||||
                      AAGTACAAGGT    GTAAT
                        ACATC
GAM212  LOC87769 3'  TAATGTTGAGATACGAA    2912      TC  A
                     TTCGTGT CAA CATTA
                     ||||||| ||| |||||
                     AAGCATA GTT GTAAT
                        GA  _
GAM212  LOC89890 3'  TAATGTTTGAAATACGAA    2574        C
                     TTCGTGTT CAAACATTA
                     |||||||| |||||||||
                     AAGCATAA GTTTGTAAT
                        A
GAM213  GDF8    5'  ACAAGAAAAAAGATTATA    1196         CA
                    TATAATCTTTTT TCTTGT
                    |||||||||||| ||||||
                    ATATTAGAAAAA AGAACA
                        __
GAM213  REGL    3'  ACCATATAGAAAAAGATTATA 1306          ATCT  A
                    TATAATCTTTTTC  TGTG GT
                    |||||||||||||  |||| ||
                    ATATTAGAAAAG   ATAC CA
                        AT__  _
GAM213  DKFZP434J214 3'  ACTCAGTGTGGAAAAGA    2586         CTTG
                         TCTTTTTCAT  TGAGT
                         ||||||||||  |||||
                         AGAAAAGGTG  ACTCA
                           TG__
GAM213  KIAA0440 5'  CTTTTAAATGAAAAGATTA   1636        C  T
                     TAATCTTTTTCAT TTG GAG
                     ||||||||||||| ||| |||
                     ATTAGAAAAGTA AAT TTC
                       _  T
GAM213  LOC152756 3'  ACTCATGATCCAAAAAGATTA 3363        CATC TG
                      TAATCTTTTT  T TGAGT
                      ||||||||||  | |||||
                      ATTAGAAAA   A ACTCA
                        ACCT GT
GAM213  LOC158428 3'  ACTCACATAGGTGAAAAA    2889         _
                      TTTTTCATCT TGTGAGT
                      |||||||||| |||||||
```

```
                         AAAAAGTGGA ACACTCA
                         T
GAM214  BHLHB3   3' TATGTAAGGGGTGAGACACAAC 2162        A A G _
                       GTTGTGTCT CA CC CT ACATA
                       |||||||||| || || || |||||
                       CAACACAGA GT GG GA TGTAT
                              _ _ G  A
GAM214  F9      3' GCGTGTGTGTAGACACAC   709    T     _ _
                       GT GTGTCTACA AC CGC
                       || ||||||||| || |||
                       CA CACAGATGT TG GCG
                         _       G  T
GAM214  FLJ31737 3' TAGCACTGTAGACACAAC   2504          ACC
                       GTTGTGTCTACA  GCTA
                       ||||||||||||  ||||
                       CAACACAGATGT  CGAT
                           CA_
GAM214  KIAA1505 5' GCATTTAGTAGACACCACG  3638    T    _ CC
                       CGT GTGTCTAC AA  GC
                       ||| ||||||||| || ||
                       GCA CACAGATG TT  CG
                         C      A TA
GAM214  PHRET1   3' GGCGCTGTAGACACAAC   1947          AC
                       GTTGTGTCTACA CGCT
                       |||||||||||| ||||
                       CAACACAGATGT GCGG
                           C_
GAM214  RYD5     3' AGCAGCCGTGGACACAACG  3103          AACC
                       CGTTGTGTCTAC  GCT
                       ||||||||||||  |||
                       GCAACACAGGTG  CGA
                           CCGA
GAM214  LOC221337 5' TAGTTCAAGTAAACACAATG 3556     C AACC
                       CGTTGTGT TAC   GCTA
                       |||||||| |||   ||||
                       GTAACACA ATG   TGAT
                          A  AACT
GAM215  ADCY9    3' GTGGTCATTTCAGCCCTA    801    T    A
                       TAGG GCTGAAAT ACCAC
                       |||| ||||||||| |||||
                       ATCC CGACTTTA TGGTG
                          _        C
GAM215  CRAT     3' GTGGGTCATCCCAGCACCTG 1079       AA A  A
                       TAGGTGCTG AT ACC CAT
                       |||||||||| || ||| |||
                       GTCCACGAC TA TGG GTG
                          CC C  _
GAM215  CRAT     3' GTGGGTCATCCCAGCACCTG  771       AA A  A
                       TAGGTGCTG AT ACC CAT
                       |||||||||| || ||| |||
```

```
                        GTCCACGAC  TA TGG GTG
                         CC  C  _
GAM215  CXCR4    3' CAGGAGTGGGTTGATTTCAGCA 1028          AA__  AT
          CCTA              TAGGTGCTGAAAT  CCAC  CTG
                        ||||||||||||  |||| |||
                        ATCCACGACTTTA  GGTG  GAC
                              GTTG  AG
GAM215  AGMAT    3' CAGACGTGGTGTGGTGCACACC 2087     C AAATA_  A
                        GGTG TG   ACCAC TCTG
                        |||| ||   ||||| ||||
                        CCAC AC   TGGTG AGAC
                         _ GTGGTG    C
GAM215  DKFZp434E0519 3' CAGATGCGGTGGCTCACACCTA 2240       C  AATA  A
                        TAGGTG TGA   ACC CATCTG
                        |||||| |||   ||| ||||||
                        ATCCAC ACT   TGG GTAGAC
                         _ CGG_  C
GAM215  DKFZp762E1312 5' CAGACATGGCCTTAGTACCTA 1823         AATAA  CA
                        TAGGTGCTGA   CCA TCTG
                        ||||||||||   ||| ||||
                        ATCCATGATT   GGT AGAC
                              CC___  AC
GAM215  FLJ20619 3' CAGTGAGGTAGCATCTA    1760        GAAATA  A T
                        TAGGTGCT    ACC CA CTG
                        ||||||||    ||| || |||
                        ATCTACGA    TGG GT GAC
                              _____  A  _
GAM215  FLJ20716 3' CAGATTGCCACCCCAGCACCTA 1768          AAATAAC  C
                        TAGGTGCTG    CA ATCTG
                        |||||||||    || |||||
                        ATCCACGAC    GT TAGAC
                          CCCACC_  _
GAM215  FRAT1    3' CAGATGTGGCTACTGACATATC 1217     C AAA_ A
           TA             TAGGTG TG   TA CCACATCTG
                        ||||||| ||   || |||||||||
                        ATCTAT AC   AT GGTGTAGAC
                         _ AGTC  C
GAM215  KIAA1656 3' CAGATGTGGCCATCCCTCCCTG 2729      TGCT AATAA
                        TAGG  GA   CCACATCTG
                        ||||  ||   |||||||||
                        GTCC  CT   GGTGTAGAC
                          CTCC ACC__
GAM215  Rab11-FIP3 3' CAGATGTGGTCACCTCAGTCC 1524     T   AATA
                        GG GCTGA  ACCACATCTG
                        || |||||  |||||||||
                        CC TGACT   TGGTGTAGAC
                         _  CCAC
GAM215  TOMM34  3' AGACATGGTTGTTGCACC   1332       TGA      CA
                        GGTGC  AATAACCA TCT
                        |||||  |||||||| |||
```

```
                              CCACG  TTGTTGGT AGA
                               ___        AC
GAM215  LOC146337 3'  CAGATGCATCTGTTTCAGCCCT 3285     T      ACCA
           A                   TAGG GCTGAAATA  CATCTG
                              |||| |||||||||  ||||||
                               ATCC CGACTTTGT  GTAGAC
                                 _      CTAC
GAM215  LOC147229 3'  AGATGCAGGCTCAGCACT   3105      AATAA A_
                          GGTGCTGA   CC CATCT
                          ||||||||   || |||||
                          TCACGACT   GG GTAGA
                            C____  AC
GAM215  LOC158332 3'  GGTACTAATTCAGCACCTA  3217         A __
                      TAGGTGCTGAA TA  ACC
                      ||||||||||| || |||
                      ATCCACGACTT AT  TGG
                          A  CA
GAM215  LOC163131 5'  AGATGTGATTACATTACT   3245    C AAA  C
                         GGTG TG  TAA CACATCT
                         |||| ||  ||| |||||||
                         TCAT AC  ATT GTGTAGA
                           T ___  A
GAM215  LOC221423 3'  AGATGTGGCTACAACAT    3551    C AAA A
                         GTG TG  TA CCACATCT
                         ||| ||  || ||||||||
                         TAC AC  AT GGTGTAGA
                           A ___  C
GAM215  LOC222182 5'  CAGACATGTGCCCAGCACCT 3639        AAATAAC  __
                         AGGTGCTG    CACA TCTG
                         ||||||||    |||| ||||
                         TCCACGAC    GTGT AGAC
                           CC_____     AC
GAM216  B3GALT3   3'  GAAGATTACAGTTATGTA   1056       CG_
                      TACGTAAC AATCTTC
                      |||||||| |||||||
                      ATGTATTG TTAGAAG
                          ACA
GAM216  LOC159199 5'  GAAGATCAAGAGGTTACGTG 3237        GA___
                      TACGTAACC   ATCTTC
                      |||||||||   ||||||
                      GTGCATTGG   TAGAAG
                          AGAAC
GAM217  ACCN2     3'  CCACCAGACACTCCTTC    1891        TCT
                      GAAGGAGTGTTT TGG
                      |||||||||||| |||
                      CTTCCTCACAGA ACC
                          CC_
GAM217  BLAME     3'  CCAAAAAAACACAAAGTGCTTC 1892      GA____      C
           TG                TAGAAG   GTGTTTT TTGG
                             ||||||   ||||||| ||||
```

```
                        GTCTTC    CACAAAA AACC
                        GTGAAA        A
GAM217  DLX4    3' TTGCCACTCCCCCACTCCTTCT 2432           TTTTCT
                        AGAAGGAGTG    TGGCAA
                        |||||||||    ||||||
                        TCTTCCTCAC    ACCGTT
                           CCCCTC
GAM217  DLX4    3' TTGCCACTCCCCCACTCCTTCT 870            TTTTCT
                        AGAAGGAGTG    TGGCAA
                        |||||||||    ||||||
                        TCTTCCTCAC    ACCGTT
                           CCCCTC
GAM217  IGSF6   3' TTTGCCAAGAAAAAAAATTCTA 1256      GGAGTG
                        TAGAA    TTTTCTTGGCAAA
                        |||||    ||||||||||||
                        ATCTT    AAAAGAACCGTTT
                          AAAA__
GAM217  ITPR2   3' CAGGAACAAAACACTGCCT 912        _    ___
                        AGG AGTGTTT  TCTTG
                        ||| |||||||  |||||
                        TCC TCACAAA  AGGAC
                          G    ACA
GAM217  IVD     5' GCTAAAAACACTCATCCTA 913     AAG     CT
                        TAG  GAGTGTTTT TGGC
                        |||  ||||||||| ||||
                        ATC  CTCACAAAA ATCG
                          CTA        __
GAM217  MAP4K2  3' TGCCAAGAGCCTGCCCCT  1127     A TT
                        AGG GTG TTCTTGGCA
                        ||| ||| |||||||||
                        TCC CGT GAGAACCGT
                          C  CC
GAM217  POLG    3' TGCCAAGAAGATTCCTTCTA 948           GT
                        TAGAAGGA GTTTCTTGGCA
                        |||||||| |||||||||||
                        ATCTTCCT TAGAAGAACCGT
                          __
GAM217  RET     3' TTGCCAAAACTCCTTCT    1920          GTTTTC
                        AGAAGGAGT    TTGGCAA
                        |||||||||    ||||||
                        TCTTCCTCA    AACCGTT
                           A_____
GAM217  SALL2   3' TTGCCAAGAGGTCTCC    2672      TGT
                        GGAG TTTCTTGGCAA
                        |||| |||||||||||
                        CCTC GGAGAACCGTT
                           T__
GAM217  SLC9A1  3' CCAAGGTCTCACACTCCTCCTG 2886     A     TT__
                        TAG AGGAGTGT  TCTTGG
                        ||| ||||||||  ||||||
```

```
                    GTC TCCTCACA   GGAACC
                     C       CTCT
GAM217  ZNF132   5' CCAAGAAAGCTAACTCCT   1020        __
                    AGGAGT  GTTTTCTTGG
                    ||||||  ||||||||||
                    TCCTCA  CGAAAGAACC
                       AT
GAM217  AD-020   3' TTTGCCAAGAAAATCTGGGCCT 1893     AGT__
                    AGG   GTTTTCTTGGCAAA
                    |||   |||||||||||||
                    TCC   TAAAAGAACCGTTT
                     GGGTC
GAM217  AD-020   3' TTTGCCAAGAAAATCTGGGCCT 2524     AGT__
                    AGG   GTTTTCTTGGCAAA
                    |||   |||||||||||||
                    TCC   TAAAAGAACCGTTT
                     GGGTC
GAM217  APOL3    3' CCAAGAAAAACAGTCTCA   1494    A  G   _
                    A GGA TGTTTT CTTGG
                    | ||| |||||| |||||
                    A TCT ACAAAA GAACC
                      C   G      A
GAM217  DJ473B4  3' TTTGCCAAAAAAGTCCCCTA 1881    AA  GTG  C
                    TAG GGA  TTTT TTGGCAAA
                    ||| |||  |||| ||||||||
                    ATC CCT  GAAA AACCGTTT
                     C_  ___     A
GAM217  KIAA0475 3' TTTGCCAAAAGCAGTCCTTC 1571     G    CT
                    GAAGGA TGTTTT TGGCAAA
                    |||||| |||||| |||||||
                    CTTCCT ACGAAA ACCGTTT
                       G      __
GAM217  KIAA1729 3' CCAGGAACACTCCTTC       3458        TT
                    GAAGGAGTGT TCTTGG
                    |||||||||| ||||||
                    CTTCCTCACA AGGACC
                          __
GAM217  PHYHIP   3' CCACCGGGACACTCCCCCTG 1541     AA      CT
                    TAG GGAGTGTTTT TGG
                    ||| |||||||||| |||
                    GTC CCTCACAGGG ACC
                     CC         CC
GAM217  SCAMP-4  3' TGCCAAGAGGCACCCCCTTC 2372     A_   T
                    GAAGG GTGTTT CTTGGCA
                    ||||| |||||| |||||||
                    CTTCC CACGGA GAACCGT
                      CC       _
GAM217  ST6GalNAcl 3' TGCTGAAAAACACTCTTC 1824    G    C TG
                    GAAG AGTGTTTT T GCA
                    |||| |||||||| | |||
```

```
                         CTTC TCACAAAA A  CGT
                         _        _GT
GAM217   TTTY2     5' TGCCAAAAAAACAGGTACTCTT 3396        G  ____        C
         CTA                TAGAAG AGT   GTTTT TTGGCA
                         |||||| |||   ||||| ||||||
                         ATCTTC TCA   CAAAA AACCGT
                           _  TGGA     A
GAM217   LOC126917 3' TTGCCAAGAAAGACCCC   3001     A G
                         GG GT TTTTCTTGGCAA
                         || || ||||||||||||
                         CC CA GAAAGAACCGTT
                            C _
GAM217   LOC128077 3' TTGCTTCTGAAACCCCTCCT 3007        T_    CTT
                         AGGAG GTTTT  GGCAA
                         ||||| |||||  |||||
                         TCCTC CAAAG  TCGTT
                           CC    TCT
GAM217   LOC152485 3' TCACCCAAACACTCCTTC   3171           TCT
                         GAAGGAGTGTTT  TGG
                         ||||||||||||  |||
                         CTTCCTCACAAA  ACT
                              CCC
GAM217   LOC159148 5' TGCCAAAAAAACAGGTACTCTT 3397        G  ____        C
         CTA                TAGAAG AGT   GTTTT TTGGCA
                         |||||| |||   ||||| ||||||
                         ATCTTC TCA   CAAAA AACCGT
                           _  TGGA     A
GAM217   LOC159989 3' GCCAAGAAAAAAGCTCT    3238        G__
                         GGAGT  TTTTCTTGGC
                         |||||  ||||||||||
                         TCTCG  AAAAGAACCG
                           AAA
GAM217   LOC164584 5' TTGCCAAGAAAACAATCT   3250     G
                         GGA TGTTTCTTGGCAA
                         ||| |||||||||||||
                         TCT ACAAAAGAACCGTT
                           A
GAM218   RAG1      3' CCAGTATTAAATTATCC     745           ACTACT
                         GGATAATTTA    ATATTGG
                         ||||||||||    |||||||
                         CCTATTAAAT    TATGACC
                             _____
GAM218   LOC221964 3' GCCAGTAATAGTCAAATTAACC 3628     A    A  CTA
                         GG TAATTT ACTA  TATTGGC
                         || |||||| ||||  |||||||
                         CC ATTAAA TGAT  ATGACCG
                            A    C  A__
GAM219   ADAM12   3' TGACTATGGATAAACTAAA   1030             AT
                         TTTAGTTTATTCATA GTTA
                         |||||||||||||| ||||
```

```
                        AAATCAAATAGGTAT CAGT
                              __
GAM219  KIAA1789 5'  TAACATTATGTGATTCTAAATG 2780       TTTATT
                        TATTTAG    CATAATGTTA
                        ||||||     ||||||||||
                        GTAAATC    GTATTACAAT
                          TTAGT_
GAM220  NR4A2    3'  AACAAACAAAAACTGTTGCTAT 1276       TC__   CTA
           TTC          GAAATAGC  GTTT  TTTGTT
                        ||||||||  ||||  ||||||
                        CTTTATCG  CAAA  AAACAA
                          TTGT  AAC
GAM220  LOC51145 3'  GCAAAAACGAGCTCTTCA    1667     AT      CTAT
                        TGAA AGCTCGTTT   TTGT
                        |||| |||||||||   ||||
                        ACTT TCGAGCAAA   AACG
                          C_       ____
GAM221  HFE     3'  GCAGGTGCTTCAGGATA      738       AC    _
                        TATCCTGA  AGCAT TGC
                        ||||||||  ||||| |||
                        ATAGGACT  TCGTG ACG
                          __     G
GAM221  HFE     3'  GCAGGTGCTTCAGGATA     2464       AC    _
                        TATCCTGA  AGCAT TGC
                        ||||||||  ||||| |||
                        ATAGGACT  TCGTG ACG
                          __     G
GAM221  PKIA    3'  CAATGCTGTATGATACTATTT 1334      A  CTGA
                        AGATA TATC   ACAGCATTG
                        ||||| ||||   |||||||||
                        TTTAT ATAG   TGTCGTAAC
                          C   TA__
GAM221  PLAG1   3'  GCAATGCTATCCATTGATGT   943      C_ AAC
                        ATATC TG  AGCATTGC
                        ||||| ||  |||||||||
                        TGTAG AC  TCGTAACG
                          TT CTA
GAM221  FLJ20371 3'  GCCTATTCAGGATATTAACT 1752     A       CA_
                        AG TAATATCCTGAA  GC
                        || ||||||||||||  ||
                        TC ATTATAGGACTT  CG
                          A        ATC
GAM221  LOC202052 3'  GCATCTGTTCAGGACAACATC 3485    AATA      CAT
                        GAT   TCCTGAACAG  TGC
                        |||   |||||||||| |||
                        CTA   AGGACTTGTC  ACG
                          CAAC       T__
GAM222  EIF2C1   3'  TGCCCTCAAGCTTATACTA 1413        CGTC  A A
                        TAGTATAG   GTTT AG GCA
                        ||||||||   |||| || |||
```

```
                            ATCATATT  CGAA TC CGT
                            ___       C C
GAM222  FMR2     3' CTCTTAAAAAGATGCTATGC  888          G_
                            GTATAGCGTC TTTAAGAG
                            |||||||||| ||||||||
                            CGTATCGTAG AAATTCTC
                                     AA
GAM222  FLJ13612 3' CTCTTAAATACTGTACTA  2146       CGTC
                            TAGTATAG  GTTTAAGAG
                            |||||||| |||||||||
                            ATCATGTC  TAAATTCTC
                                 A___
GAM223  HPS4     5' TGTTTGAACTGGAAACTTCAA  1977        AA  T
                            TTGAAGTTTCCA TTT GATA
                            |||||||||||| ||| ||||
                            AACTTCAAAGGT AAG TTGT
                                 C_  T
GAM223  TEKT1    5' GGAATTTGGAAACCTCAA  2359      A
                            TTGA GTTTCCAAATTTT
                            |||| ||||||||||||
                            AACT CAAAGGTTTAAGG
                                 C
GAM223  LOC145783 3' CGGAATTTGGAAACCCCAG  3082    AA
                            TTG GTTTCCAAATTTTG
                            ||| ||||||||||||
                            GAC CAAAGGTTTAAGGC
                                 CC
GAM223  LOC154321 3' TATTTAGCTTTGGAAACTT  3190        T T
                            AAGTTTCCAAA TT GATA
                            |||||||||| || ||||
                            TTCAAAGGTTT GA TTAT
                                 C  T
GAM224  FEZ1     3' AGGATATGTCCACATAAGAA  1993    _ ATTTT
                            TTCTT TGT  GGCATATCCT
                            ||||| |||  |||||||||
                            AAGAA ACA   CTGTATAGGA
                                 T  C____
GAM224  GOLGA4   5' AGGATATTGAACACAAAGAA  2554     A TGGC
                            TTCTTTGT TTT  ATATCCT
                            |||||||| |||  |||||||
                            AAGAAACA AAG   TATAGGA
                                 C  T___
GAM224  HAS3     3' AGGACAAATCTAAAATGCAAAG 1199         CATA_
            AA            TTCTTTGTATTTTGG   TCCT
                            ||||||||||||| ||||
                            AAGAAACGTAAAATC  AGGA
                                 TAAAC
GAM224  JUN      3' AGGATATTTAAGAAAATACAA 914       GGC__
                            TTGTATTTT  ATATCCT
                            |||||||  ||||||
```

```
                          AACATAAAA   TATAGGA
                             GAATT
GAM224   MADH9    3' ATGTGTAAATACATAGAA  1260      T      TG
                     TTCT TGTATTT  GCATAT
                     |||| ||||||| ||||||
                     AAGA ACATAAA  TGTGTA
                     T        __
GAM224   NR2C2    3' AGGACCGTTCACATACAAAGAA 1007        TTT  ATA
                     TTCTTTGTAT  GGC  TCCT
                     ||||||||| ||| ||||
                     AAGAAACATA  TTG  AGGA
                          CAC  CC_
GAM224   AP1S3    3' AGGACTATAGAAATGCAAAGAA 3010         GGCATA
                     TTCTTTGTATTTT    TCCT
                     |||||||||||    ||||
                     AAGAAACGTAAAG    AGGA
                          ATATC_
GAM224   ARHE     3' ATATGCCAAAAAATGAGAG  1190      TGTA
                     TTCTT  TTTTGGCATAT
                     |||||  ||||||||||
                     GAGAG  AAAACCGTATA
                          TAA_
GAM224   FLJ11000 3' AGGACACATGGGGTACAAAGA 1812        TT GCATA
                     TCTTTGTATT  G   TCCT
                     |||||||||| |   ||||
                     AGAAACATGG  T   AGGA
                          GG ACAC_
GAM224   FLJ11996 5' ATAGATCTAAATACAAAGGA 2120         T  CA
                     TTCTTTGTATTT GG  TAT
                     ||||||||||| || |||
                     AGGAAACATAAA CT ATA
                          T  AG
GAM224   GADD45A  3' AGGAACAAAAATTACAAAGAA 869        T  GGCATA
                     TTCTTTGTA TTT    TCCT
                     ||||||||| |||    ||||
                     AAGAAACAT AAA    AGGA
                          T AACA__
GAM224   HNRPA3   3' AGGATATGATGGTTACAATGAA 1244     T    TTTTGG
                     TTC TTGTA    CATATCCT
                     ||| |||||    ||||||||
                     AAG AACAT    GTATAGGA
                          T   TGGTA_
GAM224   KIAA0179 3' AGAATATGTCACATAAAGAA 2704         ATTT      C
                     TTCTTTGT   TGGCATAT CT
                     ||||||||   |||||||| ||
                     AAGAAATA   ACTGTATA GA
                          C___      A
GAM224   KIAA1831 3' GGAAAAAAATACAAAGAA  2667          GGCATA
                     TTCTTTGTATTTT    TCC
                     |||||||||||||    |||
```

```
                     AAGAAACATAAAA    AGG
                        AA____
GAM224  KLHL4   3' AGGATATGTGTGCTATATAAA 1880        TTTG_
                     TTTGTAT   GCATATCCT
                     |||||||   |||||||||
                     AAATATA   TGTATAGGA
                        TCGTG
GAM224  PANX3   3' AGGATAGTATAAATAAAAAGAA 2350      G   TG A
                     TTCTTT TATTT GC TATCCT
                     |||||| ||||| || ||||||
                     AAGAAA ATAAA TG ATAGGA
                        A   TA _
GAM224  TRAF3   5' ATATGCTAAACAAAAGAA   2541      GTAT
                     TTCTTT  TTTGGCATAT
                     ||||||  ||||||||||
                     AAGAAA  AAATCGTATA
                        AC__
GAM224  TRAF3   3' ATATGCTAAACAAAAGAA   1008      GTAT
                     TTCTTT  TTTGGCATAT
                     ||||||  ||||||||||
                     AAGAAA  AAATCGTATA
                        AC__
GAM224  ZFD25   3' GATTGTACAAATACAAGGAA 1672         TG  T
                     TTCTTTGTATTT GCA ATC
                     |||||||||||| ||| |||
                     AAGGAACATAAA TGT TAG
                        CA  _
GAM224  ZID     3' ATATGCCAAAAGGAA      1315    TTGTA
                     TTCT   TTTTGGCATAT
                     ||||   |||||||||||
                     AAGG   AAAACCGTATA
                        _____
GAM224  LOC151742 5' AGGACTACGAGAAAGACAAAGA 2477      A   GGCATA
          A              TTCTTTGT TTTT    TCCT
                     |||||||| ||||    ||||
                     AAGAAACA AAAG    AGGA
                        G   AGCATC
GAM224  LOC152179 3' TGCTTCAAAATCAAAGAA 3352       T   __
                     TTCTTTG ATTTTG GCA
                     ||||||| |||||| |||
                     AAGAAAC TAAAAC CGT
                        _   TT
GAM224  LOC51266 3' GATATGTATGAATGCAAA   1691       TG
                     TTTGTATTT GCATATC
                     ||||||||| |||||||
                     AAACGTAAG TGTATAG
                        TA
GAM224  LOC90317 5' AGGATACATACTACAGAGAA 2629        TTT GCA
                     TTCTTTGTA TG TATCCT
                     ||||||||| || ||||||
```

```
                        AAGAGACAT  AC  ATAGGA
                        CAT ___
GAM224  LOC90470 3' AGAATATGCTCAATACAAAG  2645        TT     C
                        CTTTGTATT GGCATAT CT
                        |||||||||| ||||||| ||
                        GAAACATAA TCGTATA GA
                        C_        A
GAM224  LOC90786 5' ATATGCCAAAATTGAGA     2678      TGT
                        TCTT ATTTTGGCATAT
                        |||| |||||||||||
                        AGAG TAAAACCGTATA
                        T__
GAM225  ATRX    3' ATCACGTCAGTAAAATACTA  751         T A   C
                        TAGTATTTT CT ACGT GGT
                        |||||||||| || |||| |||
                        ATCATAAAA GA TGCA CTA
                        T C   _
GAM225  ATRX    3' ATCACGTCAGTAAAATACTA  2431        T A   C
                        TAGTATTTT CT ACGT GGT
                        |||||||||| || |||| |||
                        ATCATAAAA GA TGCA CTA
                        T C   _
GAM225  D10S170 3' ATACCATTAGAAAATACTA   1211        T   CGTC
                        TAGTATTTT CTAA  GGTAT
                        |||||||||| ||||   |||||
                        ATCATAAAA GATT   CCATA
                        _  A___
GAM225  RAB27A 3' ACTGTAATTAGAAAAATAC    1128           CGT
                        GTATTTTTCTAA  CGGT
                        |||||||||||||   ||||
                        CATAAAAAGATT  GTCA
                        AAT
GAM225  CYLD    3' AATAGTGGTCAGAAAAATACT  1616          A GT  G
                        AGTATTTTTCT AC  CG TATT
                        |||||||||| ||  || ||||
                        TCATAAAAGA TG  GT ATAA
                        C  __ G
GAM225  LOC145945 5' ATTTATGGTGAGAAAAATAC  3279         AA_ CG
                        GTATTTTTCT  CGT GT
                        |||||||||| |||  ||
                        CATAAAAAGA  GTA TA
                        GTG  TT
GAM225  LOC200273 3' ACCGACGTCAAAAAGTCTG   2895      T    CTA
                        TAG ATTTTT  ACGTCGGT
                        ||| |||||||  ||||||||
                        GTC TGAAAA  TGCAGCCA
                        _   AC_
GAM225  LOC220758 3' GCGATTAGAAAAACACTA    3497      A      _
                        TAGT TTTTTCTAA CGT
                        |||| |||||||| |||
```

```
                            ATCA AAAAGATT GCG
                              C        A
GAM226  KNSL1    3' TTAGTGGTTATTTCTAAAAT 1123              _
                       ATTTTAGAAATAAC ATTAG
                       ||||||||||||| |||||
                       TAAAATCTTTATTG TGATT
                                    G
GAM226  PLAC1    3' TGAAGATGCTATTTCTAGAATT 1960          A   AG
                       AATTTTAGAAATA CATT  CG
                       ||||||||||| |||| ||
                       TTAAGATCTTTAT GTAG  GT
                                  C   AA
GAM226  SCP2     3' CTAATGTTATTTCTTAAAATT 977         _
                       AATTTTA GAAATAACATTAG
                       ||||||| |||||||||||
                       TTAAAAT CTTTATTGTAATC
                             T
GAM226  STIM1    3' GTGTTATTTCATAAAATT   2558         _
                       AATTTTA GAAATAACAT
                       ||||||| ||||||||||
                       TTAAAAT CTTTATTGTG
                             A
GAM226  CORTBP2 3' AATGTTACTTCTAAAATT   2334        A
                       AATTTTAGAA TAACATT
                       |||||||||| |||||||
                       TTAAAATCTT ATTGTAA
                                C
GAM226  VAMP3    3' CTACTGTTATCTCTAAAATT 1156        A    T
                       AATTTTAGA ATAACA TAG
                       ||||||||| |||||| |||
                       TTAAAATCT TATTGT ATC
                              C    C
GAM226  LOC90148 3' TCCTTGTGTTATTTCTAAAA 2603             T C
                       TTTTAGAAATAACAT AG GA
                       ||||||||||||||| || ||
                       AAAATCTTTATTGTG TC CT
                              T _
GAM227  AK2      3' TGAAAAAGGAAGTTGGTTATGC 1449    TACA  __       C
          CA               TGGC   AACT TTTCCTTTT CA
                       ||||   |||| ||||||||| ||
                       ACCG   TTGG GAAGGAAAA GT
                       TA__   TT        A
GAM227  CRTAP    3' GGAAAAGGAAGAAAGCCA   1291      ACAAAC
                       TGGCT    TTTTCCTTTTCC
                       |||||    |||||||||||
                       ACCGA    AGAAGGAAAAGG
                             A_____
GAM227  CXorf6   5' TGGAAAAGTCGGCTTGTAATCA 1218    GC   A TTTC
                       TG TACAA CT   CTTTTCCA
                       || ||||| ||   |||||||||
```

```
                              AC  ATGTT GG   GAAAAGGT
                              TA    C  CT__
GAM227  EPHB2    3' TGGAAAAGAAAAACTGGTGCCA 1113      T  AAAC   C
                              TGGC AC   TTTTC TTTTCCA
                              |||| ||   ||||| |||||||
                              ACCG TG   AAAAG AAAAGGT
                              _  GTCA      _
GAM227  FZD3     3' TGGAAAAATTTTAATTTGTAGC 1717         CTTTTCC
         CA                TGGCTACAAA    TTTTCCA
                              ||||||||||    |||||||
                              ACCGATGTTT    AAAAGGT
                                 AATTTTA
GAM227  HMGA2    3' GAAAAAAAAAGCTTGTGGCCA 1033        A    CC
                              TGGCTACAA CTTTT TTTTC
                              ||||||||| ||||| |||||
                              ACCGGTGTT GAAAA AAAAG
                                 C   A_
GAM227  SLC2A4   3' TGGAAAAGAATCCCTGCAGCC 794      A AACTT  C
                              GGCT CA    TTC TTTTCCA
                              |||| ||    ||| |||||||
                              CCGA GT    AAG AAAAGGT
                                 C CCCT_   _
GAM227  ATP10B   3' AGGGAAAAGTTATAACCA   2654      C CA
                              TGG TA  AACTTTTCCTT
                              ||| ||  |||||||||||
                              ACC AT  TTGAAAAGGGA
                                 A A_
GAM227  BCCIP    3' GAAAAGGAATAGTCA     2369        CAAACTT
                              TGGCTA    TTCCTTTTC
                              ||||||    |||||||||
                              ACTGAT    AAGGAAAAG
                                      _____
GAM227  C20orf30 3' GGAAAAGTGTTGCCTGCCA  1478      TA_  _
                              TGGC  CAA ACTTTTCC
                              ||||  ||| ||||||||
                              ACCG  GTT TGAAAAGG
                                 TCC  G
GAM227  DKFZP564O043 3' GGAAGGGAAAAATTTATAGCTA 3565     C  C
                              TGGCTA AAA TTTTCCTTTTC
                              |||||| ||| |||||||||||
                              ATCGAT TTT AAAAGGGAAGG
                                 A  A
GAM227  FLJ11710 3' TGGAAAGGGGAATCTATGCCA 2097        TACAAACT
                              TGGC    TTTCCTTTTCCA
                              ||||    |||||||||||
                              ACCG    AAGGGGAAAGGT
                                 TATCT___
GAM227  JDD1     3' TGGAAAGGCAAGTTTGTACCCA 2653     C      TTC
                              TGG TACAAACTT CTTTTCCA
                              ||| |||||||||| |||||||
```

```
                    ACC ATGTTTGAA  GGAAAGGT
                     C        C__
GAM227  KIAA0265 3'  GAAAAGGAAAAGGAATAATCA 2871    GC  CAAA
                     TG TA   CTTTTCCTTTTC
                     || ||   |||||||||||
                     AC AT   GAAAAGGAAAAG
                      TA AAG_
GAM227  KIAA0663 3'  GGAAAAGGAAGAAAGCCA   1561      ACAAAC
                     TGGCT   TTTTCCTTTCC
                     |||||   |||||||||||
                     ACCGA   AGAAGGAAAAGG
                            A_____
GAM227  KIAA1010 3'  TGGAAAGGAGAAACTTGCAGTC 2934    A  AC      T
            A                TGGCT CAA TTTTCCTTT CCA
                     ||||| ||| ||||||||| |||
                     ACTGA GTT AAGAGGAAA GGT
                       C  CA      _
GAM227  KIAA1576 3'  GGTCAAAAGTTTGAGCCA   2734      A       __
                     TGGCT CAAACTTTT CC
                     ||||| |||||||||| ||
                     ACCGA GTTTGAAAA GG
                       _        CT
GAM227  KIAA1634 3'  TGAAAAAGGAAAGAAAGTAACC 2658   C AAAC      C
            A                TGG TAC   TTTTCCTTTT CA
                     ||| |||   ||||||||| ||
                     ACC ATG   GAAAGGAAAA GT
                     A  AAA_        A
GAM227  KIAA1798 3'  GAAAGTAAGTTTGTAGC    2575          TTC
                     GCTACAAACTT CTTTT
                     ||||||||||| |||||
                     CGATGTTGAA  GAAAG
                            T__
GAM227  KNSL7    3'  AAAAATAAAAGCCTGTAGCTA 1904       AA   CC
                     TGGCTACA CTTTT TTTT
                     |||||||| ||||| ||||
                     ATCGATGT GAAAA AAAA
                        CC   TA
GAM227  LALP1    3'  GAAATGAAATTTGTAGC    1916       CT  CT
                     GCTACAAA TTTC TTTC
                     |||||||| |||| ||||
                     CGATGTTT AAAG AAAG
                          __  T_
GAM227  MGC2488  3'  GAAAAGGAAGCATGTAGC   2044       AACT
                     GCTACA   TTTCCTTTTC
                     ||||||   ||||||||||
                     CGATGT   GAAGGAAAAG
                        AC__
GAM227  nexilin  3'  AAAAGGAAACCAGGAGTGCCA 2484     T AAA __
                     TGGC AC  CT TTTCCTTTT
                     |||| ||  || |||||||||
```

```
                          ACCG TG  GA  AAAGGAAAA
                          _  AG_  CC
GAM227  NKX2B      3' TGGAAAAGAAAACCCTGTAGGC 934      G    AAC    C
        A                   TG CTACA   TTTTC TTTTCCA
                         || ||||| ||||| |||||||
                         AC GATGT   AAAAG AAAAGGT
                          G    CCC    _
GAM227  STX18      3' TGAAAAAGGAAACAGTGCACAC 1715      CTACAA  _        C
        CA                  TGG    ACT TTTCCTTTT CA
                         |||    ||| ||||||||| ||
                         ACC    TGA AAAGGAAAA GT
                          ACACG_  C       A
GAM227  ZNF271     5' AGTAAAAGTTTTAGCCA      3670      C    C
                         TGGCTA AAACTTTT CT
                         |||||| ||||||||| ||
                         ACCGAT TTTGAAAA GA
                          _       T
GAM227  LOC115207 3' GAAAGTTGGAAGTTTGTACCA 2440    C      CC
                         TGG TACAAACTTTT TTTTC
                         ||| ||||||||||| |||||
                         ACC ATGTTTGAAGG  GAAAG
                          _        TT
GAM227  LOC133482 5' AAAAGGAAAAAAGCCA      3014      ACAAAC
                         TGGCT    TTTTCCTTTT
                         |||||    ||||||||||
                         ACCGA    AAAAGGAAAA
                           A_____
GAM227  LOC147080 5' TGGAAATCGCCAAATTTGTAGC 3290          CTTTTCCT
        CA                  TGGCTACAAA    TTTCCA
                         ||||||||||    ||||||
                         ACCGATGTTT    AAAGGT
                          AAACCGCT
GAM227  LOC147990 3' GAAAAGGAAATAAAAAAGCCA 3295      ACAAACT
                         TGGCT    TTTCCTTTTC
                         |||||    ||||||||||
                         ACCGA    AAAGGAAAAG
                          AAAAAT_
GAM227  LOC149529 3' AAAAGGCAAAAGTTTGCAGC  3134    A      _
                         GCT CAAACTTTT CCTTTT
                         ||| ||||||||| ||||||
                         CGA GTTTGAAAA GGAAAA
                          C    C
GAM227  LOC158130 3' AAAGGAAAATTCTAGCCA    2847      C AC
                         TGGCTA AA  TTTTCCTTT
                         |||||| || |||||||||
                         ACCGAT TT  AAAAGGAAA
                          C  __
GAM227  LOC196478 5' GAAAATGGATTTGTAGC     3413      CTTT  _
                         GCTACAAA  TCC TTTTC
                         ||||||||  ||| |||||
```

```
                           CGATGTTT   AGG AAAAG
                            ____    T
GAM227  LOC219894 3' AGAAGAAAAGTTTGAAACCA 3595      CTA      C
                     TGG  CAAACTTTC TTTT
                     ||| ||||||||| ||||
                     ACC  GTTTGAAAAG AAGA
                      AAA      _
GAM227  LOC219988 5' GAAAGCACAAAATTTGTAGC 3535        C TC_
                     GCTACAAA TTT  CTTTT
                     |||||||| ||| |||||
                     CGATGTTT AAA  GAAAG
                        A  CAC
GAM227  LOC221272 3' GAAAAGGAAAAGTTTACCTGC 3613     TAC_
                     GC  AAACTTTTCCTTTTC
                     || |||||||||||||
                     CG  TTTGAAAAGGAAAAG
                      TCCA
GAM227  LOC221272 3' GAAAAGGAAAGTAGCTA 3614        AAACT
                     TGGCTAC   TTTCCTTTTC
                     |||||||   ||||||||||
                     ATCGATG   AAAGGAAAAG
                          _____
GAM227  LOC245771 5' TGAAAAGGAGAGATCATCAGC 3584       ACAAAC      C
          CA            TGGCT    TTTTCCTTTT CA
                     |||||    |||||||||| ||
                     ACCGA    GAGAGGAAAA GT
                        CTACTA      A
GAM227  LOC253019 3' GGAAAAGGAAGAAAGCCA 3673      ACAAAC
                     TGGCT    TTTTCCTTTTCC
                     |||||    |||||||||||
                     ACCGA    AGAAGGAAAAGG
                        A_____
GAM227  LOC253975 3' GGAAAAGGAAGAAAGCCA 3687      ACAAAC
                     TGGCT    TTTTCCTTTTCC
                     |||||    |||||||||||
                     ACCGA    AGAAGGAAAAGG
                        A_____
GAM227  LOC254873 3' TGGAAAAGAATCCCTGCAGCC 3659     A AACTT  C
                     GGCT CA   TTC TTTTCCA
                     |||| ||   ||| |||||||
                     CCGA GT   AAG AAAAGGT
                        C CCCT_  _
GAM227  LOC51634 3' AAAATGAAACCCTGTAGCCA 1655       AACT   C
                    TGGCTACA   TTTC TTTT
                    ||||||||   |||| ||||
                    ACCGATGT   AAAG AAAA
                       CCC_   T
GAM228  ABCE1   3' AAATATACAGAATGGAA 2532       GCTG
                   TTCCG  TTGTATATTT
                   |||||  |||||||||
```

```
                        AAGGT   GACATATAAA
                        AA__
GAM228  WWP1    3' ATTTAAATACCCCAGCCAAGAA 1345      C_    TTGTA
         A                 TTTC GGCTG   TATTTAAAT
                           |||| |||||   |||||||||
                           AAAG CCGAC   ATAAATTTA
                        AA   CCC__
GAM229  GDF8    3' ATGAAGAATAAACTGATGCTA 1197      C GAG   C
                        TAGCATCG TTT  ATTCT CAT
                        |||||||| |||  ||||| |||
                        ATCGTAGT AAA  TAAGA GTA
                           C  ___   A
GAM229  DIO2    3' TGGAGAGGAAGAAACGCTA 773       ATCG  GAGA
                        TAGC  CTTT  TTCTCCA
                        ||||  ||||  |||||||
                        ATCG  GAAG  GAGAGGT
                           CAAA  ____
GAM229  DIO2    3' TGGAGAGGAAGAAACGCTA 1454      ATCG  GAGA
                        TAGC  CTTT  TTCTCCA
                        ||||  ||||  |||||||
                        ATCG  GAAG  GAGAGGT
                           CAAA  ____
GAM229  FLJ21007 5' ATGAAGAATCTCAGGCTGC 2167    TC  T    C
                        GCA  GCTT GAGATTCT CAT
                        |||  |||| |||||||| |||
                        CGT  CGGA CTCTAAGA GTA
                           __  _    A
GAM229  KIAA0478 3' ATGGAGAAAAAGCAGGGATGCT 1573     ___   GAGA
         A                 TAGCATC  GCTTT  TTCTCCAT
                           |||||||  |||||  ||||||||
                           ATCGTAG  CGAAA  AAGAGGTA
                        GGA    ____
GAM229  KIAA0513 3' GATCTCAAAACAGTGCTA  1535      CGC
                        TAGCAT  TTTGAGATT
                        ||||||  |||||||||
                        ATCGTG  AAACTCTAG
                           ACA
GAM229  KIAA1323 5' ATGGAGAATGGGCTGAAGCGAT 2647        G ___
         GCT                AGCATCGCTTT AG  ATTCTCCAT
                           ||||||||||| ||  |||||||||
                           TCGTAGCGAAG TC  TAAGAGGTA
                           _  GGG
GAM229  P450RAI-2 3' GAGAATCTTGGGGATGCTG  1888     G TT
                        TAGCATC CT  GAGATTCTC
                        ||||||| ||  |||||||||
                        GTCGTAG GG  TTCTAAGAG
                           G  __
GAM229  XYLT1   3' GAAACTCACAAAGCAATGCT 3089     C __  A
                        AGCAT GCTT TGAG TTC
                        ||||| |||| |||| |||
```

```
                      TCGTA CGAA  ACTC AAG
                        A    AC    A
GAM229  LOC143282 3' ATGGAGAATCTCTGGGATAGC 3055     _  G TT
                     GC ATC CT GAGATTCTCCAT
                     || ||| ||  ||||||||||||
                     CG TAG GG  CTCTAAGAGGTA
                       A  _  T_
GAM229  LOC200132 3' ATGGAGAAAATTAGCAATGCTG 3438       C  TT GA
                     TAGCAT GCT GA  TTCTCCAT
                     |||||| ||| ||  ||||||||
                     GTCGTA CGA TT  AAGAGGTA
                       A   __ AA
GAM230  FGFR1     5' CCGCAGCGCGCGGAGGAA     759       GAGA ACA A
                     TTCCTCTG  TG  CT CGG
                     ||||||||   ||   || |||
                     AAGGAGGC  GC  GA GCC
                     ____  GC_  C
GAM230  FGFR1     5' CCGCAGCGCGCGGAGGAA     1647      GAGA ACA A
                     TTCCTCTG  TG  CT CGG
                     ||||||||   ||   || |||
                     AAGGAGGC  GC  GA GCC
                     ____  GC_  C
GAM230  FGFR1     5' CCGCAGCGCGCGGAGGAA     2031      GAGA ACA A
                     TTCCTCTG  TG  CT CGG
                     ||||||||   ||   || |||
                     AAGGAGGC  GC  GA GCC
                     ____  GC_  C
GAM230  FGFR1     5' CCGCAGCGCGCGGAGGAA     2033      GAGA ACA A
                     TTCCTCTG  TG  CT CGG
                     ||||||||   ||   || |||
                     AAGGAGGC  GC  GA GCC
                     ____  GC_  C
GAM230  FGFR1     5' CCGCAGCGCGCGGAGGAA     2035      GAGA ACA A
                     TTCCTCTG  TG  CT CGG
                     ||||||||   ||   || |||
                     AAGGAGGC  GC  GA GCC
                     ____  GC_  C
GAM230  FGFR1     5' CCGCAGCGCGCGGAGGAA     2036      GAGA ACA A
                     TTCCTCTG  TG  CT CGG
                     ||||||||   ||   || |||
                     AAGGAGGC  GC  GA GCC
                     ____  GC_  C
GAM230  ITGB3     3' CCTCTCATTCCAGAGGAA     718        A  CACTAC
                     TTCCTCTGGAG TGA    GG
                     ||||||||||| |||    ||
                     AAGGAGACCTT ACT    CC
                       _   CT____
GAM230  PCSK2     3' GCCATGCAATTCATCCCAGAGG 940        A    CACTAC_
     AA              TTCCTCTGG GATGA    GGC
                     ||||||||| |||||    |||
```

```
                              AAGGAGACC CTACT      CCG
                              _   TAACGTA
GAM230  STK24    3' CCATAGTGCACATATTCCAGG 1038        _  A_    C
                              TCTGGAG ATG  CACTA GG
                              ||||||| |||  ||||| ||
                              GGACCTT TAC  GTGAT CC
                                 A  AC   A
GAM230  TIMP3    5' CCTGCTCTCTCCAGAG     733          T _ CTAC
                              CTCTGGAGA GA CA   GG
                              ||||||||| || ||   ||
                              GAGACCTCT CT GT   CC
                                 _  C ____
GAM230  AF038169 3' GCCAGGGGGCATCTCCAAAGGA 1440      C     ACA AC
          A                   TTCCT TGGAGATG  CT GGC
                              ||||| |||||||||  || |||
                              AAGGA ACCTCTAC  GG CCG
                                  A    GG_ GA
GAM230  CRTAM    3' GCCGCAGTGTCACCTCAGTGGA 1883     T  G A    A
                              TCC CTG AG TGACACT CGGC
                              ||| ||| || ||||||| ||||
                              AGG GAC TC ACTGTGA GCCG
                                T  _  C    C
GAM230  DKFZP564J0863 3' GCCACAGGTTCATATCCAGAGG 2815      G  CA AC
           AA                 TTCCTCTGGA ATGA  CT  GGC
                              ||||||||||| |||| || |||
                              AAGGAGACCT TACT  GA  CCG
                                   A  TG CA
GAM230  FLJ14297 5' GCCATAGAATTCTCTCCAGAAG 2108      C     T CA_  C
           AG                 TTC TCTGGAGA GA  CTA GGC
                              ||| |||||||| ||  ||| |||
                              GAG AGACCTCT CT  GAT CCG
                                 A    _ TAA  A
GAM230  FLJ20508 3' GCTGTTACCATCTCAGAGGAA 1757         G   ACACT
                              TTCCTCTG AGATG   ACGGC
                              |||||||| |||||   |||||
                              AAGGAGAC TCTAC   TGTCG
                                 _  CAT__
GAM230  FLJ23462 3' GCTTCTGTCATCTCCAGAG  2096           CTAC
                              CTCTGGAGATGACA   GGC
                              ||||||||||||||   |||
                              GAGACCTCTACTGT   TCG
                                 CT__
GAM230  LOC126167 3' CCAAGAATTTATCTCCAAAGGA 2998     C     CACTAC
           A                  TTCCT TGGAGATGA    GG
                              ||||| |||||||||    ||
                              AAGGA ACCTCTATT    CC
                                  A    TAAGAA
GAM230  LOC157247 5' CCACAGTGTCATCCCACAG  3200   C A     AC
                              CT TGG GATGACACT GG
                              || ||| ||||||||| ||
```

```
                           GA ACC CTACTGTGA  CC
                            C  _       CA
GAM230  LOC161357 5' CCGTAGTGGCTCCAAAG    3240    C   ATGA
                           CT TGGAG   CACTACGG
                           || |||||   ||||||||
                           GA ACCTC   GTGATGCC
                            A   G___
GAM230  LOC201965 3' CCGTAAATTACTTCAGAG    3455       A  CAC
                           CTCTGGAG TGA   TACGG
                           ||||||||| |||  |||||
                           GAGACTTC ATT  ATGCC
                                _  AA_
GAM230  LOC253758 5' GCCGTCTCACCTCCAAAGG   3723    C   A  CACT
                           CCT TGGAG TGA   ACGGC
                           ||| ||||| |||   |||||
                           GGA ACCTC ACT   TGCCG
                            A   C  C___
GAM230  LOC91661 3' CCACTGCATCTCAGAGGAA    2438       G   A CTAC
                           TTCCTCTG AGATG CA   GG
                           |||||||| ||||| ||   ||
                           AAGGAGAC TCTAC GT   CC
                                 _  _ CA__
GAM231  SPG4    3' AATCTACAGACATTAAACAAT   1595       C   TA
                           ATTGTTTAAT GTTT  TAGATT
                           |||||||||| ||||  ||||||
                           TAACAAATTA CAGA  ATCTAA
                                _   C_
GAM231  KIAA0672 3' AATCTATAAAACAAAACAA    1569       AATC
                           TTGTTT  GTTTTATAGATT
                           ||||||  |||||||||||
                           AACAAA  CAAAATATCTAA
                               A___
GAM231  MGC32104 3' AATCTATAAAGAACTCAAACAA 2495        AATCG
                           TTGTTT  TTTTATAGATT
                           ||||||  |||||||||||
                           AACAAA  GAAATATCTAA
                           CTCAA
GAM231  PRO0082 3' AATCTATGGCTTGATTAAAAAT 1851      G     TT
             A              TATT TTTAATCG TTATAGATT
                           |||| |||||||| |||||||||
                           ATAA AAATTAGT GGTATCTAA
                               _      TC
GAM232  TRAP1   3' GATGACAGCCCCACCTCC    1678       A  A_
                           GGAGGTGG GT  TCGTC
                           |||||||| ||  |||||
                           CCTCCACC CG  AGTAG
                            C  AC
GAM232  ASAH   3' TGGTGAACTCCACCTCC      1098       A  GT
                           GGAGGTGGAGT TC  CA
                           ||||||||||| ||  ||
```

```
                          CCTCCACCTCA AG  GT
                           _          TG
GAM232  CNNM1     3' ATTATTGACTTCACCACACCCC 1913     A   GA  ATC
                          GG GGTG  GT  GTCAATAAT
                          || |||| || |||||||||
                          CC CCAC  CA  CAGTTATTA
                           _         AC  CTT
GAM232  Rab11-FIP2 3' ATTATGCATTACTCCACATCC 1582      G     TC  CA
                          GGA GTGGAGTA  GT  ATAAT
                          ||| |||||||| ||  |||||
                          CCT CACCTCAT  CG  TATTA
                            A       TA __
GAM232  RNF38     3' ATTGAATACTCCATCCC    2009   A       CG
                          GG GGTGGAGTAT  TCAAT
                          || ||||||||||  |||||
                          CC CTACCTCATA  AGTTA

                            _         __
GAM232  LOC152283 3' TGGTCGACATCCCACCTCC 3357       AG A  _
                          GGAGGTGG  T TCG TCA
                          ||||||||  | ||| |||
                          CCTCCACC  A AGC GGT
                               CT C   T
GAM232  LOC160484 5' TATTGGCCTGACAGTCCACCTC 3239         __ ATC
         C                GGAGGTGGA  GT  GTCAATA
                          |||||||||  ||  |||||||
                          CCTCCACCT  CA  CGGTTAT
                              GA  GTC
GAM232  LOC90119  3' ATTATTGACAACACCAT    2600      A  ATC
                          GTGG GT  GTCAATAAT
                          |||| ||  |||||||||
                          TACC CA  CAGTTATTA
                            A A__
GAM233  MTMR2     3' GATCAAAATCATTTGATA    1664             T
                          TATCAGATGATTTTG ATT
                          ||||||||||||||| |||
                          ATAGTTTACTAAAAC TAG

                            _
GAM233  PCDHGA8   5' GATCTAATCTGATCATTTAATA 2227     C      TTGT
                          TAT AGATGATT   ATTAGATC
                          ||| |||||||||  ||||||||
                          ATA TTTACTAG   TAATCTAG
                            A       TC__
GAM233  PCDHGA8   5' GATCTAATCTGATCATTTAATA 1460     C      TTGT
                          TAT AGATGATT   ATTAGATC
                          ||| |||||||||  ||||||||
                          ATA TTTACTAG   TAATCTAG
                            A       TC__
GAM233  PTGES     3' CTAATGATCATCTGA     1162          TTGT
                          TCAGATGATT   ATTAG
                          ||||||||||   |||||
```

```
                        AGTCTACTAG   TAATC
                        ――――
GAM233  SOX11   3' AATCATAATCATCTGATA   991         T T
                        TATCAGATGATT TG ATT
                        ||||||||||| || |||
                        ATAGTCTACTAA AC TAA
                              T _
GAM234  C6      5' TGGGAGGACAAAGGCAGT   3656      A      A_
                        ACT CCTTTGTC CCCA
                        ||| |||||||| ||||
                        TGA GGAAACAG GGGT
                          C    GA
GAM234  CGB     5' ATAAAGCCAGGTACACGAGGCA 770      A  _  C CAA
              G             CT CCTT TGT ACC  CTTTAT
                        || |||| ||| |||  ||||||
                        GA GGAG ACA TGG  GAAATA
                          C   C  _  ACC
GAM234  CUL3    3' AGTTGGGTAACAAAAATGG   1040     CC    C
                        CTA  TTTGT ACCCAACT
                        |||  ||||| ||||||||
                        GGT  AAACA TGGGTTGA
                          AA    A
GAM234  GRINL1A 3' ATAAAGTTACACAAAGGTAGT 2863        CACCC
                        ACTACCTTTGT   AACTTTAT
                        |||||||||||   ||||||||
                        TGATGGAAACA   TTGAAATA
                              CA___
GAM234  PRKG1   3' AGTTGAGAGACAAAGGTA   1283        ACC
                        TACCTTTGTC  CAACT
                        ||||||||||  |||||
                        ATGGAAACAG  GTTGA
                              AGA
GAM234  WHSC1   3' AAAGTTGGGTTGATAGG    2409     TT  _
                        CCT GTCA CCCAACTTT
                        ||| |||| |||||||||
                        GGA TAGT GGGTTGAAA
                          __   T
GAM234  CGB5    5' ATAAAGCCAGGTACACGAGGCA 2311    A  _  C CAA
              G             CT CCTT TGT ACC  CTTTAT
                        || |||| ||| |||  ||||||
                        GA GGAG ACA TGG   GAAATA
                          C   C  _  ACC
GAM234  DDX33   3' ATAAAATTGGGTTCATAAAG 1895      C_    C
                        CTTTGT ACCCAA TTTAT
                        |||||| |||||| |||||
                        GAAATA TGGGTT AAATA
                          CT     A
GAM234  FLJ20296 5' TAAAGCTGGTTAAGGTGGT 1749        TGTCAC  A
                        ACTACCTT    CCA CTTTA
                        ||||||||    ||| |||||
```

```
                        TGGTGGAA    GGT GAAAT
                      TT____   C
GAM234  IRO039700 5' GTGGGGCAGACAAAGGCAG  1858     A     A_   A
                      CT CCTTTGTC CCC AC
                      || |||||||| ||| ||
                      GA GGAAACAG GGG TG
                        C      AC  G
GAM234  KIAA0594 3' ATAAAATTAGGTGACAAGGGT  2706          C C
                      ACCTTTGTCACC AA TTTAT
                      |||||||||||| || |||||
                      TGGGAACAGTGG TT AAATA
                         A A
GAM234  MAL2    3' AGTTGAATGACAAAGCAGT  2343     AC     CC
                      ACT CTTTGTCA CAACT
                      ||| |||||||| |||||
                      TGA GAAACAGT GTTGA
                        C_     AA
GAM234  LOC145622 3' AAAGTTGTGTAAAGTGACGAA  3080          C_____
                      TTTGTCAC    CAACTTT
                      ||||||||    |||||||
                      AAGCAGTG    GTTGAAA
                         AAATGT
GAM234  LOC152982 3' ATAAAGTTACACAAAGGTAGT  3176          CACCC
                      ACTACCTTTGT   AACTTTAT
                      |||||||||||   ||||||||
                      TGATGGAAACA   TTGAAATA
                         CA___
GAM234  LOC256174 5' ATAAAGTTGGATGGAAAGG  3742     G  C
                      CCTTT TCA CCAACTTTAT
                      ||||| ||| ||||||||||
                      GGAAA GGT GGTTGAAATA
                         _  A
GAM235  CALCR   3' GAGGGGAAAAAATTAACTGCTC 854    A  A    _  G
         CA           TG AGTA TTAATTTTT CT CCTC
                      || |||| ||||||||| || ||||
                      AC TCGT AATTAAAAA GG GGAG
                        C  C      A _
GAM235  IL1F9   3' GAAGAAGCAATTACTTCA  1886       AA
                      TGAAGTAATT TTTTTC
                      |||||||||| ||||||
                      ACTTCATTAA AAGAAG
                         CG
GAM235  LTA     3' AGGCAAAAAAATTAAATTATTT 757      _   C
                      AAGTAATT AATTTTT TGCCT
                      |||||||| ||||||| |||||
                      TTTATTAA TTAAAAA ACGGA
                         A   A
GAM235  PPP1R12B 3' AGGCAGGGTCTAACCCTTCA  2229      TAA ATTT
                      TGAAG TTA TTCTGCCT
                      ||||| ||| |||||||||
```

```
                         ACTTC  AAT  GGGACGGA
                         CC_   CT__
GAM235  TFF3      3' GCAGAAAAAATACATTTCA  2661      AAT  A
                         TGAAGT  TA TTTTTCTGC
                         ||||||  ||  |||||||||
                         ACTTTA  AT AAAAAGACG
                           C__   A
GAM235  ZHX1      3' AGGAGAATCAATTCTTCA  1366      T   A
                         TGAAG AATT ATTTTTCT
                         ||||| |||| ||||||||
                         ACTTC TTAA TAAGAGGA
                           _    C
GAM235  DKFZP434C1715 3' AGGCAGAAGGATCACTT    3371      AATTA
                         AAGT    ATTTTTCTGCCT
                         ||||    ||||||||||||
                         TTCA    TAGGAAGACGGA
                           C____
GAM235  FLJ21075  3' GAGGCAGAAAATTCCACTT  2130      AATTAAT
                         AAGT    TTTTCTGCCTC
                         ||||    |||||||||||
                         TTCA    AAAAGACGGAG
                         CCTT___
GAM235  FLJ23556  3' AGGCAGAAGGATCACTT  2101      AATTA
                         AAGT    ATTTTTCTGCCT
                         ||||    ||||||||||||
                         TTCA    TAGGAAGACGGA
                           C____
GAM235  HSD17B7   3' AGGCAGAAGGATCACTT  1682      AATTA
                         AAGT    ATTTTTCTGCCT
                         ||||    ||||||||||||
                         TTCA    TAGGAAGACGGA
                           C____
GAM235  IDN3      3' AGGCAGAAAAACTTGAAATAC 2415      A_  _
                         GTA TTAA TTTTTCTGCCT
                         ||| |||| |||||||||||
                         CAT AGTT AAAAAGACGGA
                          AA   C
GAM235  KIAA1456  3' AGGCAGAAGGATCACTT  2772      AATTA
                         AAGT    ATTTTTCTGCCT
                         ||||    ||||||||||||
                         TTCA    TAGGAAGACGGA
                           C____
GAM235  NXPH3     3' AGACAGAAATGTTACTTC  2727        TAATT   C
                         GAAGTAAT    TTTCTG CT
                         ||||||||    |||||| ||
                         CTTCATTG    AAAGAC GA
                           T____      A
GAM235  PNPASE    3' GAGGCAGAAGAATCACTTCA 2901      AATTA
                         TGAAGT  ATTTTTCTGCCTC
                         ||||||  |||||||||||||
```

```
                    ACTTCA    TAAGAAGACGGAG
                         C____
GAM235  SPRY4    3' AGGCAGAAGAATCACTT   2176      AATTA
                    AAGT    ATTTTTCTGCCT
                    ||||   |||||||||||
                    TTCA    TAAGAAGACGGA
                         C____
GAM235  ZNF33A   3' AGGCAGAAGAATCACTT   3519      AATTA
                    AAGT    ATTTTTCTGCCT
                    ||||   |||||||||||
                    TTCA    TAAGAAGACGGA
                         C____
GAM235  LOC126282 3' AGGCAGGATAATCACTT   2999     A   ATTT
                    AAGT ATTA   TTCTGCCT
                    |||| ||||   ||||||||
                    TTCA TAAT    AGGACGGA
                         C  ____
GAM235  LOC144583 3' AGGCAGGATAATCACTT   3068     A   ATTT
                    AAGT ATTA   TTCTGCCT
                    |||| ||||   ||||||||
                    TTCA TAAT    AGGACGGA
                         C  ____
GAM235  LOC145231 3' AGGCAGGCGAATTACTTCA   3273        AATTTT
                    TGAAGTAATT    TCTGCCT
                    ||||||||||    |||||||
                    ACTTCATTAA    GGACGGA
                          GC____
GAM235  LOC147837 3' AGGCAGGATAATCACTT   3113     A   ATTT
                    AAGT ATTA   TTCTGCCT
                    |||| ||||   ||||||||
                    TTCA TAAT    AGGACGGA
                         C  ____
GAM235  LOC149910 3' GAGACAGAATCTTTAGTTACTT 3141           TTT   C
         CA             TGAAGTAATTAA  TTCTG CTC
                    |||||||||||| ||||| |||
                    ACTTCATTGATT  AAGAC GAG
                          TCT    A
GAM235  LOC158160 3' AGGCAGAAGGATCACTT   2967      AATTA
                    AAGT    ATTTTTCTGCCT
                    ||||   |||||||||||
                    TTCA    TAGGAAGACGGA
                         C____
GAM235  LOC158292 5' AGGCAGAAGAATCACTT   3385      AATTA
                    AAGT    ATTTTTCTGCCT
                    ||||   |||||||||||
                    TTCA    TAAGAAGACGGA
                         C____
GAM235  LOC162333 5' GAAGCAGAAGATACTACTTTA   3401        ATTAAT    C
                    TGAAGTA    TTTTCTGC TC
                    |||||||    |||||||| ||
```

```
                        ATTTCAT    AGAAGACG AG
                        CAT___        A
GAM235  LOC200057 5' GAAGCAGAAAGAGGTTACTT 3437        AA      C
                        AAGTAATT TTTTTCTGC TC
                        |||||||| |||||||| ||
                        TTCATTGG AGAAAGACG AG
                                    A
GAM235  LOC202018 3' GCTTTAAAACTAATTACTTCA 3460         A  TCT
                        TGAAGTAATTA TTTT  GC
                        ||||||||||| ||||  ||
                        ACTTCATTAAT AAAA  CG
                             C  TTT
GAM235  LOC219392 5' GCAGAGGGAACCAGCTTCA  3511       AATTAA
                        TGAAGT   TTTTTCTGC
                        ||||||   |||||||||
                        ACTTCG   AGGGAGACG
                            ACCA__
GAM236  TACC1    3' TAATTGGTAGCCATCTCATG 1285      C   _
                        CGTGA GTGGT ATCAATTA
                        ||||| ||||| ||||||||
                        GTACT TACCG TGGTTAAT
                            C    A
GAM237  EIF4G2   3' AAGCAGAGGCAGTCATTG  827      T  GTAAG
                        CAAT AGAC   TTCTGCTT
                        |||| ||||   ||||||||
                        GTTA TCTG   GAGACGAA
                          _  ACG__
GAM237  PEX12    3' AAGCAAAATACTAATCTAATTG 727          CGTAA  C
              TG             TACAATTAGA   GTT TGCTT
                        ||||||||||   ||| |||||
                        GTGTTAATCT   TAA ACGAA
                            AATCA  A
GAM237  LOC130162 3' AAGCAGAACAGATACCTAATT 3009       AC AA
                        AATTAG GT GTTCTGCTT
                        |||||| || |||||||||
                        TTAATC TA CAAGACGAA
                            CA GA
GAM237  LOC152573 3' AAGCAAAGAAAAATACCTAATT 3172         AC AG_  __
              GTA             TACAATTAG GTA  TTCT GCTT
                        |||||||||| |||  |||| ||||
                        ATGTTAATC CAT  AAGA CGAA
                            __ AAA  AA
GAM238  FACL2    3' AGAGTACATGTATTATAT 1942         TTT A
                        ATGTAATACA TG ACTCT
                        |||||||||| || |||||
                        TATATTATGT AC TGAGA
                            ___ A
GAM238  PTER    3' AGTCAAAATATATTACAT  2154       C    A
                        ATGTAATA ATTTTGA CT
                        |||||||| ||||||| ||
```

```
                         TACATTAT TAAAACT GA
                         A        _
GAM238  ATP6V1G1 3' AGAATTCAAGAACTTGTTACAT 1163         CA_     C
        GTA                 TACATGTAATA  TTTTGAA TCT
                            |||||||||| |||||| |||
                            ATGTACATTGT  AGAACTT AGA
                             TCA       A
GAM238  GFR     3' AGATGCAAATGTATTACTGTA 1423      T       T AAC
                            TACA GTAATACATTT G  TCT
                            |||| ||||||||||| |  |||
                            ATGT CATTATGTAAA C  AGA
                             _       _GT_
GAM238  KIAA0349 3' TTTGGAATGTATCATATGTA 3562        A       TG
                            TACATGT ATACATTT AA
                            ||||||| |||||||| ||
                            ATGTATA TATGTAAG TT
                              C      GT
GAM238  RGS20   3' AAGATGTGACCACTACATGTA 1049        A____
                            TACATGTA   TACATTTT
                            ||||||||   ||||||||
                            ATGTACAT   GTGTAGAA
                              CACCA
GAM238  LOC253573 3' GAGTTCAAAAGTACCACA  3725    AA  A
                            TGT TAC TTTTGAACTC
                            ||| ||| ||||||||||
                            ACA ATG AAAACTTGAG
                             CC _
GAM238  LOC83690 3' AGATGAACTAATGTATTACATT 2203  C         TTGAAC
           A                 A ATGTAATACATT    TCT
                             | ||||||||||||    |||
                             A TACATTATGTAA    AGA
                             T       TCAAGT
GAM239  RBM8A   3' AATGTTCCATTTTTGTTTTC 1186          A_
                            GAAAACAAAAAT GATATT
                            ||||||||||| ||||||
                            CTTTTGTTTTTA TTGTAA
                              CC
GAM239  SLC7A6  3' GTCTGTTTTTGTTCCCGA  1078    AA
                            TCG AACAAAAATAGAT
                            ||| |||||||||||||
                            AGC TTGTTTTTGTCTG
                              CC
GAM239  SEMA3E  3' AGTGTTTATTTCAGTTTTC 1432       AA
                            GAAAAC AAATAGATATT
                            |||||| |||||||||||
                            CTTTTG TTTATTTGTGA
                               AC
GAM239  LOC151201 3' AATGTCATTTTTGTTTTT  3339        A
                            GAAAACAAAAAT GATATT
                            |||||||||||| ||||||
```

```
                    TTTTTGTTTTTA CTGTAA
                          _
GAM239  LOC90979 3' AATAATATTTTTTTTGTTTT  2692          T
                    AAAACAAAAA AGATATTATT
                    ||||||||| ||||||||||
                    TTTTGTTTTT TTTATAATAA

                          _
GAM240  ZIC1    3' CGAATCAAAACAACCCCCACAC 1017     ATAGA  AC
           A              TGT   GG  GTTTTGATTCG
                          |||   ||  ||||||||||
                    ACA   CC  CAAAACTAAGC
                     CACCC  AA
GAM240  KIAA1550 3' CAGGACGTCCTCTACACA     2752       A
                    TGT TAGAGGACGTTTTG
                    ||| |||||||||||||
                    ACA ATCTCCTGCAGGAC
                     C
GAM240  LOC143720 3' TCAAAGCTCCCCTATACA    2568        A  C
                    TGTATAG GGA GTTTTGA
                    ||||||| ||| |||||||
                    ACATATC CCT CGAAACT
                        C  _
GAM240  LOC150848 5' TCAAATCCCTTTTGTCTCTATA 3335       G  TTTT_  C
              CA              TGTATAGAG ACG   GATT GA
                    ||||||||| |||    |||| ||
                    ACATATCTC TGT   CTAA CT
                      _  TTTCC   A
GAM241  MAIL    3' AGTCTTTGTAGATAAA     2194          AC
                    TTTATCTACAG AGACT
                    ||||||||||| |||||
                    AAATAGATGTT TCTGA

                          __
GAM241  LOC151414 3' ATTATTCTTAGATCTGTAGATA 3157        C___  C
                    TATCTACAGA   AGA TAAT
                    ||||||||||   ||| ||||
                    ATAGATGTCT   TCT ATTA
                      AGAT  T
GAM241  LOC155038 3' AGCTATTTGTAGATAAA     3197        C A
                    TTTATCTACAGA AG CT
                    |||||||||||| || ||
                    AAATAGATGTTT TC GA
                         A _
GAM242  CRH     3' TTACTTAGCATGCACAAA   772      A GA
                    TTTGT CA  CTAAGTAA
                    ||||| ||  ||||||||
                    AAACA GT  GATTCATT
                      C  AC
GAM242  C1orf24 3' AAGAATTTTCTGTACA     2351       CTAAGT
                    TGTACAGA    AATTCTT
                    ||||||||    |||||||
```

```
                              ACATGTCT    TTAAGAA
                                  T_____
GAM242  C21orf67 5' AAAGATACTCACCTGTACAAA 2367        ACTA   AT
                        TTTGTACAG   AGTA  TCTTT
                        |||||||||   ||||  |||||
                        AAACATGTC   TCAT  AGAAA
                              CAC_    __
GAM242  KIAA0940 3' AAGAAATGTCTGTACAAA  1585         TAAGTAA
                        TTTGTACAGAC    TTCTT
                        ||||||||||     |||||
                        AAACATGTCTG    AAGAA
                              TA_____
GAM242  LOC158722 3' AAAGAATTATATTGCTGACAAA 3225     A  ACTAA
                        TTTGT CAG   GTAATTCTTT
                        ||||| |||   ||||||||||
                        AAACA GTC   TATTAAGAAA
                            _ GTTA_
GAM242  LOC220705 3' AATGTCTTAGTTGTACAAA  3514        A    TA
                        TTTGTACAG CTAAG  ATT
                        ||||||||| |||||  |||
                        AAACATGTT GATTC  TAA
                              _   TG
GAM243  ACVR1    3' AAGCAAAGATTTCAGTAGA  800     _       A
                        TCT TTGAAATCTTT CTT
                        ||| ||||||||||| |||
                        AGA GACTTTAGAAA GAA
                            T       C
GAM243  CELSR1   3' AAGTAAAATGCAAAGATGT  1486        AAATC
                        ACATCTTTG    TTTACTT
                        |||||||||    |||||||
                        TGTAGAAAC    AAATGAA
                              GTA__
GAM243  GJA1     3' AAGTAGTGGATTCAAAGA  715       A  T
                        TCTTTGAA TC TTACTT
                        |||||||| || ||||||
                        AGAAACTT GG GATGAA
                            A  T
GAM243  PLN      3' AAGTAATTTTTTCAAAGA  945           TCT
                        TCTTTGAAA TTACTT
                        ||||||||| ||||||
                        AGAAACTTT AATGAA
                            TTT
GAM243  CNOT7    3' AAGTAAAGATATAATTAGAGAT 2363      A___
                        ATCTTTGA ATCTTTACTT
                        |||||||| ||||||||||
                        TAGAGATT TAGAAATGAA
                            AATA
GAM243  Grcc9    3' AAGTAAAAATAGTAAGAGATGT 2268     GAA_ C
            T                AACATCTTT  AT TTTACTT
                        ||||||||| || ||||||
```

```
                    TTGTAGAGA   TA AAATGAA
                          ATGA  A
GAM243  KIAA1287 3' AAGTAGAAATCTCAAAGAT  3106        A C
                    ATCTTTGA AT TTTACTT
                    |||||||| || |||||||
                    TAGAAACT TA AGATGAA
                          C  A
GAM243  KIAA1673 3' AAGTGTTTGATTCAGAGATGT 2894          A TT_
                    ACATCTTTGAA TC  TACTT
                    ||||||||||| ||  |||||
                    TGTAGAGACTT AG  GTGAA
                          _ TTT
GAM243  LHFP    3' AAGCAAGGTACCCCCAAAGATG 1248           AAAT__  A
              TT            AACATCTTTG   CTTT CTT
                    ||||||||||    |||| |||
                    TTGTAGAAAC    GGAA GAA
                       CCCCAT   C
GAM243  PDE10A  3' AAGTAGCAGTTCAAAAGATGT 1320          GA  CT
                    ACATCTTT AAT TTACTT
                    |||||||| ||| ||||||
                    TGTAGAAA TTG GATGAA
                          AC  AC
GAM243  TBDN100 3' AAGTAAAGATTTATCTGAT  2135      TTTG
                    ATC   AAATCTTTACTT
                    |||   |||||||||||
                    TAG   TTTAGAAATGAA
                     TCTA
GAM243  LOC149448 3' GTAATTTTCAAAGATG     3310          TCT
                    CATCTTTGAAA  TTAC
                    |||||||||||  ||||
                    GTAGAAACTTT  AATG
                        T__
GAM243  LOC155434 3' AGTGGCGATTCAAAGATG    3375        A T
                    CATCTTTGAA TC TTACT
                    |||||||||| || |||||
                    GTAGAAACTT AG GGTGA
                        _  C
GAM243  LOC221583 3' AAGTATACTACTCTCAAAGGTG 3557          AATCTT__
              T             ACATCTTTGA     TACTT
                    ||||||||||     |||||
                    TGTGGAAACT     ATGAA
                       CTCATCAT
GAM243  LOC54466 3' AAGTGGCAACTGTCAAAGATG 1871         AATCT_
                    CATCTTTGA    TTACTT
                    |||||||||    ||||||
                    GTAGAAACT    GGTGAA
                        GTCAAC
GAM244  MECP2   3' CCAGAGACAAATATTTCTAGA 1167    C     C  AA_
                    TC AGAGATAT TTGT  TGG
                    || ||||||||| ||||   |||
```

```
                        AG TCTTTATA AACA  ACC
                         A     _    GAG
GAM244  ATP10B   3' CCAGGCAATATCTCAGGATA 2655      A     CT  AA
                        TATCC GAGATAT TGT TGG
                        ||||| ||||||| ||| |||
                        ATAGG CTCTATA ACG ACC
                          A      __    G_
GAM244  BDG-29   3' CCATTACAGTGGCCTGGATA 2943       AGA  CT
                        TATCCAG TAT TGTAATGG
                        ||||||| ||| ||||||||
                        ATAGGTC GTG ACATTACC
                           CG_  __
GAM244  GW112    3' CCACTTACTTAGATATCTGCAG 1298      CAG      T_  _
       ATA              TATC  AGATATCT GTAA TGG
                        ||||  |||||||| |||| |||
                        ATAG  TCTATAGA CATT ACC
                         ACG      TT  C
GAM244  HSPB7    3' CCATTACAACAGCTCCAGGA 1498     A_ ATATC
                        TCC GAG   TTGTAATGG
                        ||| |||   |||||||||
                        AGG CTC   AACATTACC
                         AC GAC__
GAM244  KIAA1464 3' CCAGTATTTATCTCTGGA   2813       TCTT  A
                        TCCAGAGATA  GTA TGG
                        ||||||||||  ||| |||
                        AGGTCTCTAT  TAT ACC
                          T___   G
GAM244  KIAA1634 3' CCACCAACTATTTCTGGATA 2656        TC  TAA
                        TATCCAGAGATA TTG  TGG
                        |||||||||||| ||| |||
                        ATAGGTCTTTAT AAC  ACC
                          C_  C__
GAM244  NETO1    3' CCATCATCTCATCTCTGGATG 2463        ATCT  TA
                        TATCCAGAGAT  TG  ATGG
                        |||||||||||  ||  ||||
                        GTAGGTCTCTA  AC  TACC
                         CTCT  __
GAM244  PRO2533  3' CCATTACAAAATGTAATGG  1854     GAG  C
                        CCA  ATAT TTGTAATGG
                        |||  |||| |||||||||
                        GGT  TGTA AACATTACC
                         AA_  A
GAM244  LOC151201 3' TGTAAAATACCTCTGGATA 3343       A  C
                        TATCCAGAG TAT TTGTA
                        ||||||||| ||| |||||
                        ATAGGTCTC ATA AATGT
                           C  A
GAM245  FLJ14124 3' CAAAACGAGTAAAGAGCAG  2099     T TAAAG
                        CT CTT   TACTCGTTTTG
                        || |||   ||||||||||
```

```
                        GA GAG   ATGAGCAAAAC
                          C  AA___
GAM245  FLJ20039  3'  TGGGATAACTACTTTAAAGAA  1735              _____
                        TTCTTTAAAGTA    CTCG
                        |||||||||||    ||||
                        AAGAAATTTCAT    GGGT
                                CAATA
GAM245  FLJ21369  5'  CAAAACCTGAAACTTTAAAGGA  2090          ACTC_
                        TTCTTTAAAGT    GTTTTG
                        ||||||||||    ||||||
                        AGGAAATTTCA    CAAAAC
                              AAGTC
GAM245  KIAA1577 5'  ATGGGTACCCCAGAGAAG  2690          AAA
                        CTTCTTT  GTACTCGT
                        |||||||  ||||||||
                        GAAGAGA  CATGGGTA
                            CCC
GAM245  LOC144524 3'  CAAAACAAGGCATAAAGAAGT  3269          AAGTA  C
                        ACTTCTTTA   CT GTTTTG
                        |||||||||   || ||||||
                        TGAAGAAAT   GA CAAAAC
                            ACG__  A
GAM245  LOC150170 5'  CAAAATGGAACTTTAAAACAGT  3143      TC      A T
            A              TACT  TTTAAAGT C CGTTTTG
                        ||||  |||||||| | |||||||
                        ATGA  AAATTTCA G GTAAAAC
                            CA      A _
GAM245  LOC150175 5'  CAAAATGGAACTTTAAAACAGT  3144      TC      A T
            A              TACT  TTTAAAGT C CGTTTTG
                        ||||  |||||||| | |||||||
                        ATGA  AAATTTCA G GTAAAAC
                            CA      A _
GAM245  LOC150215 5'  CAAAATGGAACTTTAAAACAGT  3145      TC      A T
            A              TACT  TTTAAAGT C CGTTTTG
                        ||||  |||||||| | |||||||
                        ATGA  AAATTTCA G GTAAAAC
                            CA      A _
GAM245  LOC150218 5'  CAAAATGGAACTTTAAAACAGT  3146      TC      A T
            A              TACT  TTTAAAGT C CGTTTTG
                        ||||  |||||||| | |||||||
                        ATGA  AAATTTCA G GTAAAAC
                            CA      A _
GAM246  CCRL1     3'  TGTAACTTCCTGTGAATTTA  1697          G   A C
                        TAAATTCG CAGGAA GT ACA
                        |||||||| |||||| || |||
                        ATTTAAGT GTCCTT CA TGT
                            _    _ A
GAM246  PAFAH1B1 3'  TGTGACTTCCAAGTAGAATTTA  741        G A_  A
                        TAAATTC GC  GGAA GTCACA
                        ||||||| ||  |||| ||||||
```

```
                          ATTTAAG TG  CCTT CAGTGT
                            A  AA        _
GAM246  PSMB9     3' TGACTTTCTTCTCAAACCTGGA 956      AA  C C
                          TCTA  TT GG AGGAAAGTCA
                          |||| || || |||||||||
                          AGGT  AA CT TTCTTTCAGT
                            CC  A  C
GAM246  SLC4A4    3' TGTGACTTTTATGGAATTAAGA 1055     A   GG G
                          TCT AATTC  CA GAAAGTCACA
                          ||| |||||  || |||||||||
                          AGA TTAAG  GT TTTTCAGTGT
                            A    __  A
GAM246  TNFAIP1   3' TGACTTTCCCACAGAGACTGGA 1944     AA  GGCA
                          TCTA TTC   GGAAAGTCA
                          |||| |||   |||||||||
                          AGGT GAG   CCTTTCAGT
                            CA  ACAC
GAM246  CAT56     3' GTGACTTCCCAGCACTAGA 2149     AATTCG A A
                          TCTA    GC GG AAGTCAC
                          ||||    || || |||||||
                          AGAT    CG CC TTCAGTG
                            CA____  A C
GAM246  FLJ10520  3' TGTGACTTTCTGGACCTTAGA 1785     ATTC CA_
                          TCTAA  GG  GGAAAGTCACA
                          |||||  ||  |||||||||||
                          AGATT  CC  TCTTTCAGTGT
                            ____   AGG
GAM246  FLJ14001  5' TGCGACCCCCCTGCCCCGAAT 2081     __   AAA A
                          ATTC GGCAGG  GTC CA
                          |||| ||||||  ||| ||
                          TAAG CCGTCC  CAG GT
                            CC    CCC  C
GAM246  FLJ14917  3' TGTGACTTTCCTGGTGCATCCA 2290     AA T G
          GG              TCT AT CG CAGGAAAGTCACA
                          ||| || || |||||||||||||
                          GGA TA GT GTCCTTTCAGTGT
                            CC  C G
GAM246  KIAA0618  3' TGTGACTTTGCCCCAAATTTG 1564      C CA  _
                          TAAATT GG  GG AAAGTCACA
                          |||||| ||  || |||||||||
                          GTTTAA CC  CC TTCAGTGT
                            A  __  G
GAM246  KIAA1750  3' GACTTTCCCCATTTTAG    2812      TTC CA
                          CTAAA  GG  GGAAAGTC
                          |||||  ||  |||||||||
                          GATTT  CC  CCTTTCAG
                            TA_  __
GAM246  MAGEF1    3' GTGACTTTAAGGATTTAGA 2555         GGCAGG
                          TCTAAATTC   AAAGTCAC
                          |||||||||   ||||||||
```

```
                        AGATTTAGG   TTTCAGTG
                        AA____
GAM246  LOC253017 5' TGACTTTCACCAATTTA    3685      C CAG
                        TAAATT GG  GAAAGTCA
                        |||||| ||  ||||||||
                        ATTTAA CC  CTTTCAGT
                        _ A__
GAM246  LOC51705 3' TGACTTTCCTTAATGTTTA   1674       TCGGC
                        TAAAT   AGGAAAGTCA
                        |||||   ||||||||||
                        ATTTG   TCCTTTCAGT
                         TAAT_
GAM247  BCL11B  3' AATGGTGGGTCTATAAATTGT 2019          AT TT
                        ATAAATTTATA G CGCCATT
                        |||||||||| | ||||||
                        TGTTTAAATAT T GTGGTAA
                        C_ GG
GAM247  FGFR4   3' AATGGCGTTTTATAAATT   2022       TGTT
                        AATTTATAA  CGCCATT
                        |||||||||  ||||||
                        TTAAATATT  GCGGTAA
                        TT__
GAM247  FGFR4   3' AATGGCGTTTTATAAATT   887       TGTT
                        AATTTATAA  CGCCATT
                        |||||||||  ||||||
                        TTAAATATT  GCGGTAA
                        TT__
GAM247  FLJ22833 3' AATGGCCGGGGACTTATAAAT 2015       T  ___
                        ATTTATAA GTTC  GCCATT
                        |||||||| ||||  ||||||
                        TAAATATT CAGG  CGGTAA
                        _ GGC
GAM247  SSH2    3' AATGGCCGGCTCTGCAAATTTA 2625       A AT TC
          T              ATAAATTT TA GT GCCATT
                        |||||||| || || ||||||
                        TATTTAAA GT CG CGGTAA
                        C CT GC
GAM248  RARB   3' TTCACAAGCCATTAGGGA   792      AA  C
                        TCCCTAAT CTT GTGAA
                        |||||||| ||| |||||
                        AGGGATTA GAA CACTT
                        CC  _
GAM248  RARB   3' TTCACAAGCCATTAGGGA   1663       AA  C
                        TCCCTAAT CTT GTGAA
                        |||||||| ||| |||||
                        AGGGATTA GAA CACTT
                        CC _
GAM248  BTN2A2  3' CACTTAGAAGTTATTGAGGA 1344      C        ___
                        TCC TAATAACTTC  GTG
                        ||| |||||||||| |||
```

```
                        AGG GTTATTGAAG  CAC
                         A       ATT
GAM248  ZNF337     3' TTACCTGGGCTATTGGGGA  2806        A_ TC
                      TCCCTAATA CT GTGA
                      |||||||| || ||||
                      AGGGGTTAT GG CATT
                          CG TC
GAM248  LOC139231  3' TCACTTGAGAAGTTGTTAGG  3021           ____
                      CCTAATAACTTC  GTGA
                      ||||||||||||  ||||
                      GGATTGTTGAAG   CACT
                          AGTT
GAM248  LOC221399  5' CACTCAAGTCATTAGGGA  3622       A   C_
                      TCCCTAAT ACTT GTG
                      |||||||| |||| |||
                      AGGGATTA TGAA  CAC
                          C   CT
GAM249  DKFZp762E1511 3' AGGTTGGAAATGCACTGAA  2530      C  AT
                      TTCAG GTG TTTCCAACCT
                      ||||| ||| ||||||||||
                      AAGTC CGT AAAGGTTGGA
                        A  __
GAM249  LOC123591  5' AGGTTGGAAAAGGCTCCGC  3032      T ___
                      GCG GA  TTTTCCAACCT
                      ||| ||  |||||||||||
                      CGC CT  AAAAGGTTGGA
                       _  CGG
GAM250  EFNB2      3' GTTGAAAAGCCAAAGGT   1085      C    TTA
                      GCCT TGGCTTT  TCAGC
                      |||| |||||||  |||||
                      TGGA ACCGAAA  AGTTG
                        A      ___
GAM250  FACL4      5' AGGCTTTCAAAAGCCAAAG  2025    C     TATC
                      CT TGGCTTTT  AGCCT
                      || ||||||||  |||||
                      GA ACCGAAAA   TCGGA
                        A     CTT_
GAM250  GATA2      3' AGGCTGGGCTGAGCCAAAGC  892    CTC    TTTA
                      GC TGGCTT  TCAGCCT
                      || ||||||  |||||||
                      CG ACCGAG   GGTCGGA
                       AA_    TCG_
GAM250  IRS2       3' CTGATAAAAAGAGGC    2540        GGCT
                      GCCTCT  TTTTATCAG
                      ||||||  |||||||||
                      CGGAGA   AAAATAGTC
                               ____
GAM250  PAH        5' AGGCCCTAAAAAGCCAGAG  725             TCA
                      CTCTGGCTTTTTA GCCT
                      ||||||||||||| ||||
```

```
                         GAGACCGAAAAAT  CGGA
                              CC_
GAM250  PODXL     3' GCTGCACAGGAGGCCAGA  1207          AT_
                         TCTGGCTTTTT  CAGC
                         ||||||||||| ||||
                         AGACCGGAGGA  GTCG
                              CAC
GAM250  RPL15     3' GCTGGTGAGCCAGTGGC   973      T    TTT
                         GCC CTGGCTT  ATCAGC
                         ||| ||||||| ||||||
                         CGG GACCGAG  TGGTCG
                          T      ___
GAM250  SERPINE1 3' AGGCTGGTGACAGGCCAAAGGC 758      C    T
                         GCCT TGGCTT TTATCAGCCT
                         |||| |||||| ||||||||||
                         CGGA ACCGGA AGTGGTCGGA
                             A    C
GAM250  ABIN-2    3' GCTTAAGCCAGAGCTA    2057     C     TTTATC
                         TAGC TCTGGCTT    AGC
                         |||| ||||||||    |||
                         ATCG AGACCGAA    TCG
                          _      T_____
GAM250  C20orf48  5' GGCCGAGGGACAAAGGCTA  2118       C G TTTA A
                         TAGCCT TG CTT   TC GCC
                         |||||| || |||   || |||
                         ATCGGA AC GGG   AG CGG
                             A A ____  C
GAM250  C9orf7    3' AGACTGGCTTAAGCCAGGAGC 1724    CT    TTTA  C
                         GC CTGGCTT  TCAG CT
                         || ||||||| |||| ||
                         CG GACCGAA  GGTC GA
                          AG     TTC_  A
GAM250  DUSP10    3' CTGACAAATTAAGGAGGTTA  1364          GGCTT  A
                         TAGCCTCT   TTT TCAG
                         ||||||||   ||| ||||
                         ATTGGAGG   AAA AGTC
                          AATT_  C
GAM250  DUSP10    3' CTGACAAATTAAGGAGGTTA  2501          GGCTT  A
                         TAGCCTCT   TTT TCAG
                         ||||||||   ||| ||||
                         ATTGGAGG   AAA AGTC
                          AATT_  C
GAM250  ERMAP     3' GCTGATGGTCCTGTCCAAAGGC 1838        C  _TTT_
            TA              TAGCCT TGG C   TTATCAGC
                         |||||| ||| |  |||||||||
                         ATCGGA ACC G   GGTAGTCG
                          A  T TCCT
GAM250  FLJ12892 3' GCTGATAAAGAAGTGCTA    2802    CT GGC       C
                         TAGC CT  TTTTTATCAG C
                         |||| || ||||||||||| |
```

```
                        ATCG  GA   AGAAATAGTC G
                        T_  ___            A
GAM250  FLJ22059  5' GACTGGAGAGCCAGAGGC   2003              _
                        GCCTCTGGCTTTTTA TC
                        |||||||||||||| ||
                        CGGAGACCGAGAGGT AG
                                 C
GAM250  HEMK     3' GGCCAAAGCCAGAGACT    1669    C      TTATCA
                        AG CTCTGGCTTT    GCC
                        || |||||||||     |||
                        TC GAGACCGAAA    CGG
                           A     C_____
GAM250  KIAA0227 3' GGGCCCCAAAAGACCAGAGGC 2578        _  TATCA
                        GCCTCTGG CTTTT   GCCT
                        |||||||| |||||   ||||
                        CGGAGACC GAAAA   CGGG
                             A    CCC__
GAM250  KIAA0527 3' GAATAAAAGCCAGAGACTG  3684    C       TA
                        TAG CTCTGGCTTTT  TC
                        ||| |||||||||||  ||
                        GTC GAGACCGAAAA  AG
                          A     TA
GAM250  KIAA1244 3' AGGCTTCAGTAAAGCAGAGGCT 2930          G  TTATC
           A                TAGCCTCTG CTTT   AGCCT
                            ||||||||| ||||   |||||
                            ATCGGAGAC GAAA    TCGGA
                             _  TGACT
GAM250  KIAA1649 3' TGAAAAAAACCAGAGACT   2771    C    C    A
                        AG CTCTGG TTTTT TCA
                        || |||||| ||||| |||
                        TC GAGACC AAAAA AGT
                          A   _  A
GAM250  KIAA1981 3' AGGCCACGGGAGCCGAGGC   3431      T    TATCA
                        GCCTC GGCTTTT   GCCT
                        ||||| |||||||   ||||
                        CGGAG CCGAGGG   CGGA
                          _   CAC__
GAM250  MGC2306  3' AGGCTGGGCTGAGCCAAAGC 2266   CTC    TTTA
                        GC TGGCTT  TCAGCCT
                        || ||||||  |||||||
                        CG ACCGAG  GGTCGGA
                        AA_    TCG_
GAM250  RPL39L   5' GTGGGAAAAAAGCAGAGGC   2352        G    A A
                        GCCTCTG CTTTTT TC GC
                        ||||||| |||||| || ||
                        CGGAGAC GAAAAA GG TG
                          _    A G
GAM250  SNPH     3' CTGAAAAAGCCAGAGGC    1531           TA
                        GCCTCTGGCTTTT TCAG
                        ||||||||||||| ||||
```

```
                        CGGAGACCGAAAA AGTC
                              __
GAM250  TMG3      3' GCCCCCGGGAAGAGCCAAAGGC 2053      C       ATCA__
                    GCCT TGGCTTTTT    GC
                    |||| ||||||||    ||
                    CGGA ACCGAGAAG    CG
                     A       GGCCCC
GAM250  LOC145240 3' GCTCGAAAAGGCAAAGGCTA 3076      C G    ATC
                    TAGCCT TG CTTTT  AGC
                    |||||| || ||||||  |||
                    ATCGGA AC GAAAAG  TCG
                      A  G    C__
GAM250  LOC146287 5' AGGCTGAACAGCAAACCCAGAG 3284        C  TTA__
         GC              GCCTCTGG TTT   TCAGCCT
                    ||||||||| |||   |||||||
                    CGGAGACC AAA   AGTCGGA
                       C  CGACA
GAM250  LOC148696 5' AGACTGTACAGGAAACCTAAGG 3301      CT C   AT_  C
          C              GCCT GG TTTTT  CAG CT
                    |||| || |||||  ||| ||
                    CGGA CC AAGGA  GTC GA
                     AT A    CAT  A
GAM250  LOC150577 3' AGGCCGACAACCACCAGAAGCT 3330      C    CTTTTTA A
          G              TAGC TCTGG    TC GCCT
                    |||| |||||    || ||||
                    GTCG AGACC    AG CGGA
                     A    ACCAAC_ C
GAM250  LOC151521 3' TGTTTAAAAACCCAAAGGC  3347      C  C   T_
                    GCCT TGG TTTTTA CA
                    |||| ||| ||||||| ||
                    CGGA ACC AAAAAT GT
                     A   C   TT
GAM250  LOC157273 5' AGGCTGGATGAAGCCAGGGGCT 3379              TTA
          A              TAGCCTCTGGCTTT  TCAGCCT
                    ||||||||||||  |||||||
                    ATCGGGGACCGAAG  GGTCGGA
                      TA_
GAM250  LOC163682 5' GAGCCAAAAGCCAGAGCCTA 3398      C      TA_
                    TAG CTCTGGCTTTT  TC
                    ||| ||||||||||  ||
                    ATC GAGACCGAAAA  AG
                     C      CCG
GAM250  LOC221749 3' GCTGAGGTCACAGCCGGAGGC 3549           TTTTA_
                    GCCTCTGGCT    TCAGC
                    ||||||||||    |||||
                    CGGAGGCCGA    AGTCG
                       CACTGG
GAM250  LOC222234 3' AGGCTGATGCCCCAAAAGGC 3646      C_ CTTTT
                    GCCT TGG   TATCAGCCT
                    |||| |||    |||||||||
```

```
                              CGGA ACC   GTAGTCGGA
                              AA  CC___
GAM251   ADAMTSL1 3' AACCATTAGAGGTGCAATCTAC 2479     _  CA_ TTA
          A                  TG AGAT  ACT  TCTAATGGTT
                             || |||| ||| |||||||||
                             AC TCTA TGG  AGATTACCAA
                              A   ACG  ___
GAM251   KIAA1862 3' AACCACCAGCCGTTCCTGATCT 2834       ACTTTAT AA
          CA                  TGAGATCA   CT TGGTT
                             |||||||| ||  |||||
                             ACTCTAGT   GA ACCAA
                              CCTTGCC CC
GAM251   LOC153951 5' AACCATGAAAGACAGAGTTGAT 3184           A  A__
          CTCA                TGAGATCAACTTT TCT  ATGGTT
                             ||||||||||| ||| |||||
                             ACTCTAGTTGAGA AGA  TACCAA
                               C  AAG
GAM251   LOC221596 3' AACCATTAGACAAAACTCTTCT 3548    TCAAC  A
          AGA   TTT TCTAATGGTT
                             |||   ||| |||||||||
                             TCT   AAA AGATTACCAA
                              TCTCA  C
GAM252   ESAM    3' CTTTACTGTGGGAAAACCATCT 2461    GA  A    AC
          CA                  TG AT GTTTTTT TAGTAAAG
                             || || ||||||| ||||||||
                             AC TA CAAAAGG GTCATTTC
                              TC  C    GT
GAM252   KIAA0379 3' ACTAAGAAAACTATTTCA    2809           AC
                              TGGAATAGTTTTTT TAGT
                             ||||||||||||| ||||
                             ACTTTATCAAAGA ATCA
                                     __
GAM252   LOC161784 3' CTTTAATTTTAAAAAACGTATT 3241     _      CTAG
          CCA                 TGGAATA GTTTTTTA  TAAAG
                             ||||||| |||||||   |||||
                             ACCTTAT CAAAAAAT   ATTTC
                               G      TTTA
GAM252   LOC255229 3' CTTTAATTTTAAAAAACGTATT 3676     _      CTAG
          CCA                 TGGAATA GTTTTTTA  TAAAG
                             ||||||| |||||||   |||||
                             ACCTTAT CAAAAAAT   ATTTC
                               G      TTTA
GAM253   HIP2   3' TGTTTTTAACATGGATC    1201    G
                              GAT CCATGTTAAAAATG
                             ||| |||||||||||||
                             CTA GGTACAATTTTTGT
                                      _
GAM253   ITK    3' TATTTTTAACATGAATC    1224    GC
                              GAT CATGTTAAAAATG
                             ||| ||||||||||||
```

```
                        CTA GTACAATTTTTAT
                        A_
GAM253  ONECUT1  3' GCGGACATCTTTTAAGAT    2622      G      _
                        AT TTAAAA ATGTCCGC
                        || |||||| |||||||||
                        TA AATTTT TACAGGCG
                            G     C
GAM253  BTN3A2   5' GACATTTTTGGCAGAGCAT    1354      CA
                        ATGC TGTTAAAAATGTC
                        |||| |||||||||||||
                        TACG ACGGTTTTTACAG
                             AG
GAM253  BTN3A3   5' GACATTTTTGGCAGAGCAT    1343      CA
                        ATGC TGTTAAAAATGTC
                        |||| |||||||||||||
                        TACG ACGGTTTTTACAG
                             AG
GAM253  IDN3     3' GGCAAACATTTTTGTGG      2416      GTT     CC
                        CCAT AAAAATGT GCC
                        |||| |||||||| |||
                        GGTG TTTTTACA CGG
                        ___         AA
GAM253  KIAA1635 3' CGGACATTTATTTGCATC     2803      CAT TAA
                        GATGC GT AAATGTCCG
                        ||||| || |||||||||
                        CTACG TA TTTACAGGC
                        TT_ ___
GAM253  LOC130106 3' GGCAAACACCTGACATGGCA  3008         AAAA CC
                        TGCCATGTTA TGT GCC
                        |||||||||| ||| |||
                        ACGGTACAGT ACA CGG
                        CC__ AA
GAM253  LOC151031 3' GGCATCTTAACATGGCATT   3403         AA
                        GATGCCATGTTAA ATGTC
                        ||||||||||||| |||||
                        TTACGGTACAATT TACGG
                        C_
GAM253  LOC162545 3' GGCATCTACATGGCATC     3402         TAAAA
                        GATGCCATGT ATGTC
                        |||||||||| |||||
                        CTACGGTACA TACGG
                        TC___
GAM253  LOC165666 5' GGCAGGGTTTTTAAATAGCATC 3257        CATG     GT _
                        GATGC TTAAAAAT CC GCC
                        ||||| |||||||| || |||
                        CTACG AATTTTTG GG CGG
                        ATA_      __ A
GAM254  MEN1     5' AATGACTTGGGGATGATGC    3599         A
                        GCATCATCTTTAG TCATT
                        ||||||||||||| |||||
```

```
                              CGTAGTAGGGGTT AGTAA
                                    C
GAM254   SRD5A2     5' AATTAATGATGAGGTTACATGC 2525      C__     TAG
           T                    AGCAT  ATCTT  ATCATTAATT
                                |||||  |||||  ||||||||||
                                TCGTA  TGGAG  TAGTAATTAA
                                  CAT         ___
GAM254   DKFZP564O043 3' TGATGTCTGAAGATAATGCT 3566      C       T
                                AGCAT ATCTTTAGA CATTA
                                ||||| ||||||||| |||||
                                TCGTA TAGAAGTCT GTAGT
                                    A        _
GAM254   FLJ22794   5' AATTAATGACAGCTTTGAAGAT 3533          ____
                                ATCTTTAGA   TCATTAATT
                                |||||||||   |||||||||
                                TAGAAGTTT   AGTAATTAA
                                   CGAC
GAM254   HTMP10     3' AATTGTTATCTAAAGATGATTC 2322    C        CAT
           T                   AG ATCATCTTTAGAT  TAATT
                               || |||||||||||||  |||||
                               TC TAGTAGAAATCTA  GTTAA
                                  T          TT_
GAM254   SEC24B     3' AATTAATGGTAACGATGATGCT 1288         TTTAG
                                AGCATCATC   ATCATTAATT
                                |||||||||   ||||||||||
                                TCGTAGTAG   TGGTAATTAA
                                   CAA__
GAM254   LOC196812  5' AATGATCTAGTCAGAAGCT   3466    A ATCT
                                AGC TC   TTAGATCATT
                                ||| ||   ||||||||||
                                TCG AG   GATCTAGTAA
                                  A  ACT_
GAM255   ATRN       3' TAAGGGAGGTCTGTGCATTTTA 2480      A AAT  A
                                TAAAAT CA  GAC TTCCCTTA
                                |||||| ||  ||| ||||||||
                                ATTTTA GT  CTG GAGGGAAT
                                   C  GT_  _
GAM255   CD59       3' AATGACATTTGTATTTTA   760          A
                                TAAAATACAAATG CATT
                                ||||||||||||| ||||
                                ATTTTATGTTTAC GTAA
                                      A
GAM255   CENTD1     3' GGATCATTTGTATTTTG    1615          CAT
                                TAAAATACAAATGA  TCC
                                ||||||||||||||  |||
                                GTTTTATGTTTACT  AGG
                                      ___
GAM255   CENTD1     3' GGATCATTTGTATTTTG    2474          CAT
                                TAAAATACAAATGA  TCC
                                ||||||||||||||  |||
```

```
                        GTTTTATGTTTACT  AGG
                        ___
GAM255  CLNS1A   3' GAGGGTATTTGTAGTTTA    816      A       ACATT
                   TAAA TACAAATG    CCCTT
                   |||| ||||||||    |||||
                   ATTT ATGTTTAT    GGGAG
                        G           _____
GAM255  NDUFA5   3' AGTGTCATTTTATTTTA     1169         C
                   TAAAAATA AAATGACATT
                   |||||||| ||||||||||
                   ATTTTAT TTTACTGTGA

                        _
GAM255  PBX3     3' GGAATCATAATCATTTGTATTT 1279           C____
                   AAATACAAATGA    ATTCC
                   |||||||||||||   |||||
                   TTTATGTTTACT    TAAGG
                        AATAC
GAM255  SCD      3' TAAGGGAAGATCACTGTAGTTT 1178    A   AA  CA
            A             TAAA TACA TGA TTCCCTTA
                   |||| |||| ||| ||||||||
                   ATTT ATGT ACT AAGGGAAT
                        G   C_  AG
GAM255  SLC2A2   3' TAAGGGAACCGTCTGTTTTA   731      T  AAT  A_
                   TAAAA ACA  GAC TTCCCTTA
                   ||||| |||  ||| ||||||||
                   ATTTT TGT  CTG AAGGGAAT
                        _  ___  CC
GAM255  TCF7     3' TAAGGGAATCCCTTGTA      998       AT CA
                   TACAA GA TTCCCTTA
                   ||||| || ||||||||
                   ATGTT CT AAGGGAAT
                        CC  __
GAM255  DKFZP586B0923 3' AAGACATGTGATTTGTATTTTA 3589         G  TCC
                   TAAAATACAAAT ACAT  CTT
                   |||||||||||| ||||  |||
                   ATTTTATGTTTA TGTA  GAA
                        G   CA_
GAM255  DKFZp761K1824 3' TAAGAGAATGTTGTGTATTT 1726        AA      C
                   AAATACA TGACATTC CTTA
                   ||||||| |||||||| ||||
                   TTTATGT GTTGTAAG GAAT
                        __          A
GAM255  FLJ14624 3' TAAGGAAATATTTATTTGTATT 2913          C_  C
            TT          AAAATACAAATGA ATT CCTTA
                   ||||||||||||| ||| |||||
                   TTTTATGTTTATT TAA GGAAT
                        TA  A
GAM255  GRO3     3' TAAGGGAATGTATGTA       2636       AATG
                   TACA   ACATTCCCTTA
                   ||||   ||||||||||
```

```
                              ATGT    TGTAAGGGAAT
                                A___
GAM255  KIAA0907 3' AAGAAAGTTTTATTTGTATTTT 1596          C  CC
          A                TAAAATACAAATGA ATT CTT
                           ||||||||||||| ||| |||
                           ATTTTATGTTTATT TGA GAA
                              T  AA
GAM255  MGC14289 3' AAGGATACTGTCATTGCATTT 2382      A      TTC_
          T                AAAAT CAAATGACA   CCTT
                           ||||| |||||||||   ||||
                           TTTTA GTTTACTGT   GGAA
                              C     CATA
GAM255  NLP_1   3' AAGGGAATTTTTTTGTA     1395       T C
                           TACAAA GA ATTCCCTT
                           |||||| || |||||||||
                           ATGTTT TT TAAGGGAA
                              T _
GAM255  PARVA   3' GAGTGCTCCTTTTGTATTTTA 1802           T_  _
                           TAAAATACAAA GA CATTC
                           ||||||||||| || |||||
                           ATTTTATGTTT CT GTGAG
                              TC  C
GAM255  PRO2176 3' AAGGGCTGCATTGTATTTTA 1833        A A TT
                           TAAAATACAA TG CA  CCCTT
                           |||||||||| || || |||||
                           ATTTTATGTT AC GT  GGGAA
                              _ _ C_
GAM255  TIMM22  3' AAGGTTGGTTTATTTGTATTTT 3104          _ ATTC
          A                TAAAATACAAATGA C   CCTT
                           ||||||||||||| |   ||||
                           ATTTTATGTTTATT G   GGAA
                              T GTT_
GAM255  LOC143914 5' GAGGGAGTCATTTTATT    3061      C    AT
                           AATA AAATGAC TCCCTT
                           |||| |||||||| ||||||
                           TTAT TTTACTG AGGGAG

                              _   __
GAM255  LOC154862 3' AAGGGTGAAATTTGTGTTTTA 3193          GA TT
                           TAAAATACAAAT CA CCCTT
                           |||||||||||| || |||||
                           ATTTGTGTTTA GT GGGAA
                              AA __
GAM255  LOC158314 3' AAGGGAATGTTTAAGCCATTT 3386      ACAAAT
                           AAAT   GACATTCCCTT
                           ||||   |||||||||||
                           TTTA   TTGTAAGGGAA
                             CCGAAT
GAM255  LOC221405 3' AAGGGACTATTTGTATT    3623       ACAT
                           AATACAAATG TCCCTT
                           |||||||||| ||||||
```

```
                              TTATGTTTAT   AGGGAA
                              C___
GAM256  YES1     3' ATGATGAATTTATCAGCGT  1209     A      CCG
                           AC CTGATAAA  CATTAT
                           II IIIIIIII   IIIIII
                           TG GACTATTT  GTAGTA
                              C     AA_
GAM256  ACTR3    3' GATGGGATTTATCAGTGT   1238            _  G
                        ACACTGATAAA CC CATT
                        IIIIIIIIIII II IIII
                        TGTGACTATTT GG GTAG
                                 A _
GAM256  GENX-3414 3' CAGATAATGCTTCCAGTG   1073    ATAAACC
                           CACTG     GCATTATCTG
                           IIIII     IIIIIIIIII
                           GTGAC     CGTAATAGAC
                              CTT____
GAM256  HT007    3' ACAGATAATAAATATCCAGTGT 1832     _ AACCGC
                        ACACTG ATA    ATTATCTGT
                        IIIIII III    IIIIIIIII
                        TGTGAC TAT    TAATAGACA
                              C AAA___
GAM256  SPRY4    3' ACAGACAATGCAGGGGCAG   2175    ATAAA _   A
                           CTG   CC GCATT TCTGT
                           III   II IIIII IIIII
                           GAC   GG CGTAA AGACA
                           GG___ A   C
GAM257  POF1B    3' GAACCATGCTGCTACCCAA   2114          _ TG A
                        TTGGGTAGT GT ATG TTC
                        IIIIIIIII II III III
                        AACCCATCG CG TAC AAG
                            T __ C
GAM257  RODH-4   5' CATGGGTAGCTACCCAATAAG 1050             GT_ G
                        TTTATTGGGTAGT T ATG
                        IIIIIIIIIIII I III
                        GAATAACCCATCG  G TAC
                           ATG G
GAM257  SFRS12   3' GAATCATTGGGACTACCCA   2472        G TG
                        TGGGTAGT T ATGATTC
                        IIIIIIIII I IIIIIII
                        ACCCATCA G TACTAAG
                           G GT
GAM257  TCBAP0758 3' GAATCCCCAACACCCAATAAA 2181        AGT   AT
                        TTTATTGGGT GTTG GATTC
                        IIIIIIIIII IIII IIIII
                        AAATAACCCA CAAC CTAAG
                               ___ CC
GAM258  HYOU1    3' CTCTGTTTTCCCCATTCA    2537    T  TA
                        C AGTG  GAAAACAGAG
                        I IIII  IIIIIIIII
```

```
                            A TTAC  CTTTTGTCTC
                            C   CC
GAM258  ITGB1    3' ATCTTGTTTCACACTAGT   910        A    A  G
                            ACTAGTGT GAAA CA AGAT
                            IIIIIIII IIII II IIII
                            TGATCACA CTTT GT TCTA
                                      _   _ _
GAM258  MAGEA4   3' TATCTCTGTTTCCTTTTACA   922           ___
                            TGTAGAA  AACAGAGATA
                            IIIIIIII  IIIIIIIIII
                            ACATTTT  TTGTCTCTAT
                                 CCT
GAM258  PTTG1IP  3' ATCTCTGTTTCTAGATTTAGT 1100       _ G    A
                            ACTAG T TAGAAA CAGAGAT
                            IIIII I IIIIII IIIIIII
                            TGATT A ATCTTT GTCTCTA
                                 T G       _
GAM258  RAB27A   3' ATCTCTGTCTTTACCAGC   1129       __   AA
                            GT GTAGA ACAGAGAT
                            II IIIII IIIIIIII
                            CG CATTT TGTCTCTA
                            AC    C_
GAM258  SALL2    5' ATCTGCTTCACAGT    2671     A  T AAAA
                            ACT GTG AG   CAGAGAT
                            III III II   IIIIIII
                            TGA CAC TC   GTCTCTA
                            _   T   ____
GAM258  SFRS7    3' TGCTTTCTACATTAGTTA   2529            A
                            TAACTAGTGTAGAAA CA
                            IIIIIIIIIIIIIII II
                            ATTGATTACATCTTT GT
                                   C
GAM258  SLC19A2  3' GTCTTTCTACATAGTTA   2836     G    AAACA
                            TAACTA TGTAGA    GAGAT
                            IIIIII IIIIII    IIIII
                            ATTGAT ACATCT    TTCTG
                            _       ____
GAM258  C20orf97 3' ATCTCTGTCCTCTTGATTA  1946     GT AA
                            TAGT AGA ACAGAGAT
                            IIII III IIIIIIII
                            ATTA TCT TGTCTCTA
                            GT CC
GAM258  CYB5-M   3' TCTGTTTTTTCTACCCTAG  2150     T    __
                            CTAG GTAGAAA ACAGA
                            IIII IIIIIII IIIII
                            GATC CATCTTT TGTCT
                                 C   TT
GAM258  CYB5-M   3' TCTGTTTTTTCTACCCTAG  3658     T    __
                            CTAG GTAGAAA ACAGA
                            IIII IIIIIII IIIII
```

```
                              GATC CATCTTT  TGTCT
                                 C      TT
GAM258  FAM8A1   3' TATCCCTGGGTTACACTA  1675        AAAA  A
                      TAGTGTAG   CAG GATA
                      ||||||||   ||| ||||
                      ATCACATT   GTC CTAT
                         GG__   C
GAM258  FLJ10853  5' TCTGCCTACACTATTTA   1804    C    AAAA
                      TAA TAGTGTAG   CAGA
                      ||| ||||||||   ||||
                      ATT ATCACATC   GTCT
                         T      C___
GAM258  FLJ14327  3' ATCTCTGTCTACAAAACTAG 2111      ___   AAA
                      CTAGT  GTAGA  CAGAGAT
                      |||||  |||||  |||||||
                      GATCA  CATCT  GTCTCTA
                         AAA      ___
GAM258  FLJ14681  5' TATCTCTGCCTTCCAGGCAT 2285     A__  AA
                      GTGT  GAA  CAGAGATA
                      ||||  |||  ||||||||
                      TACG  CTT  GTCTCTAT
                         GAC  CC
GAM258  HNRPA3   3' ATCTCTATTCTACATTTA   1245   T    AAC
                      C AGTGTAGAA  AGAGAT
                      | |||||||||  ||||||
                      A TTACATCTT  TCTCTA
                         T      A__
GAM258  KIAA0426 3' TATCTCTGTTTTGGGAGACAGG 1532    A GTAG_
           T             ACT GT   AAAACAGAGATA
                         ||| ||    ||||||||||||
                         TGG CA    TTTTGTCTCTAT
                          A GAGGG
GAM258  KIAA0594 3' TATCTCTAAGTTATACTAATTA 2707   C     AAAAC
                      TAA TAGTGTAG   AGAGATA
                      ||| ||||||||   |||||||
                      ATT ATCATATT   TCTCTAT
                         A     GAA__
GAM258  KIAA0635 5' ATCTCAATTTACACTAG    1513       AAACA
                      CTAGTGTAGA   GAGAT
                      ||||||||||   |||||
                      GATCACATTT   CTCTA
                         AA___
GAM258  PDZD2    5' ATCCCTGTTTTCGGGGACTA  3181      GTA_    A
                      TAGT   GAAAACAG GAT
                      ||||   |||||||| |||
                      ATCA   CTTTTGTC CTA
                         GGGG      C
GAM258  PP1628   5' ATCTCTGTTCCCCATCCCCAGT 2145    A___  TA AA
                      ACT  GTG GA ACAGAGAT
                      |||  ||| || ||||||||
```

```
                        TGA   TAC CT TGTCTCTA
                        CCCC  CC __
GAM258  TIP120A  3' TATCCCTGTTGCGCACACTA 1829      AGAA   A
                        TAGTGT   AACAG GATA
                        ||||||   ||||| ||||
                        ATCACA   TTGTC CTAT
                        CGCG     C
GAM258  LOC220988 3' ATCTCTATTCTACATTTA  3501    T     AAC
                        C AGTGTAGAA  AGAGAT
                        | |||||||||  ||||||
                        A TTACATCTT  TCTCTA
                        T       A__
GAM258  LOC221337 5' ATCTCTGTTCTCTAAGCAC  3555      __  A
                        GTGT  AGA AACAGAGAT
                        ||||  ||| |||||||||
                        CACG  TCT TTGTCTCTA
                         AA   C
GAM258  LOC257017 5' TATCTCTGTTTTGGCAT    3737      AG
                        GTGT  AAAACAGAGATA
                        ||||  ||||||||||||
                        TACG  TTTTGTCTCTAT
                         G_
GAM258  LOC90829  5' TATCTCTGTTTTGGTACCAGT 2680     A  AG
                        ACT GTGT  AAAACAGAGATA
                        ||| ||||  ||||||||||||
                        TGA CATG  TTTTGTCTCTAT
                         C  G_
GAM259  KIAA0268  3' ACAAAACAATGCTGAAGTTAAT 2874     T  A  T
             AT         ATATTA CT CG CATTGTTTTGT
                        |||||| || || ||||||||||
                        TATAAT GA GT GTAACAAAACA
                         T  A  C
GAM259  KIAA1255  3' ACAAAACAACTCTGAGATGA 2783     A  TCA
                        TTATCT CG  TTGTTTTGT
                        |||||| ||  |||||||||
                        AGTAGA GT  AACAAAACA
                         _ CTC
GAM259  MGC5370   3' CAAAACATCAGATAATAT   2275       ACGTCAT
                        ATATTATCT    TGTTTTG
                        |||||||||    |||||||
                        TATAATAGA    ACAAAAC
                        CT_____
GAM259  UK114    3' ACAAAATGTTATATAGATAATA 1255     CG CAT
             T          ATATTATCTA T TGTTTTGT
                        |||||||||| | ||||||||
                        TATAATAGAT A GTAAAACA
                         AT TT_
GAM260  OSBPL8   3' CTACATATGAGTATAATA    1927        CC
                        TATTATACTCATG TAG
                        ||||||||||||| |||
```

```
                              ATAATATGAGTAT  ATC
                                    AC
GAM260  LOC147463 3' CTATTACTATTGCAGGAATATA 3109     C A  C_
     A                       TTATA TC TGC  TAGTAATAG
                             ||||| || ||| |||||||||
                             AATAT AG ACG  ATCATTATC
                                   A  G   TT
GAM260  LOC151201 5' ATTAGTAGCATGAGTATAA  3340         C G
                       TTATACTCATGC TA TAAT
                       |||||||||||| || ||||
                       AATATGAGTACG AT ATTA
                             _ G
GAM261  JJAZ1    3' AGCACTGTGGTTGAGTAACATC 1621      _   TT_
                     GATGTTAC CAATCG  TGCT
                     |||||||| |||||| ||||
                     CTACAATG GTTGGT  ACGA
                           A   GTC
GAM261  SIAT1    3' AGGGGATTGGAAACATCGT 986       A    G
                     ACGATGTT CCAATC TTT
                     |||||||| |||||| |||
                     TGCTACAA GGTTAG GGA
                           A       G
GAM261  ATP6V0A1 3' AGGGGACACTGGTAACAT  1191      ATC   G
                     ATGTTACCA  GTTT CT
                     |||||||||  |||| ||
                     TACAATGGT  CAGG GA
                           CA_   G
GAM261  FLJ21313 3' AGCGAATTGGTTACATCGTT 2038      T   ATC
                     AACGATGT ACCA  GTTTGCT
                     |||||||| |||| |||||||
                     TTGCTACA TGGT  TAAGCGA
                           T   ___
GAM261  FLJ23548 3' AGCAAATTTGGCTCGATAATAT 2068      _____   TC
     CG                    CGATGTTA   CCAA GTTTGCT
                           |||||||| |||| |||||||
                           GCTATAAT   GGTT TAAACGA
                           AGCTC   __
GAM261  LOC196510 3' GCAAAAGGCAACATTGTT  3414       A AATCG
                     AACGATGTT CC   TTTGC
                     ||||||||| ||   |||||
                     TTGTTACAA GG   AAACG
                           C A____
GAM261  LOC200220 3' GCAAAAGGCAACATTGTT  3443       A AATCG
                     AACGATGTT CC   TTTGC
                     ||||||||| ||   |||||
                     TTGTTACAA GG   AAACG
                           C A____
GAM261  LOC222234 3' AGCAAGATGGGTAACATC  3645       A GT
                     GATGTTACC ATC TTGCT
                     ||||||||| ||| |||||
```

```
                          CTACAATGG TAG AACGA
                          G   __
GAM262   CDKN1B   3' GACAAAATTTTCTCATTTTCTT 1082          TGT____   C
         TTCACT              GTGAAAAGAA    AAA TTTGTC
                          ||||||||||   ||| ||||||
                          CACTTTTCTT    TTT AAACAG
                          TTACTCT  A
GAM262   CSPG3    3' ACAAAGGTCTTCTTTTCCT 1107    T    TGTAAA
                          AG GAAAAGAA    CTTTGT
                          || |||||||    ||||||
                          TC CTTTTCTT    GAAACA
                          _       CTG___
GAM262   ITSN1    3' ACAAAGTTTACATTTCATACT 981     AAAA
                          AGTG  GAATGTAAACTTTGT
                          ||||  ||||||||||||||
                          TCAT   TTTACATTTGAAACA
                          AC__
GAM262   MBNL     5' GACATGCAACAGTCTTTTCACT 1937       A AAACTT
                          AGTGAAAAGA TGT    TGTC
                          |||||||||| |||    ||||
                          TCACTTTTCT ACA    ACAG
                          G  ACGT__
GAM262   MEFV     3' GACAAAGTTTTGCTCTTGTCAC 719     A  ATGT
                          GTGA AAGA   AAACTTTGTC
                          |||| ||||   ||||||||||
                          CACT TTCT   TTTGAAACAG
                          G   CGT_
GAM262   NR3C1    3' GACAAAGTAATTCCTCTCACT 716       AAA   GTAA
                          AGTGA GAAT   ACTTTGTC
                          ||||| ||||   ||||||||
                          TCACT CTTA   TGAAACAG
                          CTC   A___
GAM262   TIF1     3' ACAAAGACATTCTTCCCACT 2564     AA      AAA
                          AGTG AAGAATGT  CTTTGT
                          |||| ||||||||  ||||||
                          TCAC TTCTTACA  GAAACA
                          CC        ___
GAM262   BZW1     3' ACAAATGGGTATTCTTTTCAT 1516          AAAC
                          GTGAAAAGAATGT  TTTGT
                          |||||||||||||  |||||
                          TACTTTTCTTATG  AAACA
                          GGT_
GAM262   FLJ10998 3' GACAAAGTCTCGCTCTGTCAC 1811     AA  A TAA
                          GTGA AGA TG  ACTTTGTC
                          |||| ||| ||  ||||||||
                          CACT TCT GC  TGAAACAG
                          G_  C TC_
GAM262   FLJ12409 3' GACAAAGTGATGTTTCTTCCC 2137     AA   TG A_
         AT               GTG AAGAA TA ACTTTGTC
                          ||| ||||| || ||||||||
```

```
                            TAC TTCTT GT TGAAACAG
                             CC    TT AG
GAM262 FLJ32356 3' ACAAAGCTTGATGTTTTCACT 2492        GAATG  A
                    AGTGAAAA    TAA CTTTGT
                    ||||||||    ||| ||||||
                    TCACTTTT    GTT GAAACA
                     GTA__   C
GAM262 GRP3    3' GTTTACATCCTTCCCACT  1624    AA  A
                    AGTG AAG ATGTAAAC
                    |||| ||| ||||||||
                    TCAC TTC TACATTTG
                     CC  C
GAM262 KIAA0210 3' GACACTGTTTACGTCCCTCCCA 1538      AAA A_     TT
          CT              AGTG AG ATGTAAAC TGTC
                    |||| || |||||||| ||||
                    TCAC TC TGCATTTG ACAG
                     CC_ CC    TC
GAM262 MGC2477 3' GACAAAAGCAAGGCCCCTTTTC 2054      AAT AAAC__
          ACT             AGTGAAAAG GT   TTTGTC
                    ||||||||| ||    ||||||
                    TCACTTTTC CG    AAACAG
                     CC_ GAACGA
GAM262 MGC2742 5' ACAAAAGGGTATTTCTTTTCTC 2039    T    T AA   _
          T              AG GAAAAGAA GTA CTTT GT
                    || |||||||| ||| |||| ||
                    TC CTTTTCTT TAT GAAA CA
                     T    _ GG  A
GAM262 MRF2    3' GTTCTCATTCTTTTCACT   3056        TA
                    AGTGAAAAGAATG AAC
                    ||||||||||||| |||
                    TCACTTTTCTTAC TTG
                      TC
GAM262 P2RXL1 3' GAGGGCCACACTCTTTTCAC 1213      A AAA
                    GTGAAAAGA TGT  CTTT
                    ||||||||| ||| ||||
                    CACTTTTCT ACA  GGAG
                      C  CCG
GAM262 STK38L 3' GACAAAGTTTAACACCTTCACT 2844      AAGAATG
                    AGTGAA    TAAACTTTGTC
                    ||||||    ||||||||||||
                    TCACTT    ATTTGAAACAG
                     CCACA__
GAM262 LOC151579 3' ACAAATGGGTATTCTTTTCAT 2859       AAAC
                    GTGAAAAGAATGT  TTTGT
                    |||||||||||||  |||||
                    TACTTTTCTTATG  AAACA
                      GGT_
GAM262 LOC51312 5' GACAAAATTCATTTTTTTCA 1849       TAAAC
                    TGAAAAGAATG  TTTGTC
                    |||||||||||  ||||||
```

```
                          ACTTTTTTTAC   AAACAG
                             TTA__
GAM262  LOC91574 3' GACAAAGTTCTGTTTCTTCAC 2751     AA   TGTA
                   GTGA AGAA   AACTTTGTC
                   |||| ||||   |||||||||
                   CACT TCTT   TTGAAACAG
                      __   TGTC
GAM263  MAB21L2  5' CACTACAAACAAACAAACC  1301        CA_   C
                   GGTTTGTT  TTGT GTG
                   ||||||||  |||| |||
                   CCAAACAA  AACA CAC
                      ACA   T
GAM263  LOC220672 3' CACGAATAAACAAACTTAA  2565          CATTG
                   TTAGGTTTGTT    TCGTG
                   |||||||||||    |||||
                   AATTCAAACAA    AGCAC
                       ATA__
GAM264  FLRT2    3' AACTTCACTCTACACTATA  1437       ACAC A C
                   TATAGTGTA  GA TG AGTT
                   |||||||||  || || ||||
                   ATATCACAT  CT AC TCAA
                         ____ C T
GAM264  KDELR2   3' AACTTGCATTCCACTATA  1335       TAACAC      _
                   TATAGTG    GAATGCA GTT
                   |||||||    ||||||| |||
                   ATATCAC    CTTACGT CAA
                      _____      T
GAM264  SMT3H2   3' AAACTGCAATTTGGTTCCAC 1341     T  A   _
                   GTG AAC CGAAT GCAGTTT
                   ||| ||| ||||| |||||||
                   CAC TTG GTTTA CGTCAAA
                      C   _   A
GAM264  LOC158997 3' AAACTGCAATTTGGTTCCAC 3230     T  A   _
                   GTG AAC CGAAT GCAGTTT
                   ||| ||| ||||| |||||||
                   CAC TTG GTTTA CGTCAAA
                      C   _   A
GAM265  APOC4    3' GTTCATACTTCTCCAATAAATA 841      C   AT T
          AA             TTTAT TATTG  GG GTATGAAC
                   |||||| ||||| || |||||||||
                   AAATA ATAAC  CT CATACTTG
                      A   CT T
GAM265  DKFZP434P0721 3' TTCATACATATATAGATA   2664        TGATG
                   TATCTAT   GTGTATGAA
                   |||||||   |||||||||
                   ATAGATA   TACATACTT
                      TA___
GAM265  FLJ14082 3' TCATACACACAGATAAA    2129        ATTGATG
                   TTTATCT    GTGTATGA
                   |||||||    ||||||||
```

```
                          AAATAGA    CACATACT
                          CA_____
GAM266  LMO7     3' AATAAACTTGCTGATGCATTT  1202      TAAT T
                          AAATGC   G CAAGTTTATT
                          ||||||   | ||||||||||
                          TTTACG   C GTTCAAATAA
                          TAGT _
GAM266  LMO7     3' AATAAACTTGCTGATGCATTT  1643      TAAT T
                          AAATGC   G CAAGTTTATT
                          ||||||   | ||||||||||
                          TTTACG   C GTTCAAATAA
                          TAGT _
GAM266  CDV-1    3' AATAAACTTGGTACGTATTT   1466      TAA GT
                          AAATGC  T CAAGTTTATT
                          ||||||  | ||||||||||
                          TTTATG  A GTTCAAATAA
                          C__ TG
GAM266  KIAA1671 3' TTTGCACATCAGCATTTTA    2726      A    _
                          TAAAATGCT ATGT CAAG
                          ||||||||| |||| ||||
                          ATTTTACGA TACA GTTT
                          C   C
GAM266  SEMA5A   3' AAACCTTTGAAATTAGCATT   1075      G    __
                          AATGCTAAT TCAA  GTTT
                          ||||||||| ||||  ||||
                          TTACGATTA AGTT  CAAA
                          A   TC
GAM266  LOC127133 3' AATAAATGGGAGTTAGCATTTT 3004          G AA
          A               TAAAATGCTAAT TC  GTTTATT
                          ||||||||||| ||  |||||||
                          ATTTTACGATTG AG  TAAATAA
                          _  GG
GAM266  LOC143154 3' AATTTGACATCACATTTTA   3052      CTA
                          TAAAATG  ATGTCAAGTT
                          |||||||  ||||||||||
                          ATTTTAC  TACAGTTTAA
                          AC_
GAM266  LOC219294 3' AATTTGACATCACATTTTA   3587      CTA
                          TAAAATG  ATGTCAAGTT
                          |||||||  ||||||||||
                          ATTTTAC  TACAGTTTAA
                          AC_
GAM267  GARP     3' TGGAGTTTGAGACTATGGAA   1221       _ TGGA
                          TTCCGTAGTC CA   TCCA
                          |||||||||| ||   ||||
                          AAGGTATCAG GT   AGGT
                          A TTG_
GAM267  FLJ30213 3' GATCATGGACCACAGAA      2507    C A    G
                          TTC GT GTCCATG ATC
                          ||| || ||||||| |||
```

```
                            AAG CA CAGGTAC TAG
                            A C        _
GAM267  LOC196510 3' GGTCCATGAACTAGGAA    3415      G   C
                       TTCC TAGT CATGGATC
                       |||| |||| ||||||||
                       AAGG ATCA GTACCTGG
                            _    A
GAM267  LOC200220 3' GGTCCATGAACTAGGAA    3444      G   C
                       TTCC TAGT CATGGATC
                       |||| |||| ||||||||
                       AAGG ATCA GTACCTGG
                            _    A
GAM267  LOC220930 3' GGTCATAGACTATGGAA    3591        C   AT
                       TTCCGTAGTC ATGG  CC
                       |||||||||| ||||  ||
                       AAGGTATCAG TACT  GG
                            A    __
GAM268  ZNF161   3' ACTAGCAGAACTCTT    1359      TAGT  T
                     AAGAGTTT   TG CTAGT
                     ||||||||   || |||||
                     TTCTCAAG   AC GATCA
                          ____  _
GAM268  DKFZP566D193 3' ACTGAATAACTAAAATCTC  3353    _       C
                          GAG TTTTAGTTGT TAGT
                          ||| |||||||||| ||||
                          CTC AAAATCAATA GTCA
                           T      A
GAM268  LOC200574 3' GCTGACTACTAAAACTC    3450      T  T
                       GAGTTTTAGT GTC AGT
                       |||||||||| ||| |||
                       CTCAAAATCA CAG TCG
                            T  _
GAM269  RAD50    3' TGTTGATAAATCCATCA    1240    A       T
                     TGA TGGATTTATCA CA
                     ||| |||||||||| ||
                     ACT ACCTAAATAGT GT
                       _        T
GAM269  RAD50    3' TGTTGATAAATCCATCA    2420    A       T
                     TGA TGGATTTATCA CA
                     ||| |||||||||| ||
                     ACT ACCTAAATAGT GT
                       _        T
GAM269  SMURF1   3' ATGATGTAAATCCACCCA   3564    AA      T
                     TG  TGGATTTA CATCAT
                     ||  |||||||| ||||||
                     AC  ACCTAAAT GTAGTA
                       CC        _
GAM269  TRIM9    3' ATGAATGAAAAATCCATCCA   1611   A     A  _
                     TG ATGGATTT TCAT CAT
                     || |||||||| |||| |||
```

```
                         AC TACCTAAA AGTA GTA
                           C       A    A
GAM269  FLJ13902 3' AACGATGATGATGAACACA  2076      GA
                       TG TTTATCATCATCGTT
                       || ||||||||||||||
                       AC AAGTAGTAGTAGCAA
                            AC
GAM269  KIAA0650 3' AAACGATGATGATGTTAACC  3427    ATT_
                        GG  TATCATCATCGTTT
                        ||  |||||||||||||
                        CC  GTAGTAGTAGCAAA
                         AATT
GAM269  MGC16075 3' AAACGATGATGCAGGCTATTCA 2277        ATTTAT
                       TGAATGG    CATCATCGTTT
                       |||||||    |||||||||||
                       ACTTATC    GTAGTAGCAAA
                          GGAC__
GAM270  PAIP2   3' ACTGAAAATAGAATTGG   1687    TATA
                       CCA  TTTATTTTCAGT
                       |||  |||||||||||
                       GGT  AGATAAAAGTCA
                         TA__
GAM270  PIN4    3' CTGAAAATATTGGGCATC   1282    A ATATATT
                       GATG CC     TATTTTCAG
                       |||| ||     |||||||||
                       CTAC GG     ATAAAAGTC
                        _  GTT____
GAM271  HLA-G   3' TCCTTCCCCAATCACCTT   900         AAT
                       AAGGTGATTGG  GGGA
                       |||||||||||  ||||
                       TTCCACTAACC  TCCT
                              CCT
GAM271  HRH2    5' TTCATTCCCAACACCTTA   1984        ATT
                       TAAGGTG  GGAATGGG
                       |||||||  ||||||||
                       ATTCCAC  CCTTACTT
                            AAC
GAM271  KCNJ15  3' ATTTATTTAACCAATGACCTTA 916        G   AATG
                       TAAGGT ATTGG   GGATAAAT
                       |||||| |||||   ||||||||
                       ATTCCA TAACC   TTTATTTA
                         G   AA__
GAM271  C1orf8  5' ATCTCAGTCTCAATCACC   1161          _ A
                       GGTGATTG GA TGGGAT
                       |||||||| || ||||||
                       CCACTAAC CT ACTCTA
                             T G
GAM271  FLJ10738 3' ATCCCATCTGGGTCACTT   1798      _TG A
                       AGGTGA T GA TGGGAT
                       |||||| | || ||||||
```

```
                              TTCACT G  CT ACCCTA
                                G GT _
GAM271   FLJ23511  3' ATCCACAATCCAATTACC    2239          A _
                      GGTGATTGGA TG GGAT
                      |||||||||| || ||||
                      CCATTAACCT AC CCTA
                               A A
GAM271   GAB3     3' ATTTCAGGGTTTCCAATCACC 2377          ____ GG
                      GGTGATTGGAA   TG AT
                      ||||||||||    || ||
                      CCACTAACCTT   AC TA
                               TGGG TT
GAM271   ITPK1    3' CTCACCCCATCACCTTG      1484       T AA
                      TAAGGTGAT GG TGGG
                      |||||||||| || ||||
                      GTTCCACTA CC ACTC
                               _ CC
GAM271   TRIP-Br2 3' TCCCCCCCCATCACCTTA     1539       T AAT
                      TAAGGTGAT GG  GGGA
                      |||||||||| ||  ||||
                      ATTCCACTA CC  CCCT
                               C CC_
GAM271   LOC152313 3' ATCCCCCTGATCCAATCACCT 3355          AT___
                      AGGTGATTGGA   GGGAT
                      |||||||||||   |||||
                      TCCACTAACCT   CCCTA
                               AGTCC
GAM271   LOC256642 3' TTTAGGCCCCAATACCTTA   3701       A   AAT GA
                      TAAGGTG TTGG  GG  TAAA
                      ||||||| |||| || ||||
                      ATTCCAT AACC  CC  ATTT
                               _  ___ GG
GAM272   C22orf2  3' TTTTTTATTAAACGATGT      3655       A
                      ACGTC TTTAATAAAAAA
                      ||||| ||||||||||||
                      TGTAG AAATTATTTTTT
                               C
GAM272   LOC153277 3' ATACTTAATAAATGACGT    3369          A AAAAA
                      ACGTCATTTA TA   AGTAT
                      |||||||||| ||    |||||
                      TGCAGTAAAT AT    TCATA
                               A _____
GAM273   SH3BP4   3' CAGTGTGCAATTAGTCATTGAC 1506    G   A      AG
              A        TG CAAT ACTAATTG ATATTG
                       || |||| |||||||| ||||||
                       AC GTTA TGATTAAC TGTGAC
                               A  C    G_
GAM273   UFD1L    3' CAACATCTTGGCTTTTAGTTAC 2973    G A      ___TG  A
         TGGCA            TG CA TAACTAA  T AGAT TTG
                       || || |||||||  |  |||| |||
```

```
                                AC GT ATTGATT  G TCTA AAC
                                G  C      TTC GT   C
GAM273  FLJ20081   3' CAATACTCTCAATTATTAACCA 1736     CAA  C         _
                                TGG  TAA TAATTGAGA TATTG
                                ||| ||| |||||||||| |||||
                                ACC  ATT ATTAACTCT ATAAC
                                A__  _        C
GAM273  KIAA1635   3' GTCCAACTATTTATTGCCA  2804         C A  A
                                TGGCAATAA TA TTG GAT
                                ||||||||| || ||| |||
                                ACCGTTATT AT AAC CTG
                                         T C _
GAM273  PRO1257    5' CAATATCTCATAAGACTACTGC 1848     A ACTAAT
                                GCA TA     TGAGATATTG
                                ||| ||     ||||||||||
                                CGT AT     ACTCTATAAC
                                 C CAGAAT
GAM273  LOC153020  3' CTCAATCAGTATTGCCA    3177        A A
                                TGGCAATA CT ATTGAG
                                |||||||| || ||||||
                                ACCGTTAT GA TAACTC
                                        _ C
GAM274  BNC        3' TGTTTCTGTTTCATATC    851        T
                                GATATGA AACAGGAATA
                                ||||||| ||||||||||
                                CTATACT TTGTCTTTGT
                                        _
GAM274  PROS1      5' TGTCCTTGTTATCACTTC   3407    TA      A
                                GA  TGATAACAGG ATA
                                ||  |||||||||| |||
                                CT  ACTATTGTTC TGT
                                TC        C
GAM274  FLJ20147   3' ATGTTGTAATTGTCATATC  1738           CAGGA
                                GATATGATAA  ATAACAT
                                ||||||||||  |||||||
                                CTATACTGTT  TGTTGTA
                                        AA___
GAM274  KIAA0737   3' ATGTTATTCCCCATTATCA  1562       CA_
                                TGATAA  GGAATAACAT
                                ||||||  ||||||||||
                                ACTATT  CCTTATTGTA
                                ACC
GAM275  CA4        3' AGGCATGATTAAAATATGGAC 769          T TGAG
                                GTCCATATTTTA TC  GCCT
                                |||||||||||| ||  ||||
                                CAGGTATAAAAT AG  CGGA
                                 T TA__
GAM275  LU         3' AGGCCCCAGAATAGCTCCTGGA 1227    TATT     A
              C                 GTCCA  TTATTCTG GGCCT
                                |||||  |||||||| |||||
```

```
                          CAGGT   GATAAGAC CCGGA
                          CCTC        C
GAM275  FNBP3    5' AGGAGTTACAAAATATGGAC 3155          ATTC  GG
                          GTCCATATTTT   TGA CCT
                          |||||||||| ||| |||
                          CAGGTATAAAA   ATT GGA
                              C___  GA
GAM275  SAP18    3' AGCCCTTCTGTAAAATATG 1258        TCT   C
                          CATATTTTAT  GAGG CT
                          ||||||||| |||| ||
                          GTATAAAATG  TTCC GA
                             TC_   C
GAM275  SCYA4    3' CTTTAAAATAAAATGCAGAC 978      CA      C
                          GTC TATTTTATT TGAGG
                          ||| ||||||||| |||||
                          CAG GTAAAATAA ATTTC
                            AC       A
GAM275  SLC6A14  3' CGTGATAAATATATGGAC   1368         _   C
                          GTCCATAT TTTATT TG
                          ||||||||| |||||| ||
                          CAGGTATA AAATAG GC
                              T    T
GAM275  LOC158629 5' CCCAGGAAAACATGGAT    3393      A  TA   A
                          GTCCAT TTT TTCTG GG
                          |||||| ||| ||||| ||
                          TAGGTA AAA AGGAC CC
                              C   __   _
GAM275  LOC163115 5' AGGCCTCAGTTTATATTGAC 3243      C  TTTATT
                          GTC ATAT    CTGAGGCCT
                          ||| ||||    |||||||||
                          CAG TATA    GACTCCGGA
                            T  TTT___
GAM275  LOC200339 3' TCTTAGAAGAAAACATAGACG 3476      C A   A
                          CGTC AT TTTT TTCTGAGG
                          |||| || |||| ||||||||
                          GCAG TA AAAA AAGATTCT
                            A  C   G
GAM275  LOC200953 5' AGGCCTCAGAGGGCCCTAGGGA 3481       ATATTTTA
              C                GTCC    TTCTGAGGCCT
                          ||||       |||||||||||
                          CAGG       GAGACTCCGGA
                            GATCCCGG
GAM275  LOC255527 5' AGGCCCACATAAAATACCAAC 3718      CCA     TC A
                          GT  TATTTTAT  TG GGCCT
                          ||  ||||||||  || |||||
                          CA  ATAAAATA  AC CCGGA
                            ACC      C_  _
GAM275  LOC51334 3' CCTCAGAATGATGAAAAATATG 1706      C     _____
              AATG               CGT CATATT   TTATTCTGAGG
                          ||| ||||||    |||||||||||
```

```
                      GTA GTATAA   AGTAAGACTCC
                       A    AAAGT
GAM275 LOC92710 3' AGGCCTCAAAACAATGAAA 2884       C___
                   TTTTATT  TGAGGCCT
                   ||||||| ||||||||
                   AAAGTAA  ACTCCGGA
                        CAAA
GAM276 TSN     3' TACACTTGGGGAGATTTGCCA 1136         GCAA C_
                   TGGCAAATCT  TCA TGTA
                   |||||||||| ||| ||||
                   ACCGTTTAGA  GGT ACAT
                        GG__  TC
GAM276 FLJ20039 3' TACAGTGATAGCAACTTTCCA 1734    C TC A
                   TGG AAA TGC ATCACTGTA
                   ||| ||| ||| |||||||||
                   ACC TTT ACG TAGTGACAT
                    _  CA  A
GAM276 KIAA1204 3' ACAGGGCCAGCTTGCCATA 2849      AT  CAA A
                   TATGGCAA CTG  TC CTGT
                   |||||||| ||| || ||||
                   ATACCGTT GAC  GG GACA
                        C_  C__ _
GAM276 OR2C3    3' TACAGTGAGGCGAGATTCACCA 3023     CA  _ AA
                T         ATGG AATCT GC TCACTGTA
                          |||| ||||| || |||||||||
                          TACC TTAGA CG AGTGACAT
                           AC   G G_
GAM276 QKI     3' TACCTTGATGCAAATTTGCCA 2722       C  A CT
                   TGGCAAAT TGCA TCA GTA
                   |||||||| |||| ||| |||
                   ACCGTTTA ACGT AGT CAT
                        A  _ TC
GAM276 TIP120A 3' ACAGTAACAATTTGCCA   1828       C CAATC
                   TGGCAAAT TG   ACTGT
                   |||||||| ||   |||||
                   ACCGTTTA AC   TGACA
                        _ AA___
GAM276 LOC90750 3' CAGTGGTCCAGACTTGCCA 2673       A  CA
                   TGGCAA TCTG ATCACTG
                   |||||| |||| |||||||
                   ACCGTT AGAC TGGTGAC
                        C  C_
GAM276 LOC92912 3' ACAGTAATTTTTGCCATG 2898        TCTGC C
                   TATGGCAAA   AAT ACTGT
                   |||||||||   ||| |||||
                   GTACCGTTT   TTA TGACA
                      _____   A
GAM277 BACH2   3' ATTTCTGGTGAGTCAGTCCAC 1962    AA TA_
                   GT ATT  TCACCAGAAAT
                   || ||| |||||||||||
```

```
                         CA TGA   AGTGGTCTTTA
                         CC   CTG
GAM277  DUSP11   3' TTTGCTGATAAATTTGCAGT  1039     C        C
                         AC GTAAATTTATCA CAGA
                         || |||||||||||| ||||
                         TG CGTTTAAATAGT GTTT
                          A         C
GAM277  EPS8     3' ATTTCTGGTAATAAGAAGC  1114      AAA   C
                         GT  TTTAT ACCAGAAAT
                         ||  ||||| |||||||||
                         CG  GAATA TGGTCTTTA
                          AA_    A
GAM277  TK1      3' TCTGGTGATGGTTCCACAGG  1005     _ AAAT_
                         CC GT    TTATCACCAGA
                         || ||    |||||||||||
                         GG CA    GGTAGTGGTCT
                          A CCTTT
GAM277  TRPC6    3' ATTTCTGGGAGCATTTAC   1134        TTA A
                         GTAAAT  TC CCAGAAAT
                         ||||||  || ||||||||
                         CATTTA  AG GGTCTTTA
                           CG_ _
GAM277  KIAA0924 3' TTCTGAATAAATTTACAGT  1577     C       CAC
                         AC GTAAATTTAT  CAGAA
                         || |||||||||   |||||
                         TG CATTTAAATA  GTCTT
                          A        A__
GAM277  KIAA1946 3' ATTTTGGGTGATGAATTTACA 3247     C          _
          GT              AC GTAAATTTATCACC AGAAAT
                         || |||||||||||||| ||||||
                         TG CATTTAAGTAGTGG TTTTTA
                          A              G
GAM277  OSBPL3   3' ATTTCTGGTGAATTAC     1635      ATTTA
                         GTAA    TCACCAGAAAT
                         ||||    |||||||||||
                         CATT    AGTGGTCTTTA
                          A____
GAM277  PSKH1    3' TCTGGTGGAGGGCCATGG   2810      AAA  A
                         CCGT  TTT TCACCAGA
                         ||||  ||| ||||||||
                         GGTA  GGA GGTGGTCT
                          CCG  _
GAM277  URB      5' ATTTCTGGGACTGAATCCAGG 3162     GTAA   _ A
                         CC  ATTTA TC CCAGAAAT
                         ||   ||||| || |||||||||
                         GG   TAAGT AG GGTCTTTA
                          ACC_    C _
GAM278  PLS3     3' TAGAAGAAAAATGTACCTTA  1174          _   CA
                         TAAGGTAC TTTTTCT TA
                         |||||||| ||||||| ||
```

```
                    ATTCCATG AAAAAGA  AT
                    T        AG
GAM278  LOC121227 3'  TTATGCAAAAAAGTATCTTA  2989          CT
                    TAAGGTACTTTTT CATAA
                    IIIIIIIIIIII IIIII
                    ATTCTATGAAAA GTATT
                            AC
GAM278  LOC145786 3'  ATTATGAGAAAGGCC      3277     ACT
                    GGT  TTTTCTCATAAT
                    III  IIIIIIIIIII
                    CCG  GAAAGAGTATTA

                         ___
GAM278  LOC149650 3'  TTAAGAGAAAAAAGTACC    3136        _  A
                    GGTACTTTTT CTC TAA
                    IIIIIIIIII III III
                    CCATGAAAAA GAG ATT
                         A  A
GAM278  LOC222223 3'  TTATCACATGGTCAAGTACCTT 3641      TT TCATA
         G                TAAGGTACTT TC   ATAA
                    IIIIIIIIII II   IIII
                    GTTCCATGAA GG   TATT
                       CT TACAC
GAM279  OGT     5'  GGTAATTTATAGAACAAA   1042       C C
                    TTTGTTCTAT AA TACC
                    IIIIIIIIII II IIII
                    AAACAAGATA TT ATGG
                         T A
GAM279  TNFRSF10B 3'  TTTATAGGTAGTTGTTTACA  1065     TCTAT
                    TGT   CAACTACCTATAAA
                    III   IIIIIIIIIIIII
                    ACA   GTTGATGGATATTT
                    TTT__
GAM279  BA108L7.2 3'  TTATAGACACTAGTAGGACAAA 2180        CAACTAC
                    TTTGTTCTAT   CTATAA
                    IIIIIIIIII   IIIIII
                    AAACAGGATG   GATATT
                       ATCACA_
GAM279  FLJ12598 5'  TTTACAGGTACCATGCAGAGAA 2086        AT_ AC_  A
         CAAA            TTTGTTCT CA TACCT TAAA
                    IIIIIIII II IIIII IIII
                    AAACAAGA GT ATGGA ATTT
                       GAC ACC   C
GAM279  FLJ23071 3'  GGTAATTTATAGAACAAA   2144        C C
                    TTTGTTCTAT AA TACC
                    IIIIIIIIII II IIII
                    AAACAAGATA TT ATGG
                         T A
GAM279  LOC91266 5'  TATAGGTTAGGAACAAA    2720        ATCAACT
                    TTTGTTCT   ACCTATA
                    IIIIIIII   IIIIII
```

```
                        AAACAAGG     TGGATAT
                     AT_____
GAM280  CDH11   5' CCGCTGACTTGTGAATGGGA 2339     A  TG  AAAA
                     TCC ATT  TAA   TCAGCGG
                     ||| ||| |||   |||||||
                     AGG TAA  GTT   AGTCGCC
                     G   GT  C___
GAM280  IGF1    3' CCTGATGCAAATTGGA     761        AAAAA    C
                     TCCAATTTGT    ATCAG G
                     ||||||||||    ||||| |
                     AGGTTAAACG    TAGTC C
                     _____       A
GAM280  FKBP9   3' CCGCTAATTTTTGTATTTTTGG 3632      TTTGTA    C
                     CCAA     AAAAAT AGCGG
                     ||||     |||||| |||||
                     GGTT     TTTTTA TCGCC
                     TTTATG     A
GAM280  FLJ23045 3' TGCTTGACAAATTGGAT     2082          AAAAAATC
                     ATCCAATTTGT     AGCG
                     ||||||||||     ||||
                     TAGGTTAAACA     TCGT
                     GT_____
GAM280  FLJ30567 3' CCTGATTTGAATTGG     2510      GTAAA    C
                     CCAATTT   AAATCAG G
                     |||||||   ||||||| |
                     GGTTAAG   TTTAGTC C
                     _____       A
GAM280  FLJ30678 5' CCGCTGATTCCTTTCGTAA  2490      TA  __
                     TTG AAA  AATCAGCGG
                     ||| |||  |||||||||
                     AAT TTT  TTAGTCGCC
                     GC  CC
GAM280  KIAA1676 3' CCACTGTGGGAACCAAATTGGA 3590         TAAAAAAT  C
          T           ATCCAATTTG    CAG GG
                     ||||||||||    ||| ||
                     TAGGTTAAAC    GTC CC
                     CAAGGGT_  A
GAM280  KLF3    3' CCGCCAATTTTTTACAAAT   1693         CA
                     ATTTGTAAAAAT GCGG
                     |||||||||||| ||||
                     TAAACATTTTTTA CGCC
                     AC
GAM280  LOC146952 5' CCACTGATTTTTTTTTTCTGGA 3286      ATTTGT     C
                     TCCA     AAAAAATCAG GG
                     ||||     ||||||||| ||
                     AGGT     TTTTTAGTC CC
                     CTTTT_       A
GAM280  LOC81569 3' CCACTGATTTTTCATTGG     2616      TTGTA    C
                     CCAAT   AAAAATCAG GG
                     |||||   ||||||||| ||
```

```
                              GGTTA    TTTTTAGTC CC
                              C____           A
GAM280  LOC83690 3' CCACTGATTTTTTTTTAAAT 2204      T_        C
                    ATTTG AAAAAATCAG GG
                    ||||| |||||||||| ||
                    TAAAT TTTTTTAGTC CC
                      TT       A
GAM281  ASPH     3' AAAAAAGCATGGAAAATG   1896      C    A
                    CATTT CCATGT TTTTT
                    ||||| |||||| |||||
                    GTAAA GGTACG AAAAA
                      A    A
GAM281  ASPH     3' AAAAAAGCATGGAAAATG   2252      C    A
                    CATTT CCATGT TTTTT
                    ||||| |||||| |||||
                    GTAAA GGTACG AAAAA
                      A    A
GAM281  CABC1    3' ATAAAAATGCTCATGGGAAGTG 1908           TATTT
              A        TCATTTCCCATG    TTTTTAT
                    ||||||||||||    |||||||
                    AGTGAAGGGTAC    AAAAATA
                       TCGT_
GAM281  SLC6A12  5' ATAAAAAGGGACATGAAAATGA 987      CC    A
                    TCATTT CATGT TTTTTTTTAT
                    |||||| ||||| |||||||||
                    AGTAAA GTACA GGGAAAAATA
                      A_    _
GAM281  CSAD     3' AAAATACATAGGAAAAGA   1654      A    C
                    TC TTTCC ATGTATTTT
                    || ||||| |||||||||
                    AG AAAGG TACATAAAA
                      A    A
GAM281  DICER1   3' AAAAAAAATTAAGGGGAAA  2151        ATGT
                    TTTCCC ATTTTTTTT
                    |||||| |||||||||
                    AAAGGG TAAAAAAAA
                       GAAT
GAM281  KIAA1025 3' AAAAAAAGGGGAAATGG    2675        ATGTA
                    TCATTTCCC   TTTTTTTT
                    |||||||||   ||||||||
                    GGTAAAGGG   GAAAAAAA
                       _____
GAM281  KLF12    3' AAAAAAAATACATGGGAA   1372
                    TTCCCATGTATTTTTTTT
                    ||||||||||||||||||
                    AAGGGTACATAAAAAAAA

GAM281  NFAT5    3' AAAAAGTGTCAAAGGAAATGA 2451        CA _
                    TCATTTCC TG TATTTTTT
                    |||||||| || ||||||||
```

```
                          AGTAAAGG  AC GTGAAAAA
                              AA   T
GAM281  LOC170261 3' ATAAAAAAGGTACAAAAAGTGA 3256        CCCA
                        TCATTT   TGTATTTTTTTAT
                        ||||||   |||||||||||||
                        AGTGAA   ACATGGAAAAATA
                             AA__
GAM281  LOC222602 3' ATAAAAAAACAAAAATGGAAAT 3583         CATGTAT
           GA            TCATTTCC    TTTTTTTAT
                        ||||||||    |||||||||
                        AGTAAAGG    AAAAAAATA
                          TAAAAAC
GAM281  LOC257051 3' ATAAAAAAGGTACAAAAAGTGA 3703        CCCA
                        TCATTT   TGTATTTTTTTAT
                        ||||||   |||||||||||||
                        AGTGAA   ACATGGAAAAATA
                             AA__
GAM282  FGF7     3' TATAAAGAACCCAGTTCCA 886          C C
                        TGGAATTGGG TC TTATA
                        |||||||||| || |||||
                        ACCTTGACCC AG AATAT
                              A A
GAM282  MTNR1B   3' TGGGGCAGAAGAGCCCAACTCC 1262     A     C ATA_
                        GGA TTGGGCTC TT   CCA
                        ||| |||||||| ||   |||
                        CCT AACCCGAG AG   GGT
                           C   A ACGG
GAM282  SEPX1    3' TGTGAGGCCCAATTCCA    1681          TC
                        TGGAATTGGGC CTTATA
                        ||||||||||| ||||||
                        ACCTTAACCCG GAGTGT
                              __
GAM282  PPFIA4   3' TGGCATAAGCTGAATCCCA 2883     A  G  CCT  A
                        TGG ATT GGCT  TAT CCA
                        ||| ||| ||||  ||| |||
                        ACC TAA TCGA  ATA GGT
                          C   G  ___   C
GAM282  LOC145231 3' CTTGACACGAGACTAGTCCCAA 3274          _  C__  ATAC
         TTCCA           TGGAATTGGG CT CTT  CAAG
                        |||||||||| || ||| ||||
                        ACCTTAACCC GA GAG  GTTC
                          T TCA  CACA
GAM283  CAV3     3' AATGCCCAGTACTGCCATTTGA 2329        ATCC
                        TCAAATG  TGTTGGGCATT
                        |||||||  |||||||||||
                        AGTTTAC  ATGACCCGTAA
                             CGTC
GAM283  HOXC4    5' AATGACGTCAGAATCATTTG 1509      C  T GG
                        CAAATGAT CTG TG CATT
                        |||||||| ||| || ||||
```

```
                    GTTTACTA GAC GC  GTAA
                     A   T  A_
GAM283  MYCL1    3' CTTTTACACGACCATTTGATA 1203        A  C  T_
                   TATCAAATG TC TGT GGG
                   ||||||||| || ||| |||
                   ATAGTTTAC AG ACA  TTC
                      C   C  TT
GAM283  FLJ20666 5' AACAGGAGAATCACTTGATG 1762        A   ___
                   TATCAA TGA   TCCTGTT
                   |||||| |||  |||||||
                   GTAGTT ACT  AGGACAA
                      C  AAG
GAM283  KIAA1001 3' AATGCCTGGCAAATTACCTGA 1599    AA  CC  TG
                   TCA TGAT TGT GGCATT
                   ||| |||| ||| ||||||
                   AGT ATTA ACG CCGTAA
                      CC   A_  GT
GAM283  PGRMC2   3' AACAGAAAGATCATTTGA   1286        ___
                   TCAAATGATC  CTGTT
                   ||||||||||  |||||
                   AGTTTACTAG  GACAA
                       AAA
GAM283  LOC152286 3' AATGCAGGGAGACATTTGATA 3354      A_  GTTGG
                   TATCAAATG TCCT    GCATT
                   ||||||||| ||||    |||||
                   ATAGTTTAC AGGG    CGTAA
                      AG   A____
GAM283  LOC158549 3' AATGCTTAGGAATCATTTTATA 3392   C    _  TTG
                   TAT AAATGAT CCTG  GGCATT
                   ||| ||||||| ||||  ||||||
                   ATA TTTACTA GGAT  TCGTAA
                      T    A  ___
GAM284  DKFZp761G0313 3' AAGATAAGCTATTATTAA   2731      TA
                   TTAATAAT CTTATCTT
                   |||||||| ||||||||
                   AATTATTA GAATAGAA
                      TC
GAM285  NRCAM    3' CAGCATGCCAACAGTAATA 1170        A  T__
                   TATTATT TTGGC  CTG
                   ||||||| ||||| |||
                   ATAATGA AACCG  GAC
                      C   TAC
GAM285  C22orf23 3' TGATTAACTGGCCAATAA   2259        C__
                   TTATTGGCT TGATCA
                   ||||||||| ||||||
                   AATAACCGG ATTAGT
                      TCA
GAM285  SARM    3' GACAGCGCCAATAACAATA 1609      A   T  A
                   TATT TTATTGGC CTG TC
                   |||| ||||||||| ||| ||
```

```
                      ATAA AATAACCG GAC AG
                       C        C    _
GAM285   LOC219918 3'  CGGTGGTTAAAACAACAATAAT 3529        A  GCTC
       A                  TATTATT TTG   TGATCACCG
                          ||||||| |||   |||||||||
                          ATAATAA AAC   ATTGGTGGC
                             C  AAA_
GAM286   FABP5     3'  TTTATCATAAACATTTTACA 828          T    C
                         TGTAAAAT TTTGT GATAAA
                         |||||||| ||||| ||||||
                         ACATTTTA AAATA CTATTT
                             C     _
GAM286   ZHX1      3'  TTGACCAAAAATTTTACA   1367          _
                         TGTAAAATTTTTG TCGA
                         ||||||||||||| ||||
                         ACATTTTAAAAAC AGTT
                             C
GAM286   KIAA0981  3'  TTTGTGGCAAAAATTTTCA  2599   T        G
                         TG AAAATTTTGTC ATAAA
                         || ||||||||||| |||||
                         AC TTTTAAAACGG TGTTT

                           _        _
GAM286   KIAA1615  3'  ATTTTTATAAGAAAATTTTAC 2829         GTCG
                          GTAAAATTTTT ATAAAAT
                          ||||||||||| |||||||
                          CATTTTAAAAG TATTTTA
                             AA__
GAM286   SGP28     3'  TTTTTATCTGCATAAATTTAC 1271        T   C
           A               TGTAAAATTT TGT GATAAAAA
                           |||||||||| ||| ||||||||
                           ACATTTTAAA ACG CTATTTTT
                              T   T
GAM286   LOC201973 3'  TTTTTTGAGAAAAATTTTGCA 3456         G    T
                          TGTAAAATTTTT TCGA AAA
                          |||||||||||| |||| |||
                          ACGTTTTAAAAA AGTT TTT
                             G    T
GAM287   LOC146237 3'  CGCACGCTCAGCAGGCATGA  3283      A  CACCGA
                          TCGT CC   GAGCGTGTG
                          |||| ||   |||||||||
                          AGTA GG   CTCGCACGC
                             C  ACGA__
GAM287   LOC255146 5'  CACACGCTCCCGCCAGCGA   3679      ACCCAC  A
                          TCGT   CG GAGCGTGTG
                          ||||   || |||||||||
                          AGCG   GC CTCGCACAC
                             ACC___ C
GAM288   ATBF1     5'  CGTACTGGGTGCAATGAA    1336          A
                          TTCGTTGTAT TAGTACG
                          |||||||||| |||||||
```

```
                              AAGTAACGTG GTCATGC
                                     G
GAM289   FMR2     3' GCATCAGTGTTTTTCAACTCC 889      ATT      _   C
                      GGAG   AAAAATA TGA GC
                      ||||   ||||||| ||| ||
                      CCTC   TTTTTGT ACT CG
                              AAC       G   A
GAM289   SF1      3' GCGTGGGGTTTTTTAATCTCTG 1138              TATG_
                      CGGAGATTAAAAA   ACGC
                      |||||||||||||   ||||
                      GTCTCTAATTTTT   TGCG
                              TGGGG
GAM289   BAL      3' GCAGTTGTTCTTTAATCTCC 2201             AAT TG _
                      GGAGATTAAA  A AC GC
                      ||||||||||  | || ||
                      CCTCTAATTT  T TG CG
                             CT_ GT A
GAM289   BTN3A1   3' ATATTTTTAATCCCGTTA  1355         A
                      TAACGG GATTAAAAATAT
                      |||||| ||||||||||||
                      ATTGCC CTAATTTTTATA

                             _
GAM289   PDE4DIP  3' CGTCATATTCTCAACAGTTTCT 1512         AAA___
                      GGAGATT   AATATGACG
                      |||||||   |||||||||
                      TCTTTGA   TTATACTGC
                             CAACTC
GAM289   LOC200251 3' GCGAGTGCCTGTAATCTCCG 3447          AAAA  GA
                      CGGAGATTA   TAT CGC
                      |||||||||   ||| |||
                      GCCTCTAAT   GTG GCG
                             GTCC  A_
GAM290   CDK10    3' CGGAAGCAGCCCTACAACAAC 2354          TTGCGA
                      GTTGTTGT   CTGCTTCCG
                      ||||||||   |||||||||
                      CAACAACA   GACGAAGGC
                             TCCC__
GAM290   COL1A1   3' CGGAAACAGACAAGCAAC  704          CGA  C
                      GTTGTTTG  CTG TTCCG
                      ||||||||  ||| |||||
                      CAACGAAC  GAC AAGGC
                             A__  A
GAM290   ESPN     3' AAGCTGCTGACGCAAACAACAA 2210             ACT___
              C           GTTGTTGTTTGCG   GCTT
                      |||||||||||   ||||
                      CAACAACAACGC   CGAA
                             AGTCGT
GAM290   GRIA1    3' CAGTGCCAAAAACAACAAC 779          ___ G
                      GTTGTTGTTT  GC ACTG
                      ||||||||||  || ||||
```

```
                        CAACAACAAA  CG TGAC
                            AAC _
GAM290  PLAG1    3' AAGCAGAAAACAAAAACAAC 942        G   CGA_
                        GTTGTT TTTG   CTGCTT
                        |||||| |||| |||||||
                        CAACAA AAAC   GACGAA
                            _   AAAA
GAM290  SORCS1   3' TCAGAAGTTCCAAACAGCAAC 2345        C CT   C
                        GTTGTTGTTG GA  GCTTC GA
                        |||||||||| || ||||| ||
                        CAACGACAAAC CT  TGAAG CT
                            _ __    A
GAM290  BM046    3' AAGCAAGACAACAAC     1830        GCGAC
                        GTTGTTGTTT   TGCTT
                        ||||||||| |||||
                        CAACAACAGA   ACGAA

                            _____
GAM290  KLF12    3' AAGCAGTTGAGTAACAGCAAC 1373        TG_
                        GTTGTTGTT CGACTGCTT
                        ||||||||| |||||||||
                        CAACGACAA GTTGACGAA
                            TGA
GAM290  PSMA6    5' CGGAAGCAGTCGCTGCAAC 2880      TT
                        GTTGT GCGACTGCTTCCG
                        ||||| |||||||||||
                        CAACG CGCTGACGAAGGC
                            T_
GAM290  LOC157292 5' CAGCTCAAAAACAACAAC  3377        GC _
                        GTTGTTGTTT GA CTG
                        ||||||||| || |||
                        CAACAACAAA CT GAC
                            AA  C
GAM291  CELSR3   3' TCCCCAGTGGTGGGTG     825      T T  A
                        CACCCAT CA CTGG GA
                        ||||||| || |||| ||
                        GTGGGTG GT GACC CT
                            _ _  C
GAM291  CMAR     5' CTCCACTTGGAATGGGTACCAC 1195     AC    ATC_
            A           TGTG ACCCATTC  TGGAG
                        |||| |||||||| |||||
                        ACAC TGGGTAAG  ACCTC
                        CA       GTTC
GAM291  FCER2    3' TCTCCAGATGAGAGTACAC 881      _ ACCCA
                        GTG AC   TTCATCTGGAGA
                        ||| ||   |||||||||||
                        CAC TG   GAGTAGACCTCT
                            A A____
GAM291  FCER2    3' TCTCCAGATGAGAGTACAC 882      _ ACCCA
                        GTG AC   TTCATCTGGAGA
                        ||| ||   |||||||||||
```

```
                        CAC TG   GAGTAGACCTCT
                         A A____
GAM291  FCER2    3' TCTCCAGATGAGAGTACAC  883    _ ACCCA
                        GTG AC   TTCATCTGGAGA
                        ||| ||   ||||||||||||
                        CAC TG   GAGTAGACCTCT
                         A A____
GAM291  MEN1     3' CTCCAGAGTGGGTGTCCA  3601   T     TCA
                        TG GACACCCAT  TCTGGAG
                        || |||||||||  |||||||
                        AC CTGTGGGTG  AGACCTC

                          _    ___
GAM291  NCSTN    3' TTCTCCAGGCCCTCAGATGGCA 2979   ACAC    CA____
            CA          GTG  CCATT   TCTGGAGAA
                        |||  |||||   |||||||||
                        CAC  GGTAG   GGACCTCTT
                          ____   ACTCCC
GAM291  RBM10    3' TTCTCCACATGTTGGGTGTCCA 1235   T    TT C
                        TG GACACCCA  CAT TGGAGAA
                        || |||||||||  ||| |||||||
                        AC CTGTGGGT  GTA ACCTCTT
                          _     T_  C
GAM291  TNFSF8   3' GGATGAATGGATGTCCCA  812    T   C
                        TG GACA  CCATTCATCT
                        || ||||  ||||||||||
                        AC CTGT  GGTAAGTAGG
                          C    A
GAM291  YES1     3' TCCTTATGGGGATGGGTGCCAC 1210    A     ATCT__
            A             TGTG CACCCATTC   GGA
                        |||| |||||||||   |||
                        ACAC GTGGGTAGG    CCT
                          C    GGTATT
GAM291  ZNF256   5' TTCTCCACAGCGGGTGTCACA 1247         ATTCATC
                        TGTGACACCC   TGGAGAA
                        ||||||||||   |||||||
                        ACACTGTGGG   ACCTCTT
                          CGAC___
GAM291  BAT8     3' TCCCCAGCATGGATGGCCACA 1325     ACAC     _ A
                        TGTG  CCATTCAT CTGG GA
                        ||||  |||||||| |||| ||
                        ACAC  GGTAGGTA GACC CT
                          C___    C C
GAM291  CPLX1    3' TCTCCGGATGGAATCACA  1318     CACCCA
                        TGTGA   TTCATCTGGAGA
                        |||||   |||||||||||
                        ACACT   AGGTAGGCCTCT
                            A_____
GAM291  DKFZP566K0524 3' TTCCAGTGAAACAGATGTTACA 2855       CCCA_ T
                        TGTGACA   TTCA CTGGAG
                        ||||||   |||| ||||||
```

```
                          ACATTGT    AAGT GACCTT
                           AGACA      _
GAM291  FLJ12891  3' TCTCCAGGGCCACAACTGTCAC 2117        CCCATTCA
            A                 TGTGACA    TCTGGAGA
                          ||||||    |||||||
                          ACACTGT    GGACCTCT
                           CAACACCG
GAM291  GR6       3' CCTGAATGAATGGGTGTCAC 1396            _T
                          GTGACACCCATTCAT C GG
                          |||||||||||||| | ||
                          CACTGTGGGTAAGTA G CC
                            A T
GAM291  KIAA0455  3' CAGATGAATAGTATCACA   2947      C CC
                          TGTGA AC  ATTCATCTG
                          ||||| || |||||||||
                          ACACT TG  TAAGTAGAC
                            A A_
GAM291  KIAA0513  3' TTCCCTGCAATGGGTGCACA 1536      A   _ TCT
                          TGTG CACCCATT CA  GGAG
                          |||| |||||||| || ||||
                          ACAC GTGGGTAA GT  CCTT
                           _        C C__
GAM291  KIAA1655  5' CTCTGAGAAGAGTGTCACA 2753        CCA  A T
                          TGTGACAC  TTC TC GGAG
                          ||||||||  ||| || ||||
                          ACACTGTG  AAG AG TCTC
                            AG_  _ _
GAM291  SCAND2    3' TTCCCCAGCCAGATGGGGTCAC 2338       A    CAT  A
            A                 TGTGAC CCCATT  CTGG GAA
                          |||||| ||||||  |||| |||
                          ACACTG GGGTAG   GACC CTT
                           _   ACC   C
GAM291  WDR5B     3' TCTCCACGTCCAGGTGTACACA 1878      _   CATTC C
                          TGTG ACACC    AT TGGAGA
                          |||| |||||    || ||||||
                          ACAC TGTGG    TG ACCTCT
                           A    ACC__  C
GAM291  LOC146330 5' TCTCCAAGAAGGGTGTCA    3088       A ATC
                          TGACACCC TTC  TGGAGA
                          |||||||| |||  ||||||
                          ACTGTGGG AAG  ACCTCT
                            _  A__
GAM291  LOC148181 5' CTCCAGACCCAGATGGTGTCTC 3117    T   C CA__
            A                 TG GACACC ATT   TCTGGAG
                          || |||||| |||   |||||||
                          AC CTGTGG TAG   AGACCTC
                           T   _  ACCC
GAM291  LOC150271 5' TCTCCAGACTGGTGACACA   3326      A  CATTCA
                          TGTG CACC    TCTGGAGA
                          |||| ||||    ||||||||
```

```
                         ACAC GTGG    AGACCTCT
                          A   TC____
GAM291  LOC150605 5'  TCTCCGGTGGAACCAGTGTCAC 3331        CCA_  T
          A              TGTGACAC  TTCA CTGGAGA
                         ||||||||  |||| |||||||
                         ACACTGTG  AGGT GGCCTCT
                            ACCA  _
GAM291  LOC153277 3'  AGATAAATGTGTGTCACA    3368        C   C
                       TGTGACAC CATT ATCT
                       |||||||| |||| ||||
                       ACACTGTG GTAA TAGA
                          T   A
GAM291  LOC154990 5'  CTCCAGACCCAGATGGTGTCTC 3196     T   C  CA__
          A             TG GACACC ATT   TCTGGAG
                        || |||||| |||   |||||||
                        AC CTGTGG TAG   AGACCTC
                        T   _  ACCC
GAM291  LOC158014 5'  TTCTCCAGATAAGAAAATCACA 3209        CACCCA  C
                        TGTGA    TT ATCTGGAGAA
                        |||||    || |||||||||||
                        ACACT    AA TAGACCTCTT
                         AAAAG_  _
GAM291  LOC158056 5'  TCTCCAGGCCCCAGGTGCCAGC 3210      GA_   CATTCA
          A              TGT  CACC    TCTGGAGA
                         |||  ||||    ||||||||
                         ACG  GTGG    GGACCTCT
                          ACC   ACCCC_
GAM291  LOC202908 3'  CTCCAGACCCAGATGGTGTCTC 3462     T   C  CA__
          A             TG GACACC ATT   TCTGGAG
                        || |||||| |||   |||||||
                        AC CTGTGG TAG   AGACCTC
                        T   _  ACCC
GAM291  LOC220143 5'  CTCCCGAGATGGTGTCACA    3610        CAT  A  T
                       TGTGACACC  TC TC GGAG
                       |||||||||  || || ||||
                       ACACTGTGG  AG AG CCTC
                          T__  _  C
GAM291  LOC220143 5'  CTCCCGAGATGGTGTCACA    3611        CAT  A  T
                       TGTGACACC  TC TC GGAG
                       |||||||||  || || ||||
                       ACACTGTGG  AG AG CCTC
                          T__  _  C
GAM291  LOC222057 3'  CTCCAGACCCAGATGGTGTCTC 3576     T   C  CA__
          A             TG GACACC ATT   TCTGGAG
                        || |||||| |||   |||||||
                        AC CTGTGG TAG   AGACCTC
                        T   _  ACCC
GAM291  LOC255096 3'  CTCATGGATGAGTACCACA    3744     AC  C    CTG
                       TGTG AC CATTCAT  GAG
                       |||| || |||||||  |||
```

```
                        ACAC  TG GTAGGTA   CTC
                        CA  A        ___
GAM291  LOC255975 5' CTCCAGACCCAGATGGTGTCTC 3686    T    C  CA__
      A                 TG GACACC ATT   TCTGGAG
                        || |||||| |||   |||||||
                        AC CTGTGG TAG   AGACCTC
                        T   _  ACCC
GAM291  LOC256878 3' CTCCAGACCCAGATGGTGTCTC 3720    T    C  CA__
      A                 TG GACACC ATT   TCTGGAG
                        || |||||| |||   |||||||
                        AC CTGTGG TAG   AGACCTC
                        T   _  ACCC
GAM291  LOC51333 3' TTCTCCAGGCTCAGGTGCCA 1705    A   CATTCA
                        TG CACC       TCTGGAGAA
                        || ||||       |||||||||
                        AC GTGG       GGACCTCTT
                        C   ACTC__
GAM291  LOC89919 3' TCAGAACAGATGGATGTCACA 2580        C   CA_
                        TGTGACA CCATT  TCTGG
                        ||||||| |||||  |||||
                        ACACTGT GGTAG  AGACT
                        A   ACA
GAM292  IL2RA   3' TCCACCCTATATGTAGTATAAA 739        _  CA  CAA
      GA                TCTTT TAC ACA  AGGGTGGA
                        ||||| ||| |||  ||||||||
                        AGAAA ATG TGT  TCCCACCT
                        T  A_  ATA
GAM292  INPP5D  3' CCATCGTGCTGGTAGAAGA  3263        A  AAAG
                        TCTTTTACCA CAC   GGTGG
                        |||||||||| |||   |||||
                        AGAAGATGGT GTG   CTACC
                        C  ____
GAM292  PLXNA1  3' TCCACCCTTGCCCTCAGCAAGA 2941        ACCAACACA
      GA                TCTTTT       AAGGGTGGA
                        ||||||       |||||||||
                        AGAGAA       TTCCCACCT
                        CGACTCCCG
GAM292  PRKCN   3' TCTTTAAGTCGTGTTTGTAAAA 1253        C   AAAGGGT
      GA                TCTTTTAC AACAC    GGA
                        |||||||| |||||    |||
                        AGAAAATG TTGTG    TCT
                        T   CTGAATT
GAM292  BHMT    3' CCACTTTTCTACCAGTAAAAGA 849        CAACACA
                        TCTTTTAC     AAGGGTGG
                        ||||||||     ||||||||
                        AGAAAATG     TTTTCACC
                        ACCATC_
GAM292  DKFZP434B044 3' CCACCCCTTTAAGGAGTTGGTA 2211        AC___   _
      AAA               TTTTACCAAC   AAAGGG TGG
                        |||||||||   |||||| |||
```

```
                              AAAATGGTTG   TTTCCC ACC
                                AGGAA      C
GAM292  FLJ10458  3' CCCCGTGTTGGTAAGAGA    1777           AAA
                       TCTTTTACCAACAC  GGG
                       |||||||||||||| |||
                       AGAGAATGGTTGTG  CCC
                             C__
GAM292  FLJ20272  3' CACCTGCTGGTAAAAGA     1744        ACACAAA
                       TCTTTTACCA    GGGTG
                       ||||||||||    |||||
                       AGAAAATGGT    TCCAC
                           CG_____
GAM292  FLJ23598  3' TCCACCCTGGGTAATAAAAGA 3665       CCAAC AA
                       TCTTTTA   AC AGGGTGGA
                       ||||||||  || ||||||||
                       AGAAAAT   TG TCCCACCT
                         AA___ GG
GAM292  KIAA1755  3' CCACCCTTCATACTGGCCAGAG 2595     TA  ACACA
                       CTTT CCA   AAGGGTGG
                       |||| |||   ||||||||
                       GAGA GGT   TTCCCACC
                         CC  CATAC
GAM292  MGC21621  3' CCCTAGGCTGGTTGGTAAAAGA 2508          A A___
                       TCTTTTACCAAC CA   AGGG
                       |||||||||||| ||   ||||
                       AGAAAATGGTTG GT   TCCC
                              _ CGGA
GAM292  MGC3077   3' TCCTTGCTCTGGTAAAAGA    2048        ACACA
                       TCTTTTACCA    AAGGG
                       ||||||||||    |||||
                       AGAAAATGGT    TTCCT
                           CTCG_
GAM292  MGC4707   3' CCCTCATGTCTGGTAAAA     2055       _  CAA
                       TTTTACCA ACA  AGGG
                       |||||||| |||  ||||
                       AAAATGGT TGT  TCCC
                         C  AC_
GAM292  MGC5149   3' TCCTCATTGGTAAAAGA      2940        CACAA
                       TCTTTTACCAA   AGGG
                       |||||||||||   ||||
                       AGAAAATGGTT   TCCT
                           AC___
GAM292  RAB3IL1   3' CAGGCTTTGTTGGTAAAA     1448       CA GG
                       TTTTACCAACA AAG TG
                       ||||||||||| ||| ||
                       AAAATGGTTGT TTC AC
                            __ GG
GAM292  LOC119369 5' TCCACCCTATTTCTGGAAAAA  3026      A  ACACAA
                       TTTT CCA     AGGGTGGA
                       |||| |||     ||||||||
```

```
                    AAAA GGT    TCCCACCT
                     A  CTTTA_
GAM292  LOC150035 5' TTGTAGTACTGGTAAAAGA 3321        __ _
                    TCTTTTACCA AC ACAA
                    ||||||||| || ||||
                    AGAAAATGGT TG TGTT
                       CA  A
GAM292  LOC219649 5' TCCACCCTTTGTGCTTGGT 3586        __
                    ACCAA CACAAAGGGTGGA
                    ||||| |||||||||||||
                    TGGTT GTGTTCCCACCT
                       TC
GAM292  LOC221688 5' TCCAACCACATTGGTAAAA 3617        CACAAA G
                    TTTTACCAA   GG TGGA
                    |||||||||   || ||||
                    AAAATGGTT   CC ACCT
                        ACA___ A
GAM293  RLBP1    5' CAGGTACCAGGTAGCCCCA 729    A    CGACA G
                    TG GGCTACCT   TAC TG
                    || ||||||||   ||| ||
                    AC CCGATGGA   ATG AC
                     C    CC___  G
GAM293  MGC23280 3' GCTGGTATCGAGGTGCCCCA 2493   A T    CA GT
                    TG GGC ACCTCGA TAC GT
                    || ||| ||||||| ||| ||
                    AC CCG TGGAGCT ATG CG
                     C _    __ GT
GAM293  LOC113523 3' TATGCCGAAATAGCTTCA 2966        CC  A
                    TGAGGCTA TCG CATA
                    |||||||| ||| ||||
                    ACTTCGAT AGC GTAT
                        AA  C
GAM293  LOC150157 3' CACACGTATGCCATGGCC 3325        CCTCGA
                    GGCTA   CATACGTGTG
                    |||||   |||||||||||
                    CCGGT   GTATGCACAC
                     ACC___
GAM293  LOC196890 3' CACACGTATGCCATGGCC 3468        CCTCGA
                    GGCTA   CATACGTGTG
                    |||||   |||||||||||
                    CCGGT   GTATGCACAC
                     ACC___
GAM294  ARHGAP6  3' TGTATTCTGTAACAGATTA 807     CA
                    TAA TGTTACAGAATATA
                    ||| |||||||||||||
                    ATT ACAATGTCTTATGT
                      AG
GAM294  ARHGAP6  3' TGTATTCTGTAACAGATTA 1450    CA
                    TAA TGTTACAGAATATA
                    ||| |||||||||||||
```

```
                         ATT  ACAATGTCTTATGT
                          AG
GAM294  ATP11B   3' TAATTTGAATCTGAACATGTTA 3158       A   ATA
                          TAACATGTT CAGA   TAAATTA
                          |||||||| |||| ||||||
                          ATTGTACAA GTCT  GTTTAAT
                            _  AA_
GAM294  BNC      3' TAATTCTTGTTCTGTAACATG 850            TA
                          CATGTTACAGAATA AATTA
                          |||||||||||| |||||
                          GTACAATGTCTTGT TTAAT
                            TC
GAM294  CREBL2   3' TAATTTATATTCTTTCCATGT 817        TTAC
                          ACATG  AGAATATAAATTA
                          |||||  |||||||||||
                          TGTAC  TCTTATATTTAAT
                          CTT_
GAM294  GCNT1    3' TAATTTATATTCTGCTCTAATA 830            ___
                          TGTTA  CAGAATATAAATTA
                          |||||  |||||||||||
                          ATAAT  GTCTTATATTTAAT
                          CTC
GAM294  MBNL     3' TATACTGTATAACATGTTA 1938          __   A
                          TAACATGT  TACAG ATA
                          |||||||| ||||| |||
                          ATTGTACA ATGTC TAT
                           AT   A
GAM294  AFAP     3' TAATTTATATCTGTACATATTA 1952    C   T   A
                          TAA ATGT ACAGA TATAAATTA
                          ||| |||| |||| |||||||||
                          ATT TACA TGTCT ATATTTAAT
                           A   _   _
GAM294  LOC148195 3' TAATTTATCTGTTAACATGTT 3299        _  ATA
                          AACATGTTA CAGA   TAAATTA
                          ||||||||| |||| |||||||
                          TTGTACAAT GTCT  ATTTAAT
                           T   ___
GAM295  ATP6V1A1 3' GAGGTTTCTCAGAATATCT 847            CGCT
                          AGATATTCTGAG  AACCTT
                          ||||||||||||  ||||||
                          TCTATAAGACTC  TTGGAG
                           T___
GAM295  DAP      3' AGGTTAGGAGAAAACCTCA 2954      ATA  GAGCG
                          TGAG  TTCT   CTAACCT
                          ||||  ||||   |||||||
                          ACTC  AAGA   GATTGGA
                           CAA  G____
GAM295  LIFR     3' AAGTATAGTGACTCAGAATCCT 919       AT    _   AC
             CA             TGAG  ATTCTGAG CGCTA CTT
                          ||||  |||||||| ||||| |||
```

```
                          ACTC  TAAGACTC GTGAT  GAA
                          C_        A      AT
GAM295  RECK      3' AGCTTTCAGAATATGTCA   1941      G        C
                          TGA ATATTCTGAG GCT
                          ||| |||||||||| |||
                          ACT TATAAGACTT CGA
                          G       T
GAM295  SLC13A3  3' AAGGCCAGGGTAAAATGTCTCA 2570         CTGA  G  AA
                          TGAGATATT  GC CT  CCTT
                          |||||||||  || ||  ||||
                          ACTCTGTAA  TG GA  GGAA
                          AA__  G  CC
GAM295  TEM8     3' GGGGCCAGAATATCTCA      2236           A  G
                          TGAGATATTCTG GC CT
                          |||||||||||| || ||
                          ACTCTATAAGAC CG GG
                          _  G
GAM295  DKFZp547I224 3' GTTAGCAAGGATATCCA   1903     A      GAGC
                          TG GATATTCT   GCTAAC
                          || |||||||||   ||||||
                          AC CTATAGGA   CGATTG
                          _        A___
GAM295  OLFM3    3' AGCATCATCCTCAAATATCTCA 3232         C   C_____
                          TGAGATATT TGAG   GCT
                          ||||||||| ||||    |||
                          ACTCTATAA ACTC   CGA
                          _  CTACTA
GAM295  TSARG1   3' AGATGTTCAGAATATCTCA   2470               _
                          TGAGATATTCTGAGCG CT
                          |||||||||||||||| ||
                          ACTCTATAAGACTTGT GA
                          A
GAM295  LOC114987 3' AGGCCAAAAATATCTCA    2517          C_ A  G
                          TGAGATATT  TG GC CT
                          |||||||||  || || ||
                          ACTCTATAA  AC CG GA
                          AA _  _
GAM295  LOC152445 5' AGGCTCCGCAAATATCTCA   3360          CT__  G
                          TGAGATATT  GAGC CT
                          |||||||||  |||| ||
                          ACTCTATAA  CTCG GA
                          ACGC  _
GAM296  FLJ20139 5' ACCATATCAATCCATATA   1737       CAA
                          TGTA  ATTGATATGGT
                          ||||  ||||||||||
                          ATAT  TAACTATACCA
                          ACC
GAM296  LOC91796 3' ACGTTTTACAATCAATTTGTAC 2785              A  GTCGT
          A                 TGTACAAATTGAT TG    CGT
                          |||||||||||| ||     |||
```

```
                              ACATGTTTAACTA AC   GCA
                              _ ATTTT
GAM297  CMAR    3' CCCCATCGCCTACTCCATG 1194        A  AGA
                              CATGGAGTAG TGAT  GGGG
                              |||||||||| |||| ||||
                              GTACCTCATC GCTA  CCCC
                                 C     ___
GAM297  CRHR1   3' TTCCCCTCACTTAACCACCCCA 1105   A AGA  TA
        T                     ATGG GT  TGA GAGGGGAA
                              |||| || ||| ||||||||
                              TACC CA  ATT CTCCCCTT
                                C CCA  CA
GAM297  DTR     3' TTCCCCTCCACCAAACCCCA 874    A AGA ATA
                              TGG GT  TG GAGGGGAA
                              ||| || || ||||||||
                              ACC CA  AC CTCCCCTT
                                C A__  CAC
GAM297  FGF5    3' TCCCCTCTCCACCCACCCCA 1117   A AGA AT
                              TGG GT  TG AGAGGGGA
                              ||| || || ||||||||
                              ACC CA  AC TCTCCCCT
                                C CCC C_
GAM297  FGF5    3' TCCCCTCTCCACCCACCCCA 2315   A AGA AT
                              TGG GT  TG AGAGGGGA
                              ||| || || ||||||||
                              ACC CA  AC TCTCCCCT
                                C CCC C_
GAM297  GAA     3' CCCCTCCATCTGTTCC      713        ATA
                              GGAGTAGATG GAGGGG
                              |||||||||| ||||||
                              CCTTGTCTAC CTCCCC
                                    ___
GAM297  GNL1    3' TCCCCTCTGCCACCCCA    3550    A AGAT A
                              TGG GT  G TAGAGGGGA
                              ||| || | |||||||||
                              ACC CA  C GTCTCCCCT
                                C ____ C
GAM297  GNL1    3' TCCCCTCTGCCACCCCA    3748    A AGAT A
                              TGG GT  G TAGAGGGGA
                              ||| || | |||||||||
                              ACC CA  C GTCTCCCCT
                                C ____ C
GAM297  KCNA6   3' TCCCCTCCCTACCTCATG   915     GA  ATGATA
                              CATG GTAG   GAGGGGA
                              |||| ||||   |||||||
                              GTAC CATC   CTCCCCT
                                TC  C_____
GAM297  LDHB    5' CCCCATACACCATCTATTCCAT 918            ATAGA_
                              ATGGAGTAGATG   GGGG
                              |||||||||||   ||||
```

```
                        TACCTTATCTAC    CCCC
                               CACATA
GAM297  LTBP2   3' TTCCCCTCCACTCAGAAACCCC 740      A AGA  TA_
                        GG GT  TGA  GAGGGGAA
                        || || ||| ||||||||
                        CC CA  ACT  CTCCCCTT
                         C AAG  CAC
GAM297  MARK1   5' CCCCTCCTCTTACTCCG    1856       AT TA
                        TGGAGTAG GA GAGGGG
                        |||||||| || ||||||
                        GCCTCATT CT CTCCCC
                              __ C_
GAM297  PLAT    3' TTCCCCTTTCCCCACTCCCTG 2306    T   AGAT TA
                        CA GGAGT   GA GAGGGGAA
                        || |||||   || ||||||||
                        GT CCTCA   CT TTCCCCTT
                         C    CCC_ __
GAM297  PLAT    3' TTCCCCTTTCCCCACTCCCTG 788     T   AGAT TA
                        CA GGAGT   GA GAGGGGAA
                        || |||||   || ||||||||
                        GT CCTCA   CT TTCCCCTT
                         C    CCC_ __
GAM297  PTGIR   3' CCCCTCTACCAAGCCACTCCA 791        AGA_ A
                        TGGAGT   TG TAGAGGGG
                        ||||||   || ||||||||
                        ACCTCA   AC ATCTCCCC
                           CCGA C
GAM297  PXN     3' CCCCTCTTTCACTTCAT     965       AGAT T
                        ATGGAGT   GA AGAGGGG
                        |||||||   || |||||||
                        TACTTCA   CT TCTCCCC
                           ____ T
GAM297  RNH     5' TCCCCTCTACCAAGGGTTCC  2536      AGA A
                        GGAGT  TG TAGAGGGGA
                        |||||  || |||||||||
                        CCTTG  AC ATCTCCCCT
                         GGA  C
GAM297  SCN4A   3' TCCCTTCTCATCTCCCCA    730       AGT   TA
                        TGG  AGATGA GAGGGGA
                        |||  |||||| |||||||
                        ACC  TCTACT CTTCCCT
                         CC_      __
GAM297  SH3GL1  3' TCCCTTCCCCACTCCATG    982         AGATGATA
                        CATGGAGT     GAGGGGA
                        ||||||||     |||||||
                        GTACCTCA     CTTCCCT
                            CCC_____
GAM297  ZNF261  3' TTCCCCTCTATTGTTCCCC   1184     AGTA TG
                        GG  GA ATAGAGGGGAA
                        ||  || |||||||||||
```

```
                        CC   TT TATCTCCCTT
                        CC__ GT
GAM297 AKAP3   3' CCCCTCTATATCCTC      1300     TA   A
                        GAG  GATG TAGAGGGG
                        ||| |||| ||||||||
                        CTC  CTAT ATCTCCCC


                              __  _
GAM297 C3F     3' TCCCCTCTGATTCCCCCATG 1246      AGTA TGA
                        CATGG  GA  TAGAGGGGA
                        |||||  ||  |||||||||
                        GTACC  CT  GTCTCCCT
                          CC__ TA_
GAM297 CL24751 5' CTCCTTCATCTACTCC      2698       TAG
                        GGAGTAGATGA  AGGGG
                        ||||||||||| |||||
                        CCTCATCTACT  TCCTC


                             ___
GAM297 DIS3    3' TTCCCCTAAGTTCTATTCCAT 1597       TGATAG
                        ATGGAGTAGA   AGGGGAA
                        ||||||||||   |||||||
                        TACCTTATCT   TCCCCTT
                          TGAA__
GAM297 FLJ10700 3' CCTTCATCCACTCCATG   1794     A   TAG
                        CATGGAGT GATGA  AGG
                        |||||||| ||||| |||
                        GTACCTCA CTACT  TCC
                              C    ___
GAM297 FLJ13102 3' TCCCCTCTACCAATCCCTG 2104   T GTAGA A
                        CA GGA   TG TAGAGGGGA
                        || |||   || |||||||||
                        GT CCT   AC ATCTCCCCT
                          C A____  C
GAM297 FLJ32978 3' TCCCATTGGTCACCTTACTCCA 2488       A_  AGAG
                        TGGAGTAG TGAT  GGGA
                        |||||||| ||||  ||||
                        ACCTCATT ACTG  CCCT
                          CC  GTTA
GAM297 HSPB7   3' TTCCCCTCTACCAGCCTCCA 1499      TAGA A
                        TGGAG  TG TAGAGGGGAA
                        |||||  || ||||||||||
                        ACCTC  AC ATCTCCCCTT
                          CG__  C
GAM297 HTCD37  3' TTCCCCTTTTTCCTACCCCA 2796     A  AT T
                        TGG GTAG GA AGAGGGGAA
                        ||| |||| || |||||||||
                        ACC CATC CT TTTCCCCTT
                          C   __ T
GAM297 KIAA0280 3' TTCCCCTCCATCTGATCC   3537     G    ATA
                        GGA TAGATG  GAGGGGAA
                        ||| ||||||  |||||||
```

```
                      CCT GTCTAC  CTCCCCTT
                       A     ___
GAM297 KIAA0450 5' TCCCCTCTACTACCCC    1511    A   ATGA
                      GG GTAG   TAGAGGGGA
                      || |||| |||||||||
                      CC CATC   ATCTCCCCT
                       C     ____
GAM297 KIAA0731 3' CCCCTCCTCTCTCCATG    2767      T TGATA
                      CATGGAG AGA   GAGGGG
                      ||||||| |||   ||||||
                      GTACCTC TCT   CTCCCC
                       _    C____
GAM297 KIAA1462 3' TCCCCTCTGTGTCTCCATG   3523        TAGATG
                      CATGGAG   ATAGAGGGGA
                      |||||||   ||||||||||
                      GTACCTC   TGTCTCCCCT
                        TG____
GAM297 LIMK2    3' CCCCTTTCTACTCCA      1710        TGATA
                      TGGAGTAGA   GAGGGG
                      |||||||||   ||||||
                      ACCTCATCT   TTCCCC

                        _____
GAM297 LIMK2    3' CCCCTTTCTACTCCA      1225        TGATA
                      TGGAGTAGA   GAGGGG
                      |||||||||   ||||||
                      ACCTCATCT   TTCCCC

                        _____
GAM297 MGC2541  5' TCCCCTTCCTAGCTCCATG   2385        _ ATGATA
                      CATGGAGT AG    GAGGGGA
                      |||||||| ||    |||||||
                      GTACCTCG TC    TTCCCCT
                        A C_____
GAM297 MGC3101  3' CCCTTCTTCTACTCCA     2046        TGAT
                      TGGAGTAGA   AGAGGGG
                      |||||||||   |||||||
                      ACCTCATCT   TCTTCCC

                        ____
GAM297 NCOA2    3' TTCCCCTCTCTCATTCCCCAT 1307     AGTA   T
                      ATGG   GATGA AGAGGGGAA
                      ||||   ||||| ||||||||||
                      TACC   TTACT TCTCCCCTT
                        CC__    C
GAM297 RBM14    3' TTCCCCTCTACCCTGCCTCC  1289     _ ATGA
                      GGAG TAG   TAGAGGGGAA
                      |||| |||   ||||||||||
                      CCTC GTC   ATCTCCCCTT
                       C CC__
GAM297 SCYA5    3' TTCCCCTCACTATCCTACCCCA 979    A  AT  __
                      TGG GTAG GATA GAGGGGAA
                      ||| |||| |||| ||||||||
```

```
                    ACC CATC CTAT CTCCCCTT
                     C  __   CA
GAM297 U5-116KD 3' CCCCTTGCTCCCACTCCATG  1095      AGAT TA
                    CATGGAGT  GA GAGGGG
                    |||||||| || ||||||
                    GTACCTCA  CT TTCCCC
                        CC__ CG
GAM297 WSB1     3' TCCCCCACCTACTCCA     2429      A ATAGA
                    TGGAGTAG TG   GGGGA
                    |||||||| ||   |||||
                    ACCTCATC AC   CCCCT
                        C _____
GAM297 LOC144501 3' TCCCCTTCCTCCCTCCATG  3268       TAGAT TA
                    CATGGAG  GA GAGGGGA
                    ||||||| || |||||||
                    GTACCTC  CT TTCCCCT
                        C____ CC
GAM297 LOC146940 3' TCCCTTCCCCACTCCATG   3101       AGATGATA
                    CATGGAGT    GAGGGGA
                    ||||||||    |||||||
                    GTACCTCA    CTTCCCT
                        CCC_____
GAM297 LOC197003 3' TCCCCTTCTCCACTCC     3418     A T TAG
                    GGAGT GA GA  AGGGGA
                    ||||| || ||  ||||||
                    CCTCA CT CT  TCCCCT
                        C _  ___
GAM297 LOC200953 5' CCCCTCCACCTGCTCCA    3482      A ATA
                    TGGAGTAG TG  GAGGGG
                    |||||||| ||  ||||||
                    ACCTCGTC AC  CTCCCC
                        C ___
GAM297 LOC257541 3' TCCCCTCTGCCACCCCA    3746    A AGAT A
                    TGG GT  G TAGAGGGGA
                    ||| ||  | |||||||||
                    ACC CA  C GTCTCCCCT
                        C ____ C
GAM298 G2       5' TGGGACAGCCGACTT      2756         ATCTTA
                    AAGTTGGCTGTC   CCA
                    |||||||||||    |||
                    TTCAGCCGACAG    GGT
                         _____
GAM298 REM      5' ATTGGCTGACAGCCAATT   1462       TCTTA
                    AGTTGGCTGTCA   CCAAT
                    ||||||||||||   |||||
                    TTAACCGACAGT   GGTTA
                        C____
GAM298 LOC90321 3' GTAAGATGACAGGGCTGACTT 2631      TG __
                    AAGT GCT GTCATCTTAC
                    |||| ||| ||||||||||
```

```
                              TTCA CGG  CAGTAGAATG
                              GT   GA
GAM298  LOC91650 5'  ATTGGTAAACAACCAAT    2766        C  CATC
                              GTTGG TGT   TTACCAAT
                              ||||| |||   ||||||||
                              TAACC ACA   AATGGTTA
                              A    ____
GAM299  CD28    3'  ATAATTAATGGTACTCCTATAA 1274         ATAC
          TT              AATTATAG  GCTATTAATTAT
                              ||||||||  |||||||||||
                              TTAATATC  TGGTAATTAATA
                              CTCA
GAM299  ABCA6   3'  ATAATTAATAGTATGTTTA  2374      CG
                              TAGATA CTATTAATTAT
                              |||||| ||||||||||
                              ATTTGT GATAATTAATA
                              AT
GAM299  FLJ21302 3' GTAGCACAATCTATAATT   2021         AC_
                              AATTATAGAT GCTAT
                              |||||||||| |||||
                              TTAATATCTA CGATG
                              ACA
GAM299  SLC7A11 3'  TAATAGTCCCATATCTGTAAT 1492          C___
                              ATTATAGATA  GCTATTA
                              ||||||||||  |||||||
                              TAATGTCTAT  TGATAAT
                              ACCC
GAM300  AP2B1   3'  AGTGTTACACTGTTTGA    814         TCC
                              TTAGATA GTAACACT
                              ||||||| ||||||||
                              AGTTGT CATTGTGA
                              CA_
GAM300  GOT1    3'  TGGTAAGAAGGATATTTAA  897          GTAACAC
                              TTAGATATCC    TACCA
                              ||||||||||    |||||
                              AATTTATAGG    ATGGT
                              AAGA___
GAM300  ZNF14   3'  TGGTAGTGCATGCCTCTAA  1934        TATC AA
                              TTAGA  CGT CACTACCA
                              |||||  ||| ||||||||
                              AATCT  GTA GTGATGGT
                              CC__  C_
GAM300  FLJ11827 3' TAGTGTTTAGAATATCTAA  2136         CCGT
                              TTAGATAT AACACTA
                              |||||||| |||||||
                              AATCTATA TTGTGAT
                              AGAT
GAM300  HEYL    3'  TGGGTTGTTGCGGACATC   1507     A      CTA
                              GAT TCCGTAACA CCA
                              ||| ||||||||| |||
```

```
                         CTA AGGCGTTGT  GGT
                         C          TG_
GAM300  LOC158722 5' TGGTAGTGCAGCTCATCTGA 3226      ATCC AA
                         TTAGAT  GT CACTACCA
                         ||||||  || |||||||||
                         AGTCTA  CG GTGATGGT
                         CT__ AC
GAM301  ADAMTS5   3' AAAATTCATAGTAATCCTGCCA 1350      A      GCTC
                         TGGTA GATTACTG  GTTTT
                         ||||| ||||||||  |||||
                         ACCGT CTAATGAT  TAAAA
                         C      ACT_
GAM301  SLC38A4   3' GACGTTTACCAGTAATATCACC 1774      AAG      CT__
              A           TGGT  ATTACTGG  CGTT
                          ||||  ||||||||  ||||
                         ACCA  TAATGACC  GCAG
                         CTA      ATTT
GAM302  SLC19A2   3' ATGGAATGTGGTACAAATTGTT 2835      G   A  AAAT
                         AA AATTT TAT  CATTCCAT
                         || ||||| |||  |||||||||
                         TT TTAAA ATG  GTAAGGTA
                         G   C  GT__
GAM302  COLEC12   3' ATGGACTGAATCACATAGATTC 2165      ATAAA  T
              T          AGAATTTAT   TCA TCCAT
                         |||||||||   ||| |||||
                         TCTTAGATA   AGT AGGTA
                         CACTA  C
GAM302  COLEC12   3' ATGGACTGAATCACATAGATTC 2395      ATAAA  T
              T          AGAATTTAT   TCA TCCAT
                         |||||||||   ||| |||||
                         TCTTAGATA   AGT AGGTA
                         CACTA  C
GAM302  SH3BGRL   3' ATGGAATGATATATCCAAGTTC 2615      AT  A
                         GAATTT ATA ATCATTCCAT
                         |||||| ||| ||||||||||
                         CTTGAA TAT TAGTAAGGTA
                         CC  A
GAM302  LOC150848 5' GAATGATTTGGAGTTCTT   3334      ATA
                         AAGAATTT  TAAATCATTC
                         ||||||||  ||||||||||
                         TTCTTGAG  GTTTAGTAAG
                             ___
GAM302  LOC219846 3' ATGAAATGATTTTTATAATTCT 3504      T  T    C
                         AGAATT ATA AAATCATT CAT
                         |||||| ||| |||||||| |||
                         TCTTAA TAT TTTAGTAA GTA
                         _ T    A
GAM303  DRD1      3' ATTAACTCCGTTTCCAAATACA 774       GCTCCT
                         TGTAT   AGCGGAGTTAAT
                         |||||   |||||||||||
```

```
                         ACATA   TTGCCTCAATTA
                         AACCT_
GAM303  KIAA0182 3' AAGTCCTAGGAGCACACA   2931      A      GC  G
                         TGT TGCTCCTA GGA TT
                         ||| |||||||| ||| ||
                         ACA ACGAGGAT CCT AA
                           C        G
GAM303  SSH2     3' AGCCCCAGGAGCATACA    2626          AGC  A
                         TGTATGCTCCT GG GTT
                         ||||||||||| || |||
                         ACATACGAGGA CC CGA
                            C__ _
GAM303  LOC90918 5' ATTAAATCCAGGAACATATA 2687      C  AGC  G
                         TGTATG TCCT  GGA TTAAT
                         |||||| ||||  ||| |||||
                         ATATAC AGGA  CCT AATTA
                           A    ___ A
GAM304  PAFAH1B2 3' ACATTCATTGAATTATTATCAC 937      A           _
        TG            CAGT ATAATAATTCAGT AATGT
                         |||| ||||||||||| |||||
                         GTCA TATTATTAAGTTA TTACA
                            C         C
GAM305  GL004    3' CGACAGAATAAGGTACAAATGT 2736        A  G  C_  A
        AG                CTACATTT TAT TT  TCT TCG
                         |||||||| ||| ||  ||| |||
                         GATGTAAA ATG AA  AGA AGC
                            C  G  TA  C
GAM305  KIAA1336 3' CGATTTTCATATAAATGTATGA 2942     _       TTCTCT
                         TC TACATTTATATG    ATCG
                         || |||||||||||    ||||
                         AG ATGTAAATATAC    TAGC
                            T       TTT___
GAM305  LOC147711 3' GAGAAAAACCATATAAATG   3112           ____
                         CATTTATATG  TTCTC
                         ||||||||||  |||||
                         GTAAATATAC  AAGAG
                            CAAA
GAM306  B3GALT3  3' TACTACACTGCCAGTTGTA   1058      ATA
                         TACAA  GCAGTGTAGTG
                         |||||  |||||||||||
                         ATGTT  CGTCACATCAT
                            GAC
GAM306  CSNK1G3  3' TACTGATGGTACTGTTATT   1106          TA  G
                         AATAGCAGTG GT CAGTA
                         |||||||||| || |||||
                         TTATTGTCAT TA GTCAT
                            GG _
GAM306  DSC3     3' TACTGCACTACCAAATTCATTT 2061        AGCAGT_
        G                 CAAAT   GTAGTGCAGTA
                         |||||   |||||||||||
```

```
                    GTTTA    CATCACGTCAT
                 CTTAAAC
GAM306  DSC3    3' TACTGCACTACCAAATTCATTT 872      AGCAGT_
     G              CAAAT    GTAGTGCAGTA
                 |||||    ||||||||||
                    GTTTA    CATCACGTCAT
                 CTTAAAC
GAM306  STK24   3' CAGAACACTCCTATTTGTA 1037      C   AG
                    TACAAATAG AGTGT  TG
                 |||||||||| ||||| ||
                    ATGTTTATC TCACA  AC
                       C   AG
GAM306  SUV39H2 3' TACTCACTGTACTTGTA    2080     ATA    T
                    TACAA   GCAGTG AGTG
                 |||||  |||||| ||||
                    ATGTT   TGTCAC TCAT
                       CA_    _
GAM306  TAC1    3' TATTACACTGTATTTGTA 1456       G
                    TACAAATA CAGTGTAGTG
                 |||||||| ||||||||||
                    ATGTTTAT GTCACATTAT
                                 _
GAM306  TAC1    3' TATTACACTGTATTTGTA 1457       G
                    TACAAATA CAGTGTAGTG
                 |||||||| ||||||||||
                    ATGTTTAT GTCACATTAT
                                 _
GAM306  TAC1    3' TATTACACTGTATTTGTA 1458       G
                    TACAAATA CAGTGTAGTG
                 |||||||| ||||||||||
                    ATGTTTAT GTCACATTAT
                                 _
GAM306  TAC1    3' TATTACACTGTATTTGTA 996        G
                    TACAAATA CAGTGTAGTG
                 |||||||| ||||||||||
                    ATGTTTAT GTCACATTAT
                                 _
GAM306  UBQLN1  3' TACTGCATGCATCACTTCTG 1452     C  TA__
                    TAG AGTG   GTGCAGTA
                 ||| ||||   ||||||||
                    GTC TCAC   TACGTCAT
                     T   TACG
GAM306  ZNF207  3' GCTTACATTGCTATTTGTA 1023               T
                    TACAAATAGCAGTGTAG GC
                 |||||||||||||||| ||
                    ATGTTTATCGTTACATT CG
                                 _
GAM306  AKAP12  3' TACTACATGCTTTTTGTA 1185       T  G
                    TACAAA AGCA TGTAGTG
                 |||||| |||| |||||||
```

```
                    ATGTTT TCGT ACATCAT
                       T    _
GAM306  AKAP12   3'  TACTACATGCTTTTTGTA    2481        T    G
                    TACAAA AGCA TGTAGTG
                    ||||||  ||||  |||||||
                    ATGTTT TCGT ACATCAT
                       T    _
GAM306  FLJ10352 3'  CACTACAATTATGCTTTTGTA 2232        T    G___
                    TACAAA AGCA  TGTAGTG
                    ||||||  ||||   |||||||
                    ATGTTT TCGT   ACATCAC
                       _      ATTA
GAM306  FLJ11222 3'  CACTACAGAGCACTGTTTG   1819        __   AG
                    CAAATA GC TGTAGTG
                    ||||||  ||  |||||||
                    GTTTGT CG ACATCAC
                       CA  AG
GAM306  FLJ14641 3'  TACTGCCTGTGCTGCTA    2284       TG   T
                    TAGCAG  TAG GCAGTA
                    ||||||   |||  ||||||
                    ATCGTC  GTC CGTCAT
                       GT    _
GAM306  FLJ23537 3'  ACTGCAGTACTGTTTGTA    2105        GCAGT  G
                    TACAAATA   GTA TGCAGT
                    ||||||||    |||  ||||||
                    ATGTTTGT   CAT ACGTCA
                       _____   G
GAM306  KIAA1161 5'  ACTGCACTAACCCATTTGTG  3212        AGCA  G
                    TACAAAT   GT TAGTGCAGT
                    ||||||    ||  |||||||||
                    GTGTTTA   CA ATCACGTCA
                       CC__   _
GAM306  MGC10646 3'  CACTACGCTGCCATTTTA    2270     C    A
                    A AAAT GCAGTGTAGTG
                    | ||||  |||||||||||
                    A TTTA CGTCGCATCAC
                       T    C
GAM306  MLL5     3'  TACAGTCTCACACTGCTATCGT 3644    AA       _ T A
                 A         TAC  ATAGCAGTGT AG GC GTA
                    ||||  |||||||||| || || |||
                    ATG  TATCGTCACA TC TG CAT
                       C_     C  _ A
GAM306  ZAK      3'  ACTGCACATATTGCTTTTG   2426      T      A
                    CAAA AGCAGTGT GTGCAGT
                    |||| ||||||||  ||||||
                    GTTT TCGTTATA CACGTCA
                       _      _
GAM306  ZNF387   3'  ACTGTTATTACTGTTACCTG  1520     AA      TAGT
                    CA TAGCAGTG  GCAGT
                    ||  ||||||||   |||||
```

```
                        GT ATTGTCAT   TGTCA
                        CC       TAT_
GAM306  LOC126661 3'  ACTGCAGCCTCCGCTTCCTGT  3000     C_   T __
                        ATAG AGTG AG TGCAGT
                        ||||  ||||  ||  ||||||
                        TGTC TCGC TC ACGTCA
                         CT   C CG
GAM306  LOC139770 3'  CACTACCGCTGTATCTGTA  3022      A  G    _
                        TACA ATA CAGTG TAGTG
                        ||||  |||  |||||  |||||
                        ATGT TAT GTCGC ATCAC
                          C  _   C
GAM306  LOC150577 3'  ACCGCATTTGCTGCTATCTGTG 3329     A      T   A
                        TACA ATAGCAGTG AGTGC GT
                        ||||  ||||||||||  |||||  ||
                        GTGT TATCGTCGT TTACG CA
                          C   _    C
GAM306  LOC89919 5'  TACTACACACATTGCTATTTG 2579          A  C
                        CAAATAGCAGTGT GTG AGTA
                        |||||||||||||  |||  ||||
                        GTTTATCGTTACA CAC TCAT
                          _   A
GAM306  LOC92573 5'  ACCGCAGGCTATGCTCTTTGTA 2869       T  GT AG  A
                        TACAAA AGCA  GT  TGC GT
                        ||||||  ||||  ||  |||  ||
                        ATGTTT TCGT  CG  ACG CA
                          C   AT G_   C
GAM307  NTRK2    3' GATGGCTTCCGTGAGACA    1275      C     GA
                        TGTC CACGGAAGT  ATC
                        ||||  |||||||||  |||
                        ACAG GTGCCTTCG  TAG
                         A      G_
GAM307  ING3     3' AGGATTTACATAGACAAT    1879        CCACGGAA
                        ATTGTC     GTGAATCCT
                        ||||||       |||||||||
                        TAACAG     CATTTAGGA
                          ATA_____
GAM307  KIAA1164 5' AAGGAACGCTTCCCGGGACAAT 2861        AC    AA
                        ATTGTCCC GGAAGTG TCCTT
                        |||||||||  |||||||  |||||
                        TAACAGGG CCTTCGC AGGAA
                          C_   A_
GAM307  LOC150577 5' AAGGAATTATTTCCACGAGACA 3328        CCAC    A
          A             TTGTC  GGAAGTGA TCCTT
                        |||||   |||||||| |||||
                        AACAG   CCTTTATT AGGAA
                         AGCA      A
GAM307  LOC199936 3' AAGGGGCCCCCATGGGACAA  3474        C AA GAA
                        TTGTCCCA GG  GT  TCCTT
                        |||||||| ||  ||   |||||
```

```
                          AACAGGGT CC  CG   GGGAA
                            A  CC  ___
GAM307  LOC257235 3' AAGGATTTCAGTATTCATGGGA 3727        C  AG_   _
        CAA                TTGTCCCA GGA  TGAA TCCTT
                          ||||||||| |||   |||| |||||
                          AACAGGGT CTT  ACTT AGGAA
                            A  ATG   T
GAM308  COL19A1  3' ATCCACATGGTACAAGCCTTTC 863         ACCA  G  _
        TCA                TGAGAAAG   GTA TAT TGGAT
                          ||||||||   ||| ||| |||||
                          ACTCTTTC   CAT GTA ACCTA
                            CGAA  G  C
GAM308  EFEMP1   3' ATCCACTAAACTGGTCTTCTTC 1089     GA       AG  T
        A                  TGA  AAGACCAGT  TA TGGAT
                          |||  ||||||||| || |||||
                          ACT  TTCTGGTCA  AT ACCTA
                            TC     A_  C
GAM308  EFEMP1   3' ATCCACTAAACTGGTCTTCTTC 1864     GA       AG  T
        A                  TGA  AAGACCAGT  TA TGGAT
                          |||  ||||||||| || |||||
                          ACT  TTCTGGTCA  AT ACCTA
                            TC     A_  C
GAM308  FACL2    3' ATCCCTGCTACTGTCCCTTCTC 1943      A_  C    TT
        A                  TGAGAA  GAC AGTAGTA  GGAT
                          ||||||  ||| |||||| ||||
                          ACTCTT  CTG TCATCGT  CCTA
                            CC  _     C_
GAM308  HDGF     3' CCTCTTCCTACTGGTCTCTCT 1120     A        TATT_
                          AGA AGACCAGTAG    GG
                          ||| ||||||||||    ||
                          TCT TCTGGTCATC    CC
                            C     CTTCT
GAM308  HGF      3' ATCCAACTAGTTGCTGGTCTCT 3642      GAA        _  _
        ATCA               TGA  AGACCAGTAG TA TTGGAT
                          |||  ||||||||| || ||||||
                          ACT  TCTGGTCGTT AT AACCTA
                            ATC        G  C
GAM308  NFE2L1   3' CCAATATATCTTCTCA      999        A  CCAGTA
                          TGAGAA GA     GTATTGG
                          |||||| ||    |||||||
                          ACTCTT CT    TATAACC
                            _  A_____
GAM308  NLGN1    5' CCATTATACAGTCTTTCTCA 1592         CA  GTAT
                          TGAGAAAGAC  GTA   TGG
                          |||||||||| |||   |||
                          ACTCTTTCTG CAT   ACC
                            A_  ATT_
GAM308  SLC21A2  3' ACTAACCCTGGTCTTTCCCA 1232     A         ___
                          TG GAAAGACCAG   TAGT
                          || ||||||||||   ||||
```

```
                          AC CTTTCTGGTC  ATCA
                          C        CCA
GAM308   FHR5     3' ATCCAATACTAAATACCCCTTA 2166        AAAGACCAG
                          TGAG     TAGTATTGGAT
                          ||||     ||||||||||
                          ATTC     ATCATAACCTA
                               CCCATAA__
GAM308   FLJ13710 3' CTGGTGCTACTGGTCTTTCT 2091               TG
                          AGAAAGACCAGTAGTAT G
                          ||||||||||||||| |
                          TCTTTCTGGTCATCGTG C
                                  GT
GAM308   KIAA1155 3' ATCACGGGCTAATAATCTTTCT 2628      CCAG  ATTG
          CA              TGAGAAAGA TAGT  GAT
                          ||||||||| |||| |||
                          ACTCTTTCT ATCG  CTA
                              AATA  GGCA
GAM308   SEF      3' TCTCTCACTACCTTTCTCA 2860      ACCA   ATT
                          TGAGAAAG  GTAGT  GGA
                          ||||||||  |||||  |||
                          ACTCTTTC  CATCA  TCT
                              ____   CTC
GAM308   TREX1    5' ATCCAGTAATCCAGTCTCCCTC 2337      AA   CAGTAG
          A              TGAG AGAC    TATTGGAT
                          |||| ||||   ||||||||
                          ACTC TCTG    ATGACCTA
                            CC  ACCTA_
GAM308   TRIM6    3' ATCCAATACATATTTTTCTC 2366      CCA A
                          GAGAAAGA  GT GTATTGGAT
                          ||||||||  || |||||||||
                          CTCTTTTT  TA CATAACCTA
                              A__ _
GAM308   VEST1    3' ATTCTCTACCACTGCTCTTTCT 2349      C  A TT
          CA              TGAGAAAGA CAGT GTA GGAT
                          ||||||||| |||| ||| ||||
                          ACTCTTTCT GTCA CAT CTTA
                              C  C  CT
GAM308   LOC149076 5' ATGCCCACTGACCTTTTTCA 3128      AC  A_
                          TGAGAAAG CAGT GTAT
                          |||||||| |||| ||||
                          ACTTTTTC GTCA CGTA
                              CA  CC
GAM308   LOC254043 3' ATCTTTCTCTCTAGTCTTTCTC 3667      C T TATT
          A              TGAGAAAGAC AG AG   GGAT
                          |||||||||| || ||   ||||
                          ACTCTTTCTG TC TC   TCTA
                              A _ TCTT
GAM309   BUB3     3' AAAGGTATTTGGGCAAAC  1149      A_ T
                          GTTT TCA ATACCTTT
                          |||| ||| ||||||||
```

```
                      CAAA  GGT TATGGAAA
                        CG   T
GAM309  CLCN6    3' TAAAGGTATGTGCTATGATAAA 815              _____        III
                      TTTATCATA    TACCTTT  A
                      IIIIIIIII    IIIIIII  I
                      AAATAGTAT    ATGGAAA  T
                        CGTGT      III
GAM309  CLCN6    3' TAAAGGTATGTGCTATGATAAA 1957             _____        III
                      TTTATCATA    TACCTTT  A
                      IIIIIIIII    IIIIIII  I
                      AAATAGTAT    ATGGAAA  T
                        CGTGT      III
GAM309  CLCN6    3' TAAAGGTATGTGCTATGATAAA 1958             _____        III
                      TTTATCATA    TACCTTT  A
                      IIIIIIIII    IIIIIII  I
                      AAATAGTAT    ATGGAAA  T
                        CGTGT      III
GAM309  CMAR     3' AAAGGAAGTGATAAACTA   1193          ATA
                      TAGTTTATCAT  CCTTT
                      IIIIIIIIIII  IIIII
                      ATCAAATAGTG  GGAAA
                        AA_
GAM309  CTPS     3' AAAGGTATTTGGGAAACT   3441       AT T
                      AGTTT  CA ATACCTTT
                      IIIII  II IIIIIIII
                      TCAAA  GT TATGGAAA
                        GG  T
GAM309  RB1      3' AAAGGTGTATTTAAACTA   3505          TC
                      TAGTTTA ATATACCTTT
                      IIIIIII IIIIIIIIII
                      ATCAAAT TATGTGGAAA
                        T_
GAM309  RP2      3' AAAGGTATATGCAATGCTA  1339       TTAT
                      TAGT  CATATACCTTT
                      IIII  IIIIIIIIIII
                      ATCG  GTATATGGAAA
                        TAAC
GAM309  WHSC1    3' AAAGGTATATGTGATAAAT  1394             __
                      GTTTATCAT ATACCTTT
                      IIIIIIIII IIIIIIII
                      TAAATAGTG TATGGAAA
                        TA
GAM309  ARHGAP11A 3' AAGGGTAGAGATAAACT    1546          ATA
                      AGTTTATC  TACCTTT
                      IIIIIIII  IIIIIII
                      TCAAATAG  ATGGGAA
                        AG_
GAM309  FLJ20533 3' AAAGGTATGTGAATAAAT   1758           _
                      GTTTAT CATATACCTTT
                      IIIIII IIIIIIIIII
```

```
                              TAAATA GTGTATGGAAA
                                   A
GAM309  MGC16063  3' AAAGGCTTACTGATAAACT  2356          _ TA
                      AGTTTATCA TA  CCTTT
                      |||||||| || |||||
                      TCAAATAGT AT  GGAAA
                              C  TC
GAM309  SEMA3C   3' AAAGGTATAATTAAACT   1293       TCA
                      AGTTTA  TATACCTTT
                      |||||| |||||||||
                      TCAAAT  ATATGGAAA
                             TA_
GAM309  LOC135293 3' AAGGTATAATAAACTG    3047        CA
                      TAGTTTAT TATACCTT
                      |||||||| ||||||||
                      GTCAAATA ATATGGAA

                           __
GAM309  LOC153883 3' AAAGGTATATTTGACTA    3182      TATC
                      TAGTT  ATATACCTTT
                      ||||| |||||||||
                      ATCAG   TATATGGAAA
                         TT__
GAM309  LOC199692 3' GAGGGTGTAATAAACTG   2521        CA
                      TAGTTTAT TATACCTTT
                      |||||||| |||||||||
                      GTCAAATA ATGTGGGAG

                           __
GAM310  MGC5242  5' CCTTACAATCCGAGACTA   2042          ___
                      TGGTCTCGGATT AGG
                      |||||||||||| |||
                      ATCAGAGCCTAA TCC
                             CAT
GAM310  LOC197259 3' GCCAATCAAGACCAGAA    3422      CG  A
                      TTCTGGTCT GATT GGC
                      ||||||||| |||| |||
                      AAGACCAGA CTAA CCG
                           A_  _
GAM311  CRYBA4   3' AAAACTCAAACGAATAAAAAAG 865        _ ATC
                      CTTTTTTAT CGTT  GGTTTT
                      ||||||||| |||| ||||||
                      GAAAAAATA GCAA  TCAAAA
                           A  AC_
GAM311  UCHL1    3' GCTGATAAGATAAAAAA   1093        G
                      TTTTTTATC TTATCGGT
                      ||||||||| ||||||||
                      AAAAAATAG AATAGTCG

                          _
GAM311  BDG-29   3' GAAAACCGTCTCATAACAAAAG 2944     _  CGTTAT
            G              CCTTTT TTAT   CGGTTTTC
                      |||||| |||| ||||||||
```

```
                              GGAAAA AATA    GCCAAAAG
                               C   CTCT__
GAM311   ERG-1    5' GAAATTTCAATGATAAAAAAGG 1972          ATC
                          CCTTTTTTATCGTT  GGTTTT
                          ||||||||||||| |||||
                          GGAAAAAATAGTAA  TTAAAG
                                  CT_
GAM311   LOC199837 5' GAAAGAAGAAACAATAGAAAAG 3434          C  A GG
          G                 CCTTTTTTAT GTT TC  TTTTC
                          ||||||||| ||| || |||||
                          GGAAAAGATA CAA AG  GAAAG
                                A  _  AA
GAM312   BHLHB3   3' AAGTCCAAACTGATATATCCTA 2160     A      TTAAA
                          TAG ATATATT   GGACTT
                          ||| |||||||    ||||||
                          ATC TATATAG    CCTGAA
                              C    TCAAA
GAM312   CLN2     3' AAGTCCTTCCAATTATATTT 735       T TA
                          GAATATA TT AAGGACTT
                          |||||| || ||||||||
                          TTTATAT AA TTCCTGAA
                              T CC
GAM312   ZFP36L1  3' TCCATAGAATATATTCT     1165          AA
                          AGAATATATTTTA GGA
                          |||||||||||| |||
                          TCTTATATAAGAT CCT
                                A_
GAM312   C8orf2   3' TCCATTTAAAATACATTC     1361     A     _
                          GAAT TATTTTAAA GGA
                          |||| ||||||||| |||
                          CTTA ATAAAATTT CCT
                                C    A
GAM312   DKFZP566K0524 3' AAGGATTTAAAATATATTC   2854         GGA
                          GAATATATTTTAAA  CTT
                          |||||||||||||  |||
                          CTTATATAAAATTT  GAA
                                AG_
GAM312   FIGNL1   3' TTTTTAAGAATATATTCTA   1980         A
                          TAGAATATATTTT AAGGA
                          ||||||||||||| |||||
                          ATCTTATATAAGA TTTTT
                                A
GAM312   FLJ10704 3' TTTTTTAAAATATATTTTA   1796
                          TAGAATATATTTTAAAGGA
                          ||||||||||||||||||
                          ATTTTATATAAAATTTTTT


GAM312   HDAC9-PENDING 3' TCTTTTAAAATACATTTTA   1528       A
                          TAGAAT TATTTTAAAGGA
                          |||||| |||||||||||
```

```
                            ATTTTA ATAAAATTTCT
                                 C
GAM312  KIAA1384  3'  AAGCCTAAAATATATTTTA  2695        AA  A
                       TAGAATATATTTT AGG CTT
                       |||||||||||| ||| |||
                       ATTTTATATAAAA TCC GAA

                                  __  _
GAM312  SOX30     3'  TTTCTTAAAATATATTCTG  1346        AG
                       TAGAATATATTTTAA GA
                       ||||||||||||| ||
                       GTCTTATATAAAATT TT
                                CT
GAM312  LOC221810 3'  AGTCTTTAAAATATATTCTG  3625         G
                       TAGAATATATTTTAAAG ACT
                       ||||||||||||||||| |||
                       GTCTTATATAAAATTTC TGA

                               _
GAM312  LOC255177 3'  AGTTCTTTAAAAATATTCTA  3712      A
                       TAGAATAT TTTTAAAGGACT
                       ||||||||| |||||||||||
                       ATCTTATA AAAATTTCTTGA

                              _
GAM313  ADRA1A    3'  TTCCCATAGACACCCAGCCCAT 2327        CCA___    A
          AG                 CTATGGGT   TCTATG GAA
                       ||||||||   |||||| |||
                       GATACCCG   AGATAC CTT
                         ACCCAC     C
GAM313  ARF3      3'  TTCTCATAAATGGATCTG  845       C
                       TGGGTCCAT TATGAGAA
                       ||||||||| ||||||||
                       GTCTAGGTA ATACTCTT
                            A
GAM313  C14orf1   3'  TCTCTGCTGCTGGACCCAAGA 1362    A      TCTAT_
                       TCT TGGGTCCA    GAGA
                       ||| ||||||||    ||||
                       AGA ACCCAGGT    CTCT
                        _     CGTCGT
GAM313  CTNNA2    3'  TTCTCATAAAATTGGGCACA  1108    G    TC__
                       TG GTCCA   TATGAGAA
                       || |||||   ||||||||
                       AC CGGGT   ATACTCTT
                        A   TAAA
GAM313  FAT2      3'  TTCTCATACCTGCCCACAG  829    A   CCATC
                       CT TGGGT   TATGAGAA
                       || |||||   ||||||||
                       GA ACCCG    ATACTCTT
                        C   TCC__
GAM313  GALNT3    3'  TTCAATGGACCCACAGG    1118    A    CTA
                       TCT TGGGTCCAT TGAG
                       ||| ||||||||| ||||
```

```
                      GGA  ACCCAGGTA   ACTT
                      C          ___
GAM313  HMG20A  3' TCTCATAGTATGCCCATA   1801         CCAT
                      TATGGGT   CTATGAGA
                      |||||||   ||||||||
                      ATACCCG   GATACTCT
                        TAT_
GAM313  HPCA    3' TCTCACACACACAGGCCCAT 903         CATCTA____
            AGA             TCTATGGGTC       TGAGA
                      ||||||||||       |||||
                      AGATACCCGG       ACTCT
                        ACACACACAC
GAM313  MTMR3   3' CTCACAGATGGATAAATG   1939    GG    A
                      TAT GTCCATCT TGAG
                      ||| |||||||| ||||
                      GTA TAGGTAGA ACTC
                        AA      C
GAM313  PIGR    3' CTCACATGGACCCAAGA    2955    A    CTA
                      TCT TGGGTCCAT TGAG
                      ||| ||||||||| ||||
                      AGA ACCCAGGTA  ACTC
                      _        C__
GAM313  PIWIL1  3' TTCTCATAGATATTTGTG   2959    GG TCC
                      TAT G  ATCTATGAGAA
                      ||| |  |||||||||||
                      GTG T  TAGATACTCTT
                      TT TA_
GAM313  SORBS1  3' TTCTCATAGAACACCA     1625    _ CCA
                      TGG GT  TCTATGAGAA
                      ||| ||  |||||||||||
                      ACC CA  AGATACTCTT
                        A ___
GAM313  TOP3A   3' TTCTCATAGACGTCCTGAGA 1132    A  TCCA
                      TCT TGGG   TCTATGAGAA
                      ||| ||||   |||||||||||
                      AGA GTCC   AGATACTCTT
                      _   TGC_
GAM313  UC28    3' TTCTCAATCTTGAACTCATAGA 1951        C TCTA
                      TCTATGGGT CA   TGAGAA
                      ||||||||| ||   ||||||
                      AGATACTCA GT   ACTCTT
                        A TCTA
GAM313  ARL5    3' TTCTCATAGATTTGTA     1406    GG TCC
                      TAT G  ATCTATGAGAA
                      ||| |  |||||||||||
                      ATG T  TAGATACTCTT
                      TT ___
GAM313  DDM36   3' TCTCATAGGAGCATAGA    1932       GG ATC
                      TCTATG TCC  TATGAGA
                      |||||| |||  |||||||
```

```
                         AGATAC AGG  ATACTCT
                            G_    ___
GAM313  FLJ21596  3' TCTCAGGGTGGGACCCATA  2093          _   A
                         TATGGGTCC ATCT TGAGA
                         |||||||||| |||| |||||
                         ATACCCAGG TGGG ACTCT
                            G    _
GAM313  FLJ22202  5' TCCAGGAGATGGACCAACAGA  2102     ATG      A_ A
                         TCT GGTCCATCT TG GA
                         ||| ||||||||| || ||
                         AGA CCAGGTAGA AC CT
                          CAA     GG _
GAM313  GPNMB  3' TCTCATAAATGGGTGGGA  935      ATGGG   C
                         TCT   TCCAT TATGAGA
                         |||   ||||| |||||||
                         AGG   GGGTA ATACTCT
                          GT___    A
GAM313  HSZFP36  3' CAGGAGATGGACCCCAGA  2659    AT      A_
                         TCT GGGTCCATCT TG
                         ||| ||||||||| ||
                         AGA CCCAGGTAGA AC
                          C_      GG
GAM313  IPLA2(GAMMA) 3' TTCTCATAAATGAAGGTCTGT 2577    GT __  C
                         ATGG  C CAT TATGAGAA
                         ||||  | ||| ||||||||
                         TGTC  G GTA ATACTCTT
                          TG AA  A
GAM313  KIAA0648  3' TTCTCATAGATAATCAAGA  3258    A GTCC
                         TCT TGG   ATCTATGAGAA
                         ||| |||   |||||||||||
                         AGA ACT   TAGATACTCTT
                           _  AA___
GAM313  KIAA1239  3' TTCATGTAACCCATAGA   2915         CCATC
                         TCTATGGGT   TATGAG
                         |||||||||   ||||||
                         AGATACCCA   GTACTT
                            AT___
GAM313  KIAA1577  5' TTCTCATGGGTACCCCAGA  2691    AT  CC
                         TCT GGGT ATCTATGAGAA
                         ||| |||| |||||||||||
                         AGA CCCA TGGGTACTCTT
                           C_     __
GAM313  KIAA1821  3' CTCATCCTGTACCTATAGA  2926         C TCT
                         TCTATGGGT CA  ATGAG
                         ||||||||| ||  |||||
                         AGATATCCA GT  TACTC
                           T CC_
GAM313  KIAA1853  5' CTCAGGATGGACCCTCAGA  2857    AT      A
                         TCT GGGTCCATCT TGAG
                         ||| ||||||||| ||||
```

```
                        AGA  CCCAGGTAGG ACTC
                        CT          _
GAM313  MGC3169  3' TCTCTGCCAGGACCCCATAGA 2051       _  ATCTAT
                     TCTATGGG TCC    GAGA
                     ||||||||| |||    ||||
                     AGATACCC AGG    CTCT
                        C  ACCGT_
GAM313  MST4     3' TTCATATGGACCCAGAGA  1696    A    TC
                     TCT TGGGTCCA TATGAG
                     ||| |||||||| ||||||
                     AGA ACCCAGGT ATACTT
                        G      __
GAM313  PDE10A   3' ATTCTCACAGATCAGATCACTC 1321     ____  C_  A   |||
              CATAGA         TGG  GTC ATCT TGAGAA  T
                     ||| ||| |||| |||||| |
                     ACC  TAG TAGA ACTCTT  A
                       TCAC AC  C    |||
GAM313  SKD3     3' TTCTAAGGGGAAGGGACCCATA 2170        A_  ATG_
              GA           TCTATGGGTCC TCT  AGAA
                     |||||||||||| ||| ||||
                     AGATACCCAGG AGG  TCTT
                        GA  GGAA
GAM313  STX18    3' CTCATGGGCACTCACAGA  1714    A   CCA
                     TCT TGGGT  TCTATGAG
                     ||| ||||| ||||||||
                     AGA ACTCA  GGGTACTC
                        C  C__
GAM313  LOC115811 5' CTCTGTGGACCTACAGA   2441    A     CTAT
                     TCT TGGGTCCAT  GAG
                     ||| |||||||||  |||
                     AGA ATCCAGGTG  CTC
                        C    T___
GAM313  LOC131308 3' TTCCAGCCTGAACCCATGGA 3013      C TCTA A
                     TCTATGGGT CA   TG GAA
                     ||||||||| ||   || |||
                     AGGTACCCA GT   AC CTT
                        A  CCG_ _
GAM313  LOC139221 3' TCTCATAGATACTAGTTGA 3036    TATG  CC
                     TC   GGT ATCTATGAGA
                     ||   ||| ||||||||||
                     AG   TCA TAGATACTCT
                        TTGA   __
GAM313  LOC158490 5' TCTCATAGGACTGTCCTAGA 3220    T TCCA
                     TCTA GGG   TCTATGAGA
                     |||| |||   |||||||||
                     AGAT CCT   GGATACTCT
                        _ GTCA
GAM313  LOC221466 5' CTCAGGATCCATAGA    3618         ATCTA
                     TCTATGGGTCC  TGAG
                     |||||||||||  ||||
```

```
                        AGATACCTAGG   ACTC
                           _____
GAM313  LOC221540 3' TTCTCATAAATCCCCGCCCA 3621      CC__ C
                         TGGGT   AT TATGAGAA
                         |||||   || ||||||||
                         ACCCG   TA ATACTCTT
                           CCCC  A
GAM313  LOC222233 5' CTCAGCAGAGACAGACCCCAGA 3648     AT   CA__  A_
                         TCT GGGTC   TCT TGAG
                         ||| |||||   ||| ||||
                         AGA CCCAG   AGA ACTC
                          C_  ACAG  CG
GAM313  LOC255042 3' TTCTCACAGATGGGCAGCA 3671     G_    A
                         TG GTCCATCT TGAGAA
                         || |||||||| ||||||
                         AC CGGGTAGA ACTCTT
                           GA      C
GAM313  LOC256117 3' CTCATTCGAGACCCCATAGA 3705        _ CATCT
                         TCTATGGG TC   ATGAG
                         |||||||| ||   |||||
                         AGATACCC AG   TACTC
                           C AGCT_
GAM313  LOC257545 3' TTCTCATAAATCCCCGCCCA 3747      CC__ C
                         TGGGT   AT TATGAGAA
                         |||||   || ||||||||
                         ACCCG   TA ATACTCTT
                           CCCC  A
GAM313  LOC257598 3' TTCTCATAAATCCCCGCCCA 3750      CC__ C
                         TGGGT   AT TATGAGAA
                         |||||   || ||||||||
                         ACCCG   TA ATACTCTT
                           CCCC  A
GAM314  CHAC     3' TGCCCATATGTCCATTTAT 1612          AGAT
                         ATAAGTGGACATAT  GCA
                         |||||||||||||   |||
                         TATTTACCTGTATA  CGT
                             CC__
GAM314  GGCX     3' CTGCACCCTGCCACTTGT 778       A TATAGA
                         ATAAGTGG CA    TGCAG
                         |||||||| ||    |||||
                         TGTTCACC GT    ACGTC
                            _ CCC___
GAM314  ITPKB    3' TCTGCATCTGTCCAC 911         TATA
                         GTGGACA  GATGCAGA
                         |||||||  ||||||||
                         CACCTGT  CTACGTCT
                            _____
GAM314  KCNAB1   3' TCTAATGTTATGTCCACTTA 2584            ____
                         TAAGTGGACATA  TAGA
                         ||||||||||||  ||||
```

```
                        ATTCACCTGTAT   ATCT
                           TGTA
GAM314  KLRC4    5' CTGTCAAAATATACACCACTTA 1451          ACA   GA_ _
          T                ATAAGTGG  TATA  TG CAG
                        ||||||||  ||||  || |||
                        TATTCACC  ATAT  AC GTC
                          AC_   AAA  T
GAM314  MLF2     3' TCTGCATCTACTGACTTG  1212       _ ACATA
                        TAAGT GG   TAGATGCAGA
                        ||||| ||  |||||||||||
                        GTTCA TC   ATCTACGTCT
                          G  _____
GAM314  NR1I2    3' TCTGCATCCATTTGAACAC  1971     GA T A
                        GTG  CA AT GATGCAGA
                        ||| || || ||||||||
                        CAC  GT TA CTACGTCT
                         AA  T  C
GAM314  NR1I2    3' TCTGCATCCATTTGAACAC  1067     GA T A
                        GTG  CA AT GATGCAGA
                        ||| || || ||||||||
                        CAC  GT TA CTACGTCT
                         AA  T  C
GAM314  CEP3     3' TTCTACATCAGATGTTGTCACT 1304        __    ATA  C
          TAT                ATAAGTG GACAT  GATG AGAA
                        |||||||| |||||  |||| ||||
                        TATTCAC  TTGTA  CTAC TCTT
                           TG  GA_  A
GAM314  FHX      3' TCATGGATCATGTCCAC  1825       ATA  G _
                        GTGGACAT  GAT CA GA
                        ||||||||  ||| || ||
                        CACCTGTA  CTA GT CT
                           ___  G A
GAM314  FLJ10352 3' TTCTGCATCTACAACTCAACAT 2233        GACATA__
          TTA                TAAGTG    TAGATGCAGAA
                        |||||||        |||||||||||
                        ATTTAC        ATCTACGTCTT
                          AACTCAAC
GAM314  FLJ22127 3' TCGAGTCCATATGTCCAC   2008        A GCA
                        GTGGACATAT GAT  GA
                        |||||||||| ||| ||
                        CACCTGTATA CTG  CT
                          C  AG_
GAM314  GDAP1L1  3' TCTGCATCCATGCCAC    2043     A ATA
                        GTGG CAT  GATGCAGA
                        |||| |||  ||||||||
                        CACC GTA  CTACGTCT
                          _  C__
GAM314  H-L(3)MBT 3' TCTGCTCTCTACCCACT   2230     ACA T T
                        AGTGG  TA AGA GCAGA
                        |||||  || ||| |||||
```

```
                    TCACC  AT TCT CGTCT
                      C__ C    _
GAM314  KIAA1340 3' TCTAAGCTATGCCCATTTAT 2846      A   ___
                    ATAAGTGG CATA  TAGA
                    |||||||| |||| ||||
                    TATTTACC GTAT  ATCT
                       C    CGA
GAM314  KNSL7    3' TTCTGCATCCATATACACCCT 1905    T AC_   A
                    AG GG  ATAT GATGCAGAA
                    || || |||| |||||||||
                    TC CC  TATA CTACGTCTT
                     _ ACA   C
GAM314  P5-1     3' CTCCATTTATGTACCCAC    1322    AC     C
                    GTGG  ATATAGATG AG
                    ||||  ||||||||| ||
                    CACC  TGTATTTAC TC
                      CA        C
GAM314  PP1044   5' CTGCATCTTTACCTATATCCAT 1956      C  T____
       TTA            TAAGTGGA ATA   AGATGCAG
                    ||||||||| |||   ||||||||
                    ATTTACCT TAT   TCTACGTC
                       A  CCATT
GAM314  SIRPB1   3' TGCATGTGTCCACTTA     1272      ATAG
                    TAAGTGGACAT  ATGCA
                    ||||||||||| |||||
                    ATTCACCTGTG  TACGT
                        ____
GAM314  LOC148811 3' CTGCATCTCTCCCCTTA    3126     T CATAT
                    TAAG GGA   AGATGCAG
                    |||| |||   ||||||||
                    ATTC CCT   TCTACGTC
                       C  C____
GAM314  LOC149711 3' TCCATATGTCTATCCACTTA 3315       ____   A
                    TAAGTGGA   CATAT GA
                    |||||||| |||||| ||
                    ATTCACCT   GTATA CT
                      ATCT    C
GAM314  LOC150630 5' CTGCATCTTCTGCCACT    3332     A TAT
                    AGTGG CA  AGATGCAG
                    ||||| || ||||||||
                    TCACC GT  TCTACGTC
                     _ CT_
GAM314  LOC150819 5' CTGCATTTTAGTCCAACT   3333     _ ATAT
                    AGT GGAC   AGATGCAG
                    ||| |||| ||||||||
                    TCA CCTG   TTTACGTC
                      A  AT__
GAM314  LOC154877 3' TCTGCATCCATTCCACT    3373     CAT A
                    AGTGGA  AT GATGCAGA
                    ||||||  || ||||||||
```

```
                        TCACCT  TA CTACGTCT
                        ___  C
GAM314  LOC158327 3' TTCTGCAGGGACACCACTTAT 3216        ACATATAGA
                        ATAAGTGG      TGCAGAA
                        ||||||||      |||||||
                        TATTCACC      ACGTCTT
                          ACAGGG___
GAM314  LOC196540 3' TCTGCATCCATGTACTCC  3467     C_  A
                        GGA ATAT GATGCAGA
                        ||| |||| ||||||||
                        CCT TGTA CTACGTCT
                          CA   C
GAM314  LOC220394 5' TCTCAGAATATGTCCAT    3581        AGA  C
                        GTGGACATAT  TG AGA
                        ||||||||||  || |||
                        TACCTGTATA  AC TCT
                            AG_  _
GAM314  LOC254428 3' CTGTTGACCCATGTCCACCTAT 3677    A       ATAGAT
                        ATA GTGGACAT   GCAG
                        ||| ||||||||   ||||
                        TAT CACCTGTA   TGTC
                          C      CCCAGT
GAM314  LOC92405 3' TTCTGTTACACATGTCTACTTA 2848         ATAGAT
                        TAAGTGGACAT   GCAGAA
                        |||||||||||   ||||||
                        ATTCATCTGTA   TGTCTT
                           CACAT_
GAM315  PIGH    3' CAAGATCATAGTATTTCAGTCA 1126    T _  GTA
                        TG CT AAAT  ATTATGATCTTG
                        || || ||||  ||||||||||||
                        AC GA TTTA  TGATACTAGAAC
                          T C  ___
GAM315  PRSC    3' CAAGATCATAATTTTATAGA 1313      AATGT
                        TCTA    AATTATGATCTTG
                        ||||    ||||||||||||
                        AGAT    TTAATACTAGAAC
                          ATT__
GAM315  PXMP4   3' CAAGATCATAGGCCTCAGAC 1370       AAATGTAA
                        GTCT     TTATGATCTTG
                        ||||     |||||||||||
                        CAGA     GATACTAGAAC
                          CTCCG___
GAM316  C1orf1  5' TATGCTGACAGAAGAACCA 809        CC A A
                        TGGTTCTTT GT CA CATA
                        ||||||||| || || ||||
                        ACCAAGAAG CA GT GTAT
                           A_ _ C
GAM316  LRAT    3' AGTATGCATACATAAAAGCAAC 2556     _  CC_  CAA
             CA              TGGTT CTTT  GTA  CATACT
                        ||||| |||| ||| ||||||
```

```
                          ACCAA GAAA  CAT  GTATGA
                            C    ATA  AC_
GAM316  MYBL1    3' AGTATGTTATACAAATGCCA 2679      TCTTTCC  C
                   TGGT    GTA AACATACT
                   |||||   ||| ||||||||
                   ACCG    CAT TTGTATGA
                       TAAA___    A
GAM316  KIAA1028 3' TATGTCTGCATTGAAAAGAACC 3547      C  TA_ _
          A              TGGTTCTTT CG  CA ACATA
                         |||||||||| ||  || |||||
                         ACCAAGAAA GT  GT TGTAT
                          A TAC  C
GAM316  MGC2488  3' TGTAGTGGAAAGAAGCAT    2045      G      _
                   ATG TTCTTTCCG TACA
                   ||| ||||||||| ||||
                   TAC AAGAAAGGT ATGT
                     G      G
GAM317  CX3CR1   3' ACTGCCTACTGCATCGAGTCA 2891      TCCCTTAA
                   TGACTCG    TAGGCAGT
                   |||||||    ||||||||
                   ACTGAGC    ATCCGTCA
                      TACGTC__
GAM317  WNT14    3' CTGCAAGGGACGAGTC      1014      AATAG
                   GACTCGTCCCTT  GCAG
                   ||||||||||||  ||||
                   CTGAGCAGGGAA  CGTC
                        _____
GAM317  FLJ20275 3' TACTGCCTTCATAAGATCAAGT 1745     CGTCC  AT_
        CA             TGACT  CTTA AGGCAGTA
                       |||||  |||| ||||||||
                       ACTGA  GAAT TCCGTCAT
                        ACTA_  ACT
GAM317  FLJ22390 5' TACTGCCTATCAAACG      2002    CCC A
                   CGT  TT ATAGGCAGTA
                   |||  || ||||||||||
                   GCA  AA TATCCGTCAT
                     ___  C
GAM318  LOC120864 5' CAAGGTCCAAACTGATATAA 2986       CGTAG
                    TTGTATCAGTTT   TCTTG
                    ||||||||||||   |||||
                    AATATAGTCAAA   GGAAC
                         CCT__
GAM319  KIAA0626 3' AACATCAGGGTGCAGAATTGAT 1954     C_ A_
                   ATCGATTC CAT  TGATGTT
                   |||||||| |||  |||||||
                   TAGTTAAG GTG  ACTACAA
                       AC  GG
GAM319  KIAA1239 3' AACATCATGATTATTGATG   2914      TCCCA
                   CATCGAT   TATGATGTT
                   |||||||   |||||||||
```

```
                         GTAGTTA    GTACTACAA
                         TTA__
GAM319  LOC201475 5' AACATCATATATTTTGATGTTA 3428          TTCCC
                         TAACATCGA    ATATGATGTT
                         ||||||||    ||||||||||
                         ATTGTAGTT    TATACTACAA
                         TTA__
GAM320  CAPN2    3' AAAACTTTATGAACTTCACCA 855      A    _    AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| |||||  ||||||
                         AC ACTTCA GTATT  TCAAAA
                         C    A    ___
GAM320  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559         CG  A
                A         TGATGGAGT TA AAAAGTTTT
                         ||||||||| || |||||||||
                         ACTACCTCA AT TTTTTAAAA
                         AA  C
GAM320  SELE    3' AAAACTCTCCTACACTTCCATT 747         _ C  AAAA
                A         TGATGGA GT GTA   AGTTTT
                         |||||||| || |||   ||||||
                         ATTACCT CA CAT   TCAAAA
                         T _  CCTC
GAM320  KIAA0475 3' AAAACCTTGCATTCCATCA 1570        C   AAAA
                         TGATGGAGT GTAA   GTTTT
                         ||||||||| ||||   |||||
                         ACTACCTTA CGTT   CAAAA
                         _  C___
GAM320  LOC222671 5' GCTTCTACGACTCCGCCA 3582      A      AAA
                         TG TGGAGTCGTA  AAGT
                         || ||||||||||  ||||
                         AC GCCTCAGCAT  TTCG
                         C      C__
GAM320  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                         TG TGGAGTC GT AA AAGTT
                         || |||||| || || |||||
                         AC ACCTCAG CA TT TTTAA
                         C    T C  C
GAM320  LOC257615 5' GCTTCTACGACTCCGCCA 3749      A      AAA
                         TG TGGAGTCGTA  AAGT
                         || ||||||||||  ||||
                         AC GCCTCAGCAT  TTCG
                         C      C__
GAM321  CAPN2    3' AAAACTTTATGAACTTCACCA 855      A    _    AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| |||||  ||||||
                         AC ACTTCA GTATT  TCAAAA
                         C    A    ___
GAM321  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559         CG  A
                A         TGATGGAGT TA AAAAGTTTT
                         ||||||||| || |||||||||
```

```
                         ACTACCTCA  AT TTTTTAAAA
                           AA  C
GAM321   SELE     3' AAAACTCTCCTACACTTCCATT 747         _  C  AAAA
         A                 TGATGGA GT GTA   AGTTTT
                     ||||||| || |||    ||||||
                     ATTACCT CA CAT   TCAAAA
                         T _  CCTC
GAM321   KIAA0475 3' AAAACCTTGCATTCCATCA  1570         C  AAAA
                           TGATGGAGT GTAA   GTTTT
                     ||||||||| ||||    |||||
                     ACTACCTTA CGTT   CAAAA
                           _  C___
GAM321   LOC222671 5' GCTTCTACGACTCCGCCA   3582   A       AAA
                           TG TGGAGTCGTA  AAGT
                     || ||||||||||  ||||
                     AC GCCTCAGCAT   TTCG
                         C       C__
GAM321   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A   _ A A
                           TG TGGAGTC GT AA AAGTT
                     || |||||||| || || |||||
                     AC ACCTCAG CA TT TTTAA
                         C    T C  C
GAM321   LOC257615 5' GCTTCTACGACTCCGCCA   3749   A       AAA
                           TG TGGAGTCGTA  AAGT
                     || ||||||||||  ||||
                     AC GCCTCAGCAT   TTCG
                         C       C__
GAM322   CAPN2    3' AAAACTTTATGAACTTCACCA 855    A   _   AAA
                           TG TGGAGT CGTAA  AGTTTT
                     || |||||| |||||  ||||||
                     AC ACTTCA GTATT  TCAAAA
                         C  A   ___
GAM322   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559      CG A
         A                 TGATGGAGT TA AAAAGTTTT
                     ||||||||| || |||||||||
                     ACTACCTCA  AT TTTTTAAAA
                           AA  C
GAM322   SELE     3' AAAACTCTCCTACACTTCCATT 747         _  C  AAAA
         A                 TGATGGA GT GTA   AGTTTT
                     ||||||| || |||    ||||||
                     ATTACCT CA CAT   TCAAAA
                         T _  CCTC
GAM322   KIAA0475 3' AAAACCTTGCATTCCATCA  1570         C  AAAA
                           TGATGGAGT GTAA   GTTTT
                     ||||||||| ||||    |||||
                     ACTACCTTA CGTT   CAAAA
                           _  C___
GAM322   LOC222671 5' GCTTCTACGACTCCGCCA   3582   A       AAA
                           TG TGGAGTCGTA  AAGT
                     || ||||||||||  ||||
```

```
                              AC GCCTCAGCAT  TTCG
                              C        C__
GAM322  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A     _ A A
                        TG TGGAGTC GT AA AAGTT
                        || |||||||| || || |||||
                        AC ACCTCAG CA TT TTTAA
                        C    T C C
GAM322  LOC257615 5' GCTTCTACGACTCCGCCA   3749    A      AAA
                        TG TGGAGTCGTA  AAGT
                        || ||||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C        C__
GAM323  CAPN2    3' AAAACTTTATGAACTTCACCA 855     A    _  AAA
                        TG TGGAGT CGTAA  AGTTTT
                        || |||||| ||||| |||||
                        AC ACTTCA GTATT  TCAAAA
                        C    A    ___
GAM323  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559       CG A
             A              TGATGGAGT TA AAAAGTTTT
                        ||||||||| || |||||||||
                        ACTACCTCA AT TTTTTAAAA
                            AA  C
GAM323  SELE     3' AAAACTCTCCTACACTTCCATT 747        _ C AAAA
             A              TGATGGA GT GTA   AGTTTT
                        |||||||| || ||| |||||||
                        ATTACCT CA CAT   TCAAAA
                        T _  CCTC
GAM323  KIAA0475 3' AAAACCTTGCATTCCATCA  1570       C  AAAA
                        TGATGGAGT GTAA   GTTTT
                        ||||||||| |||| |||||
                        ACTACCTTA CGTT   CAAAA
                        _  C___
GAM323  LOC222671 5' GCTTCTACGACTCCGCCA   3582    A      AAA
                        TG TGGAGTCGTA  AAGT
                        || ||||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C        C__
GAM323  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A     _ A A
                        TG TGGAGTC GT AA AAGTT
                        || |||||||| || || |||||
                        AC ACCTCAG CA TT TTTAA
                        C    T C C
GAM323  LOC257615 5' GCTTCTACGACTCCGCCA   3749    A      AAA
                        TG TGGAGTCGTA  AAGT
                        || ||||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C        C__
GAM324  CAPN2    3' AAAACTTTATGAACTTCACCA 855     A    _  AAA
                        TG TGGAGT CGTAA  AGTTTT
                        || |||||| ||||| |||||
```

```
                              AC ACTTCA GTATT  TCAAAA
                              C      A     ___
GAM324  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
          A                   TGATGGAGT  TA AAAAGTTTT
                              |||||||| || ||||||||
                              ACTACCTCA  AT TTTTTAAAA
                                  AA  C
GAM324  SELE     3' AAAACTCTCCTACACTTCCATT 747        _ C  AAAA
          A                   TGATGGA GT GTA   AGTTTT
                              ||||||| || |||   ||||||
                              ATTACCT CA CAT   TCAAAA
                                  T _  CCTC
GAM324  KIAA0475 3' AAAACCTTGCATTCCATCA  1570        C  AAAA
                              TGATGGAGT GTAA   GTTTT
                              ||||||||| |||    |||||
                              ACTACCTTA CGTT   CAAAA
                                   _  C___
GAM324  LOC222671 5' GCTTCTACGACTCCGCCA   3582   A      AAA
                              TG TGGAGTCGTA  AAGT
                              || |||||||||  ||||
                              AC GCCTCAGCAT  TTCG
                                 C      C__
GAM324  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699   A    _ A A
                              TG TGGAGTC GT AA AAGTT
                              || |||||| || || |||||
                              AC ACCTCAG CA TT TTTAA
                                 C    T C  C
GAM324  LOC257615 5' GCTTCTACGACTCCGCCA   3749   A      AAA
                              TG TGGAGTCGTA  AAGT
                              || |||||||||  ||||
                              AC GCCTCAGCAT  TTCG
                                 C      C__
GAM325  CAPN2    3' AAAACTTTATGAACTTCACCA 855    A   _  AAA
                              TG TGGAGT CGTAA  AGTTTT
                              || |||||| ||||| ||||||
                              AC ACTTCA GTATT  TCAAAA
                                 C      A     ___
GAM325  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
          A                   TGATGGAGT  TA AAAAGTTTT
                              ||||||||| || |||||||||
                              ACTACCTCA  AT TTTTTAAAA
                                  AA  C
GAM325  SELE     3' AAAACTCTCCTACACTTCCATT 747        _ C  AAAA
          A                   TGATGGA GT GTA   AGTTTT
                              ||||||| || |||   ||||||
                              ATTACCT CA CAT   TCAAAA
                                  T _  CCTC
GAM325  KIAA0475 3' AAAACCTTGCATTCCATCA  1570        C  AAAA
                              TGATGGAGT GTAA   GTTTT
                              ||||||||| |||    |||||
```

```
                        ACTACCTTA CGTT   CAAAA
                        _    C___
GAM325  LOC222671 5'  GCTTCTACGACTCCGCCA    3582     A       AAA
                        TG TGGAGTCGTA   AAGT
                        || |||||||||| |||| 
                        AC GCCTCAGCAT   TTCG
                        C         C__
GAM325  LOC254901 5'  AATTTCTTCACTGACTCCACCA 3699    A      _  A A
                        TG TGGAGTC GT AA AAGTT
                        || ||||||| || || ||||| 
                        AC ACCTCAG CA TT TTTAA
                        C     T C C
GAM325  LOC257615 5'  GCTTCTACGACTCCGCCA    3749     A       AAA
                        TG TGGAGTCGTA   AAGT
                        || |||||||||| ||||
                        AC GCCTCAGCAT   TTCG
                        C         C__
GAM326  CAPN2    3'  AAAACTTTATGAACTTCACCA  855      A    _   AAA
                        TG TGGAGT CGTAA  AGTTTT
                        || |||||| |||||  ||||||
                        AC ACTTCA GTATT  TCAAAA
                        C     A   ___
GAM326  DAAM2    3'  AAAATTTTTCTAAAACTCCATC 3559          CG  A
                  A            TGATGGAGT  TA AAAAGTTTT
                        ||||||||| || |||||||||
                        ACTACCTCA  AT TTTTTAAAA
                            AA  C
GAM326  SELE     3'  AAAACTCTCCTACACTTCCATT 747          _  C  AAAA
                  A            TGATGGA GT GTA   AGTTTT
                        |||||||| || |||   ||||||
                        ATTACCT CA CAT   TCAAAA
                          T  _  CCTC
GAM326  KIAA0475 3'  AAAACCTTGCATTCCATCA    1570         C   AAAA
                        TGATGGAGT GTAA   GTTTT
                        ||||||||| ||||   |||||
                        ACTACCTTA CGTT   CAAAA
                        _    C___
GAM326  LOC222671 5'  GCTTCTACGACTCCGCCA    3582     A       AAA
                        TG TGGAGTCGTA   AAGT
                        || |||||||||| |||| 
                        AC GCCTCAGCAT   TTCG
                        C         C__
GAM326  LOC254901 5'  AATTTCTTCACTGACTCCACCA 3699    A      _  A A
                        TG TGGAGTC GT AA AAGTT
                        || ||||||| || || ||||| 
                        AC ACCTCAG CA TT TTTAA
                        C     T C C
GAM326  LOC257615 5'  GCTTCTACGACTCCGCCA    3749     A       AAA
                        TG TGGAGTCGTA   AAGT
                        || |||||||||| ||||
```

```
                         AC GCCTCAGCAT  TTCG
                          C       C__
GAM327  CAPN2    3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| ||||| ||||||
                         AC ACTTCA GTATT  TCAAAA
                          C      A   ___
GAM327  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559       CG  A
              A          TGATGGAGT TA AAAAGTTTT
                         ||||||||| || |||||||||
                         ACTACCTCA  AT TTTTTAAAA
                           AA  C
GAM327  SELE     3' AAAACTCTCCTACACTTCCATT 747       _ C  AAAA
              A          TGATGGA GT GTA   AGTTTT
                         ||||||| || ||| ||||||
                         ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM327  KIAA0475 3' AAAACCTTGCATTCCATCA   1570     C  AAAA
                         TGATGGAGT GTAA  GTTTT
                         ||||||||| |||| |||||
                         ACTACCTTA CGTT  CAAAA
                             _  C___
GAM327  LOC222671 5' GCTTCTACGACTCCGCCA  3582    A     AAA
                         TG TGGAGTCGTA  AAGT
                         || |||||||||  ||||
                         AC GCCTCAGCAT  TTCG
                          C       C__
GAM327  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A   _ A A
                         TG TGGAGTC GT AA AAGTT
                         || ||||||| || || |||||
                         AC ACCTCAG CA TT TTTAA
                          C      T C C
GAM327  LOC257615 5' GCTTCTACGACTCCGCCA  3749    A     AAA
                         TG TGGAGTCGTA  AAGT
                         || |||||||||  ||||
                         AC GCCTCAGCAT  TTCG
                          C       C__
GAM328  CAPN2    3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| ||||| ||||||
                         AC ACTTCA GTATT  TCAAAA
                          C      A   ___
GAM328  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559       CG  A
              A          TGATGGAGT TA AAAAGTTTT
                         ||||||||| || |||||||||
                         ACTACCTCA  AT TTTTTAAAA
                           AA  C
GAM328  SELE     3' AAAACTCTCCTACACTTCCATT 747       _ C  AAAA
              A          TGATGGA GT GTA   AGTTTT
                         ||||||| || ||| ||||||
```

```
                        ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM328  KIAA0475 3' AAAACCTTGCATTCCATCA    1570      C   AAAA
                       TGATGGAGT GTAA    GTTTT
                       ||||||||| ||||    |||||
                       ACTACCTTA CGTT    CAAAA
                                _   C___
GAM328  LOC222671 5' GCTTCTACGACTCCGCCA    3582    A      AAA
                       TG TGGAGTCGTA   AAGT
                       || |||||||||   ||||
                       AC GCCTCAGCAT   TTCG
                          C        C__
GAM328  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                       TG TGGAGTC GT AA AAGTT
                       || |||||||| || || |||||
                       AC ACCTCAG CA TT TTTAA
                          C       T  C  C
GAM328  LOC257615 5' GCTTCTACGACTCCGCCA    3749    A      AAA
                       TG TGGAGTCGTA   AAGT
                       || |||||||||   ||||
                       AC GCCTCAGCAT   TTCG
                          C        C__
GAM329  CAPN2     3' AAAACTTTATGAACTTCACCA 855      A    _   AAA
                       TG TGGAGT CGTAA   AGTTTT
                       || |||||| |||||   ||||||
                       AC ACTTCA GTATT   TCAAAA
                          C      A      ___
GAM329  DAAM2     3' AAAATTTTTCTAAAACTCCATC 3559       CG  A
         A                 TGATGGAGT TA AAAAGTTTT
                       ||||||||| || |||||||||
                       ACTACCTCA  AT TTTTTAAAA
                             AA  C
GAM329  SELE      3' AAAACTCTCCTACACTTCCATT 747         _ C  AAAA
         A                 TGATGGA GT GTA   AGTTTT
                       ||||||| || ||||   ||||||
                       ATTACCT CA CAT   TCAAAA
                             T _  CCTC
GAM329  KIAA0475 3' AAAACCTTGCATTCCATCA    1570      C   AAAA
                       TGATGGAGT GTAA    GTTTT
                       ||||||||| ||||    |||||
                       ACTACCTTA CGTT    CAAAA
                                _   C___
GAM329  LOC222671 5' GCTTCTACGACTCCGCCA    3582    A      AAA
                       TG TGGAGTCGTA   AAGT
                       || |||||||||   ||||
                       AC GCCTCAGCAT   TTCG
                          C        C__
GAM329  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                       TG TGGAGTC GT AA AAGTT
                       || |||||||| || || |||||
```

```
                          AC ACCTCAG CA TT TTTAA
                           C       T C C
GAM329  LOC257615 5' GCTTCTACGACTCCGCCA   3749     A       AAA
                     TG TGGAGTCGTA   AAGT
                     || |||||||||||  ||||
                     AC GCCTCAGCAT   TTCG
                      C         C__
GAM330  CAPN2     3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                     TG TGGAGT CGTAA   AGTTTT
                     || |||||| |||||   ||||||
                     AC ACTTCA GTATT   TCAAAA
                      C      A        ___
GAM330  DAAM2     3' AAAATTTTTCTAAAACTCCATC 3559         CG  A
         A                  TGATGGAGT  TA AAAAGTTTT
                            ||||||||| || |||||||||
                            ACTACCTCA  AT TTTTTAAAA
                             AA  C
GAM330  SELE      3' AAAACTCTCCTACACTTCCATT 747         _  C  AAAA
         A                  TGATGGA GT GTA   AGTTTT
                            ||||||| || |||   ||||||
                            ATTACCT CA CAT   TCAAAA
                             T  _  CCTC
GAM330  KIAA0475  3' AAAACCTTGCATTCCATCA   1570         C   AAAA
                            TGATGGAGT GTAA    GTTTT
                            ||||||||| ||||    |||||
                            ACTACCTTA CGTT    CAAAA
                              _  C___
GAM330  LOC222671 5' GCTTCTACGACTCCGCCA   3582     A       AAA
                     TG TGGAGTCGTA   AAGT
                     || |||||||||||  ||||
                     AC GCCTCAGCAT   TTCG
                      C         C__
GAM330  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699     A    _ A A
                     TG TGGAGTC GT AA AAGTT
                     || ||||||| || || |||||
                     AC ACCTCAG CA TT TTTAA
                      C       T C C
GAM330  LOC257615 5' GCTTCTACGACTCCGCCA   3749     A       AAA
                     TG TGGAGTCGTA   AAGT
                     || |||||||||||  ||||
                     AC GCCTCAGCAT   TTCG
                      C         C__
GAM331  ITGB7     5' AGAGAAAGTCTGACTTGCCCCA 783       AAAA_   TTAT
         C                   GT   AAGTT   CTTTCTCT
                            ||   |||||   ||||||||
                            CA   TTCAG   GAAAGAGA
                             CCCCG   TCT_
GAM331  RPP30     3' AGAGAAAGACAACTGTTCTGCG 1297       A  A  TTA
                            CGTA AA AGTT   TCTTTCTCT
                            |||| || ||||   |||||||||
```

```
                        GCGT TT TCAA   AGAAAGAGA
                          C  G   C__
GAM331  FLJ13263 3' AGAGAAAGATTTTAGCTTTT 2139        TT_
                        AAAAGTT  ATCTTTCTCT
                        ||||||| |||||||||||
                        TTTTCGA  TAGAAAGAGA
                          TTT
GAM331  FLJ23074 5' AGAGAAAGACAAGGGTTT  2133     G   A
                        AAA TTTT TCTTTCTCT
                        ||| |||| |||||||||
                        TTT GGAA AGAAAGAGA
                          G   C
GAM331  GTF2A2   3' AGAAAAAATATGACTTTTTTAC 1119          T  C_
                        GTAAAAAAGTT TAT  TTTCT
                        ||||||||||| ||| |||||
                        CATTTTTTCAG ATA  AAAGA
                            T  AA
GAM331  IMP-2    3' AGAGAAAGCAGGCTTTTCTA 1308    A     TAT
                        TA AAAAGTTT  CTTTCTCT
                        || |||||||| ||||||||
                        AT TTTTCGGA  GAAAGAGA
                          C    C__
GAM331  KIAA0212 3' AGAAAGGTAAATCTTTTTAC 1518        A T
                        GTAAAAA G TTTATCTTTCT
                        ||||||| | |||||||||||
                        CATTTTT C AAATGGAAAGA
                          _T
GAM331  OSBPL2   5' AGAGAAAGTTTGTAAAATTCCT 1566       AAA        ___
          TAC          GTAA  AGTTTTAT  CTTTCTCT
                        ||||  |||||||| |||||||||
                        CATT  TTAAAATG  GAAAGAGA
                        CC_       TTT
GAM331  OSBPL2   5' AGAGAAAGTTTGTAAAATTCCT 2482       AAA        ___
          TAC          GTAA  AGTTTTAT  CTTTCTCT
                        ||||  |||||||| |||||||||
                        CATT  TTAAAATG  GAAAGAGA
                        CC_       TTT
GAM331  RBM9     3' AGAAAGAATACTTTTTTAT 1489           TTTA
                        GTAAAAAAGT  TCTTTCT
                        ||||||||||  |||||||
                        TATTTTTTCA  AGAAAGA
                          TA__
GAM331  LOC254826 3' AGAGAAAGTCTTGCTTTTT 3732        TTTAT
                        AAAAAGT   CTTTCTCT
                        |||||||   ||||||||
                        TTTTTCG   GAAAGAGA
                          TTCT_
GAM332  DSC3     3' TAAAATCTATGTGTTTTAGACT 871         AGT     A
          TA             TAAGTT  AATACATA ATTTTA
                        |||||| |||||||| ||||||
```

```
                              ATTCAG  TTGTGTAT TAAAAT
                              ATT        C
GAM332  DSC3    3' TAAAATCTATGTGTTTTAGACT 2060      AGT     A
        TA                  TAAGTT  AATACATA ATTTTA
                            ||||||  |||||||| ||||||
                            ATTCAG  TTGTGTAT TAAAAT
                            ATT        C
GAM332  FLJ20366 3' AAGTTTACATGTACTAACTTA 1751          ATACA
                         TAAGTTAGTA   TAAATTT
                         ||||||||||   |||||||
                         ATTCAATCAT   ATTTGAA
                              GTAC_
GAM333  CAPN2   3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                      TG TGGAGT CGTAA  AGTTTT
                      || |||||| |||||  ||||||
                      AC ACTTCA GTATT  TCAAAA
                         C   A       ___
GAM333  DAAM2   3' AAAATTTTTCTAAAACTCCATC 3559      CG  A
        A                 TGATGGAGT TA AAAAGTTTT
                          ||||||||| || |||||||||
                          ACTACCTCA AT TTTTTAAAA
                             AA  C
GAM333  SELE    3' AAAACTCTCCTACACTTCCATT 747        _  C  AAAA
        A                   TGATGGA GT GTA   AGTTTT
                            |||||||| || ||   ||||||
                            ATTACCT CA CAT   TCAAAA
                              T _  CCTC
GAM333  KIAA0475 3' AAAACCTTGCATTCCATCA 1570        C   AAAA
                            TGATGGAGT GTAA   GTTTT
                            ||||||||| ||||   |||||
                            ACTACCTTA CGTT   CAAAA
                               _   C___
GAM333  LOC222671 5' GCTTCTACGACTCCGCCA   3582   A      AAA
                            TG TGGAGTCGTA  AAGT
                            || |||||||||| ||||
                            AC GCCTCAGCAT  TTCG
                               C       C__
GAM333  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A   _ A A
                            TG TGGAGTC GT AA AAGTT
                            || |||||||| || || |||||
                            AC ACCTCAG CA TT TTTAA
                               C   T C  C
GAM333  LOC257615 5' GCTTCTACGACTCCGCCA   3749   A      AAA
                            TG TGGAGTCGTA  AAGT
                            || |||||||||| ||||
                            AC GCCTCAGCAT  TTCG
                               C       C__
GAM334  CAPN2   3' AAAACTTTATGAACTTCACCA 855     A    _   AAA
                      TG TGGAGT CGTAA  AGTTTT
                      || |||||| |||||  ||||||
```

```
                        AC ACTTCA GTATT  TCAAAA
                         C     A      ___
GAM334   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
         A                  TGATGGAGT  TA AAAAGTTTT
                        |||||||||| || |||||||||
                        ACTACCTCA  AT TTTTTAAAA
                           AA C
GAM334   SELE    3' AAAACTCTCCTACACTTCCATT 747        _  C  AAAA
         A                  TGATGGA GT GTA   AGTTTT
                        ||||||| || |||   ||||||
                        ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM334   KIAA0475 3' AAAACCTTGCATTCCATCA  1570        C   AAAA
                        TGATGGAGT GTAA   GTTTT
                        ||||||||| |||   |||||
                        ACTACCTTA CGTT   CAAAA
                            _  C___
GAM334   LOC222671 5' GCTTCTACGACTCCGCCA    3582     A      AAA
                        TG TGGAGTCGTA  AAGT
                        || |||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C        C__
GAM334   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _  A A
                        TG TGGAGTC GT AA AAGTT
                        || ||||||| || || |||||
                        AC ACCTCAG CA TT TTTAA
                        C    T C C
GAM334   LOC257615 5' GCTTCTACGACTCCGCCA   3749     A      AAA
                        TG TGGAGTCGTA  AAGT
                        || |||||||||  ||||
                        AC GCCTCAGCAT  TTCG
                        C        C__
GAM335   CAPN2    3' AAAACTTTATGAACTTCACCA 855     A   _  AAA
                        TG TGGAGT CGTAA  AGTTTT
                        || ||||||| |||||   ||||||
                        AC ACTTCA GTATT  TCAAAA
                         C     A      ___
GAM335   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
         A                  TGATGGAGT  TA AAAAGTTTT
                        |||||||||| || |||||||||
                        ACTACCTCA  AT TTTTTAAAA
                           AA C
GAM335   SELE    3' AAAACTCTCCTACACTTCCATT 747        _  C  AAAA
         A                  TGATGGA GT GTA   AGTTTT
                        ||||||| || |||   ||||||
                        ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM335   KIAA0475 3' AAAACCTTGCATTCCATCA  1570        C   AAAA
                        TGATGGAGT GTAA   GTTTT
                        ||||||||| |||   |||||
```

```
                         ACTACCTTA CGTT   CAAAA
                              _   C___
GAM335  LOC222671 5' GCTTCTACGACTCCGCCA    3582    A       AAA
                         TG TGGAGTCGTA   AAGT
                         || |||||||||| ||||
                         AC GCCTCAGCAT   TTCG
                              C        C__
GAM335  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699     A     _ A A
                         TG TGGAGTC GT AA AAGTT
                         || ||||||| || || |||||
                         AC ACCTCAG CA TT TTTAA
                              C      T C  C
GAM335  LOC257615 5' GCTTCTACGACTCCGCCA     3749    A       AAA
                         TG TGGAGTCGTA   AAGT
                         || |||||||||| ||||
                         AC GCCTCAGCAT   TTCG
                              C        C__
GAM336  CAPN2    3' AAAACTTTATGAACTTCACCA 855      A    _   AAA
                         TG TGGAGT CGTAA  AGTTTT
                         || |||||| |||||  ||||||
                         AC ACTTCA GTATT  TCAAAA
                              C      A    ___
GAM336  DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559       CG A
          A               TGATGGAGT  TA AAAAGTTTT
                         |||||||||| || |||||||||
                         ACTACCTCA  AT TTTTTAAAA
                                AA  C
GAM336  SELE     3' AAAACTCTCCTACACTTCCATT 747        _ C  AAAA
          A               TGATGGA GT GTA   AGTTTT
                         |||||||| || |||   ||||||
                         ATTACCT CA CAT   TCAAAA
                             T _  CCTC
GAM336  KIAA0475 3' AAAACCTTGCATTCCATCA  1570       C   AAAA
                         TGATGGAGT GTAA   GTTTT
                         ||||||||| ||||   |||||
                         ACTACCTTA CGTT   CAAAA
                              _   C___
GAM336  LOC222671 5' GCTTCTACGACTCCGCCA    3582    A       AAA
                         TG TGGAGTCGTA   AAGT
                         || |||||||||| ||||
                         AC GCCTCAGCAT   TTCG
                              C        C__
GAM336  LOC254901 5' AATTTCTTCACTGACTCCACCA 3699     A     _ A A
                         TG TGGAGTC GT AA AAGTT
                         || ||||||| || || |||||
                         AC ACCTCAG CA TT TTTAA
                              C      T C  C
GAM336  LOC257615 5' GCTTCTACGACTCCGCCA     3749    A       AAA
                         TG TGGAGTCGTA   AAGT
                         || |||||||||| ||||
```

```
                              AC GCCTCAGCAT  TTCG
                              C        C__
GAM337  FGF2     3' ATATTTTTGTGGCTGCTTTTT 884         T_
                         AAAAAGT TTACAAAAATAT
                         ||||||| |||||||||||
                         TTTTTCG GGTGTTTTTATA
                              TC
GAM337  MPHOSPH1 3' ATATTTTTATAAGGCTTTTTT 1670              C
                         AAAAAAGTTTTA AAAAATAT
                         |||||||||||| |||||||
                         TTTTTTCGGAAT TTTTTATA
                                A
GAM337  FLJ11274 3' ATATCTTTGTAGTAGCTTTTTT 1820          _     A
          TA                TAAAAAAAGTT TTACAAA ATAT
                         |||||||||| |||||| ||||
                         ATTTTTTTCGA GATGTTT TATA
                              T   C
GAM337  FLJ31101 3' ATATTTTTGTAAAATGTATTTG 1771      AAAA
            T                ATAAA   GTTTTACAAAAATAT
                         ||||| |||||||||||||
                         TGTTT   TAAAATGTTTTTATA
                         ATG_
GAM337  GPT2     3' ATATTTTTGTAACAATTGCTTT 2417          T____
            TTT                AAAAAAGT   TTACAAAAATAT
                         |||||||| |||||||||||
                         TTTTTTCG    AATGTTTTTATA
                              TTAAC
GAM337  RMP      3' TTTTGTAAAACTTTTTTTTTC 2430    T
                         A AAAAAAAGTTTTACAAAA
                         | |||||||||||||||||
                         C TTTTTTTCAAAATGTTTT
                             T
GAM337  RMP      3' TTTTGTAAAACTTTTTTTTTC 1059    T
                         A AAAAAAAGTTTTACAAAA
                         | |||||||||||||||||
                         C TTTTTTTCAAAATGTTTT
                             T
GAM337  SOX6     3' ATATTTTTGTCTTACTTTTTTT 2328          TTT
                         AAAAAAAGT ACAAAAATAT
                         ||||||||| |||||||||
                         TTTTTTTCA TGTTTTTATA
                              TTC
GAM337  LOC136288 3' ATATTCTGAGGCTTTTTTTGT 3018              CAA
                         ATAAAAAAAGTTTTA AAATAT
                         ||||||||||||| |||||
                         TGTTTTTTTCGGAGT TTTATA
                                C__
GAM338  AICDA    3' AGAAAGAGAACAATATTT 1922       TTTA
                         AAATATT TTCTCTTTCT
                         ||||||| ||||||||||
```

```
                          TTTATAA   AAGAGAAAGA
                              C___
GAM338  AS3       3' AGAAAGATTTAAAGTATTTTA 1652          TATTC
                          TAAAATATTTT   TCTTTCT
                          |||||||||| ||||||
                          ATTTTATGAAA   AGAAAGA
                               TTT__
GAM338  EPM2A     3' AGAAAGAGAAGTGTTTT   1234      TTTTA
                          AAAATAT   TTCTCTTTCT
                          ||||||| ||||||||||
                          TTTTGTG   AAGAGAAAGA

                             _____
GAM338  HRH1     3' AGAAAGAGAAATGAAATATTTT 780           TA
                          AAAATATTTT TTCTCTTTCT
                          |||||||||| ||||||||||
                          TTTTATAAAG AAGAGAAAGA
                               TA
GAM338  MAPK14   3' GAGAAAGGGCAAATTATTTTA 818      T TATT
                          TAAAATA TTT   CTCTTTCTC
                          ||||||| ||| |||||||||
                          ATTTTAT AAA   GGGAAAGAG
                             T C___
GAM338  MAPK14   3' GAGAAAGGGCAAATTATTTTA 2465      T TATT
                          TAAAATA TTT   CTCTTTCTC
                          ||||||| ||| |||||||||
                          ATTTTAT AAA   GGGAAAGAG
                             T C___
GAM338  MAPK14   3' GAGAAAGGGCAAATTATTTTA 2466      T TATT
                          TAAAATA TTT   CTCTTTCTC
                          ||||||| ||| |||||||||
                          ATTTTAT AAA   GGGAAAGAG
                             T C___
GAM338  NOTCH2   3' GAGAATTAAAATATTTTA   2058          T
                          TAAAATATTTT ATTCTC
                          |||||||||| ||||||
                          ATTTTATAAAA TAAGAG
                               T
GAM338  SIM1     3' GAGAAAGAGAGAGATA     1181       TAT
                          TATTTT TCTCTTTCTC
                          |||||| ||||||||||
                          ATAGAG AGAGAAAGAG
                              ___
GAM338  C11orf25 3' AAAGAGAAAAATATTTTA   2193          TAT
                          TAAAATATTTT TCTCTTT
                          |||||||||| ||||||
                          ATTTTATAAAA AGAGAAA
                              __
GAM338  DKFZP564D116 3' GAAAAGCAATAAAAATATTTTA 2938            _ C
                          TAAAATATTTTTATT CT TTTC
                          |||||||||||||| || ||||
```

```
                        ATTTTATAAAAATAA GA AAAG
                             C  _
GAM338  DSCR6    3' GAGAAAGAGAAGGTCTATGTCA 1866   A   TTTTA
                        A ATAT    TTCTCTTTCTC
                        | ||||    |||||||||||
                        A TGTA    AAGAGAAAGAG
                         C   TCTGG
GAM338  FLJ10006 3' GAGAAAGAAGATATTTTA    3152        A
                        TAAAATATTTTT TTCTC
                        ||||||||||| |||||
                        ATTTTATAGAAG AAGAG
                              A
GAM338  HTPAP    3' GAGAATAAAAAGATTTTA    2255        A
                        TAAAAT TTTTTATTCTC
                        |||||| |||||||||||
                        ATTTTA AAAAATAAGAG
                             G
GAM338  KIAA0979 3' AGAAAGATTTAAAGTATTTTA 1601          TATTC
                        TAAAATATTTT   TCTTTCT
                        |||||||||||   |||||||
                        ATTTTATGAAA   AGAAAGA
                            TTT__
GAM338  KIAA1634 3' GAGAATAAAACTATTTTA    2657       T
                        TAAAATA TTTTATTCTC
                        ||||||| ||||||||||
                        ATTTTAT AAAATAAGAG
                             C
GAM338  PTD012   3' GAGATTGGGAACAAAAATAT  1465        A   TT
                        ATATTTTT TTCTC  TCTC
                        |||||||| |||||  ||||
                        TATAAAAA AAGGG  AGAG
                           C    TT
GAM338  SAMHD1   3' AGAAAGAGAAAGAAATAT    2593        A
                        ATATTTTT TTCTCTTTCT
                        |||||||| ||||||||||
                        TATAAAGA AAGAGAAAGA
                             _
GAM338  LOC196758 3' GAGAAAGAGCAGGTGAAATATT 3410       TATT_
          TT              AAAATATTTT   CTCTTTCTC
                        ||||||||||   |||||||||
                        TTTTATAAAG   GAGAAAGAG
                           TGGAC
GAM338  LOC219790 3' GAGAATAAAAATAATTTA   3520      A
                        TAAA TATTTTTATTCTC
                        |||| |||||||||||||
                        ATTT ATAAAAATAAGAG
                           A
GAM339  CAPN2    3' AAAACTTTATGAACTTCACCA  855      A   _   AAA
                        TG TGGAGT CGTAA  AGTTTT
                        || |||||| |||||  ||||||
```

```
                        AC ACTTCA GTATT   TCAAAA
                          C      A        ___
GAM339   DAAM2    3' AAAATTTTTCTAAAACTCCATC 3559        CG  A
       A                 TGATGGAGT  TA AAAAGTTTT
                        IIIIIIIII II IIIIIIIII
                        ACTACCTCA  AT TTTTTAAAA
                                AA  C
GAM339   SELE     3' AAAACTCTCCTACACTTCCATT 747        _  C  AAAA
       A                 TGATGGA GT GTA   AGTTTT
                        IIIIIIII II III   IIIIII
                        ATTACCT CA CAT   TCAAAA
                            T _  CCTC
GAM339   KIAA0475 3' AAAACCTTGCATTCCATCA  1570        C   AAAA
                         TGATGGAGT GTAA   GTTTT
                        IIIIIIIIII IIII   IIIII
                        ACTACCTTA CGTT   CAAAA
                             _  C___
GAM339   LOC222671 5' GCTTCTACGACTCCGCCA   3582    A      AAA
                         TG TGGAGTCGTA  AAGT
                        II IIIIIIIIII  IIII
                        AC GCCTCAGCAT  TTCG
                           C       C__
GAM339   LOC254901 5' AATTTCTTCACTGACTCCACCA 3699    A    _ A A
                         TG TGGAGTC GT AA AAGTT
                        II IIIIIII II II IIIII
                        AC ACCTCAG CA TT TTTAA
                           C    T C C
GAM339   LOC257615 5' GCTTCTACGACTCCGCCA   3749    A      AAA
                         TG TGGAGTCGTA  AAGT
                        II IIIIIIIIII  IIII
                        AC GCCTCAGCAT  TTCG
                           C       C__
GAM340   ADCY6    3' TTGTACAATATTTGTACAAAG 1617     G     TTCAC
       A                 TCTTTG TACAAAAT   ACAA
                        IIIIII IIIIIIII    IIII
                        AGAAAC ATGTTTTA   TGTT
                          _     TAACA
GAM340   ADCY6    3' TTGTACAATATTTGTACAAAG 1933     G     TTCAC
       A                 TCTTTG TACAAAAT   ACAA
                        IIIIII IIIIIIII    IIII
                        AGAAAC ATGTTTTA   TGTT
                          _     TAACA
GAM340   APBB2    5' TGAGCTTTGTACCAAAGA   2946         AT
                         TCTTTGGTACAAA TTCA
                        IIIIIIIIIIIII IIII
                        AGAAACCATGTTT GAGT
                                C_
GAM340   ATP8B2   3' TGATTTTTATACCAAAGA   2716     C  TT
                         TCTTTGGTA AAAA  TCA
                        IIIIIIIII IIII III
```

```
                          AGAAACCAT TTTT  AGT
                             A   T_
GAM340  CEACAM1  3' TGTGTGAACTAGCAAAGA  848        G  CAAAAT
                       TCTTTG TA    TTCACACA
                       |||||| ||    ||||||||
                       AGAAAC AT    AAGTGTGT
                             G  C_____
GAM340  CHST1    3' TGTGATATTCTTTGTGCCAAA 1046          ___  T
                       TTTGGTACAAA  AT TCACA
                       |||||||||||  || |||||
                       AAACCGTGTTT  TA AGTGT
                             CTT  T
GAM340  FBXL7    3' TGCGTGTTTTCCACCAAAGA 1425        AC   TTT  A
                       TCTTTGGT AAAA  CAC CA
                       |||||||| ||||  ||| ||
                       AGAAACCA TTTT  GTG GT
                             CC  ___  C
GAM340  HOXC9    3' TGCGTGCAGATTTTGTAC  2592          _  A
                       GTACAAAATTT CAC CA
                       ||||||||||| ||| ||
                       CATGTTTTAGA GTG GT
                             C  C
GAM340  IGF1     3' TGTGGCATTTGTACCAAA  763          ATT
                       TTTGGTACAAA  TCACA
                       |||||||||||  |||||
                       AAACCATGTTT  GGTGT
                             AC_
GAM340  ITGAL    3' TGTGAAATTCTGTCCAAA  907        T  A
                       TTTGG ACA AATTTCACA
                       ||||| ||| |||||||||
                       AAACC TGT TTAAAGTGT
                             _  C
GAM340  LBR      3' TGTACTGGATTGCACCAAGGA 2522        A  AAT  C_
                       TCTTTGGT CAA  TTCA ACA
                       |||||||| |||  |||| |||
                       AGGAACCA GTT  AGGT TGT
                             C  ___  CA
GAM340  MIP      3' TGTGTGAAATCTTTCAAG  1399        TACAAA
                       TTTGG    ATTTCACACA
                       |||||    ||||||||||
                       GAACT    TAAAGTGTGT
                             TTC___
GAM340  RLN2     3' TGTTGGTTGTACCAAA   1175        AATT  C
                       TTTGGTACAA   TCA ACA
                       ||||||||||   ||| |||
                       AAACCATGTT   GGT TGT
                             ___  _
GAM340  SART2    3' TGATTTTCATACCAAAGA  1444        CA  TT
                       TCTTTGGTA AAA TCA
                       ||||||||| ||| |||
```

```
                        AGAAACCAT TTT AGT
                        AC  T_
GAM340  TPK1     3' AAATTTTGCTACCAAAGA  1987          _
                        TCTTTGGTA CAAAATTT
                        |||||||| ||||||||
                        AGAAACCAT GTTTTAAA
                        C
GAM340  TRIP12   3' TGTGTGAAATTTAAAAAAGG  1094      GGTACA
                        TCTTT    AAATTTCACACA
                        |||||    |||||||||||
                        GGAAA    TTTAAAGTGTGT
                        AAA___
GAM340  BRD3     3' GTGTGAGATTCGTACCGAAGA  1398          AA
                        TCTTTGGTAC AATTTCACAC
                        |||||||||| ||||||||||
                        AGAAGCCATG TTAGAGTGTG
                        C_
GAM340  FLJ13397 3' GTGTGAAATTTACTAGCAAA  2116      G CA
                        TTTG TA AAATTTCACAC
                        |||| || |||||||||||
                        AAAC AT TTTAAAGTGTG
                        G CA
GAM340  FLJ22202 3' TGTATCATTTTGTACCAAA  2103            TTC
                        TTTGGTACAAAAT ACA
                        ||||||||||||| |||
                        AAACCATGTTTTA TGT
                        CTA
GAM340  GROS1    3' TGTGTAGACAACCAAAGA  1986      ACAAAATT _
                        TCTTTGGT    TC ACACA
                        ||||||||    || |||||
                        AGAAACCA    AG TGTGT
                        AC_____ A
GAM340  KIAA0981 3' TGTGTAAAACTGCCAAGGA  2598          CAAAA  C
                        TCTTTGGTA  TTT ACACA
                        |||||||||  ||| |||||
                        AGGAACCGT  AAA TGTGT
                        C____ A
GAM340  KIAA1243 3' TGTGACATGACCAAAGA  2978       A AAATT
                        TCTTTGGT CA  TCACA
                        |||||||| ||  |||||
                        AGAAACCA GT  AGTGT
                        _ AC___
GAM340  KIAA1462 3' TTGTGTGAGAGGAACCCAAAGA 3524       TACAAAA
                        TCTTTGG   TTTCACACAA
                        |||||||   ||||||||||
                        AGAAACC   AGAGTGTGTT
                        CAAGG__
GAM340  MGC1136  3' TTGTGTGAAACCCCTAGCATAG 2041      T G CAAAA
           A            TCT TG TA   TTTCACACAA
                        ||| || ||   ||||||||||
```

```
                        AGA AC AT    AAAGTGTGTT
                        T  G  CCCC_
GAM340  MSTP043   3' TGTCTTTATTTTTACCAAAGA 2223        C    TTC_
                        TCTTTGGTA AAAAT   ACA
                        ||||||||| |||||   |||
                        AGAAACCAT TTTTA   TGT
                         _    TTTC
GAM340  Nup43     3' TGTGCAAAATTTTAGTATCAGA 2075        _      CA
                        TTTGGTAC AAAATTT CACA
                        ||||||||| ||||||| ||||
                        AGACTATG TTTTAAA GTGT
                            A    AC
GAM340  RPS6KA4   3' TGTGCAATTACGTCCACCAAAG 1072           __ AA   T
             A              TCTTTGGT AC AATT CACA
                        ||||||||| || |||| ||||
                        AGAAACCA TG TTAA GTGT
                          CC CA   C
GAM340  SLC17A6   3' TGAAACTTGTGCCACAGA   1911      T     AA
                        TCT TGGTACAA TTTCA
                        ||| ||||||| |||||
                        AGA ACCGTGTT AAAGT
                          C    C_
GAM340  TERA      3' TGTATGAATAGTACCAAAG  1949        AAAAT   C
                        CTTTGGTAC   TTCA ACA
                        |||||||||   |||| |||
                        GAAACCATG   AAGT TGT
                          AT___  A
GAM340  VAV3      3' TTGTGTAGAGTTCTAATACCAA 1273        CAA_  TC
          AGA            TCTTTGGTA  AATT ACACAA
                        |||||||||  |||| ||||||
                        AGAAACCAT  TTGA TGTGTT
                          AATC  GA
GAM340  LOC120892 3' TGCAATTTTTTTTACCAAAGA 2987        C__    T
                        TCTTTGGTA  AAAATT CA
                        |||||||||  |||||| ||
                        AGAAACCAT  TTTTAA GT
                          TTT    C
GAM340  LOC155434 3' TTGTGTGATTTCGTACCAAA 3376        A  TT
                        TTTGGTAC AAA TCACACAA
                        ||||||||| ||| ||||||||
                        AAACCATG TTT AGTGTGTT
                          C  __
GAM340  LOC169966 3' ATTTTGCCTTTACCAAAGA  3252           ____
                        TCTTTGGTA  CAAAAT
                        |||||||||  ||||||
                        AGAAACCAT  GTTTTA
                          TTCC
GAM340  LOC221272 3' TGTCTGCTCTGTACCAGAGA 3616              AAATTT C
                        TCTTTGGTACA   CA ACA
                        ||||||||||   || |||
```

```
                      AGAGACCATGT    GT TGT
                         CTC___  C
GAM340  LOC221968 3' TTGTGTGAAATTTTGTCGAA 3569     GT
                     TTTG ACAAAATTTCACACAA
                     |||| |||||||||||||||
                     AAGC TGTTTTAAAGTGTGTT


                         __
GAM340  LOC86651 5' TTGTGTGAAAGATGTTTCATAC 2830        CA    ____
            CAAGGA            CTTTGGTA AAAT  TTCACACAA
                     |||||||| ||||  |||||||||
                     GGAACCAT TTTG  AAGTGTGTT
                       AC   TAGA
GAM340  LOC90322 3' GAGATTCCATACTAAAGA  2632       CAA
                     TCTTTGGTA AATTTC
                     ||||||||| ||||||
                     AGAAATCAT TTAGAG
                        ACC
GAM341  MYO1E    5' ATGGAGTCCCCTCTAGGGTT 1168    ATC A A
                     GACC  GA GG GACTCCAT
                     ||||  || || |||||||||
                     TTGG  CT CC CTGAGGTA
                      GAT  C _
GAM341  ROCK2   3' ATGAAGTCTTTTAACAGTCTC 2737      CATCGA    C
                     GAGAC    AGGAGACT CAT
                     |||||    |||||||| |||
                     CTCTG    TTTTCTGA GTA
                       ACAA__       A
GAM341  MGC15937 5' GAGTTTCTTCTTCAAGGTCTCA 2383       ATC      __
                     TGAGACC  GAAGGAGA CTC
                     |||||||  |||||||| |||
                     ACTCTGG  CTTCTTCT GAG
                        AA_     TT
GAM341  STK16    5' GAGCTCTTCGGTAGCCTCA 2937     ACC    G A
                     TGAG  ATCGAAG AG CTC
                     ||||  ||||||| || |||
                     ACTC  TGGCTTC TC GAG
                        CGA      _ _
GAM341  LOC148029 5' GGAGTCTCCATCCTCA    3116     ACCATC A
                     TGAG    GA GGAGACTCC
                     ||||    || |||||||||
                     ACTC    CT CCTCTGAGG
                       _____  A
GAM341  LOC169436 5' TGGAGTTCAATGAGCTCA 3261     AC  C AGGAG
                     TGAG CAT GA   ACTCCA
                     |||| ||| ||   ||||||
                     ACTC GTA CT   TGAGGT
                       GA  A _____
GAM341  LOC256267 3' ATGGAGTCTCCCTCTGTC  3713    CATC A
                     GAC  GA GGAGACTCCAT
                     |||  || |||||||||||
```

```
                              CTG   CT CCTCTGAGGTA
                              T___  C
GAM341  LOC257426 3' GAGTCCTTCGGTGGCCTCA  2755      A        GA
                              TGAG CCATCGAAGGA CTC
                              |||| ||||||||||| |||
                              ACTC GGTGGCTTCCT GAG
                              C              __
GAM341  LOC92466  3' ATGGAGTCTCCCTCTGTC   2858    CATC A
                              GAC   GA GGAGACTCCAT
                              |||   || |||||||||||
                              CTG   CT CCTCTGAGGTA
                              T___  C
GAM342  MME       3' AAAAAAAGTTACAGAAATA   785        AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                                    __
GAM342  MME       3' AAAAAAAGTTACAGAAATA   1377       AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                                    __
GAM342  MME       3' AAAAAAAGTTACAGAAATA   1378       AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                                    __
GAM342  MME       3' AAAAAAAGTTACAGAAATA   1379       AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                                    __
GAM342  DKFZP434C212 3' AAAAAGTACACAGAAATATT  2832       AAA
                              AATATTTTTGT ACTTTT
                              |||||||||| |||||||
                              TTATAAAGACA TGAAAAA
                                  CA_
GAM342  FLJ11275  3' TAAAATGGGATTTATAAAAATA 1821         A TT
          TT              AATATTTTTGTAAA CT TTTTA
                              |||||||||||| || |||||
                              TTATAAAAATATTT GG  AAAAT
                                  A GT
GAM342  GOLPH3    3' TAAAAAAAGTTTTACTGCCATA 1981        TTTT
          TT              AATAT  GTAAAACTTTTTTTA
                              |||||  |||||||||||||
                              TTATA  CATTTTGAAAAAAAT
                                  CCGT
GAM342  KIAA0563  5' TAAAAAAAAGGAGCAAAAGTAT 1565         AAAA
                              ATATTTTGT  CTTTTTTTA
                              |||||||||  |||||||||
```

```
                              TATGAAAACG   GAAAAAAAT
                              AG__
GAM342   TAF2      3' AGAAAGTTTGACAAAATA  997          A
                              TATTTTTGT AAACTTTTT
                              |||||||||| ||||||||
                              ATAAAAACA TTTGAAAGA
                              G
GAM342   LOC147071 5' TAAAAAAAGGAGCAAAAGTAT 2965           AAAA
                              ATATTTTTGT   CTTTTTTTA
                              ||||||||||   |||||||||
                              TATGAAAACG   GAAAAAAAT
                              AG__
GAM342   LOC147639 5' AAAAGTGCTGCAAAAATATT  3110          AA
                              AATATTTTTGTA ACTTTT
                              |||||||||||| ||||||
                              TTATAAAAACGT TGAAAA
                              CG
GAM342   LOC201173 5' TAAAAAAAGGAGCAAAAGTAT 3405           AAAA
                              ATATTTTTGT   CTTTTTTTA
                              ||||||||||   |||||||||
                              TATGAAAACG   GAAAAAAAT
                              AG__
GAM342   LOC201220 5' TAAAAAAAGGAGCAAAAGTAT 3406           AAAA
                              ATATTTTTGT   CTTTTTTTA
                              ||||||||||   |||||||||
                              TATGAAAACG   GAAAAAAAT
                              AG__
GAM343   MME       3' AAAAAAAGTTACAGAAATA  785          AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                              __
GAM343   MME       3' AAAAAAAGTTACAGAAATA  1377          AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                              __
GAM343   MME       3' AAAAAAAGTTACAGAAATA  1378          AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                              __
GAM343   MME       3' AAAAAAAGTTACAGAAATA  1379          AA
                              TATTTTTGTA ACTTTTTTT
                              |||||||||| |||||||||
                              ATAAAGACAT TGAAAAAAA
                              __
GAM343   DKFZP434C212 3' AAAAAGTACACAGAAATATT 2832            AAA
                              AATATTTTTGT ACTTTTT
                              |||||||||||| ||||||
```

```
                    TTATAAAGACA  TGAAAAA
                         CA_
GAM343  FLJ11275 3'  TAAAATGGGATTTATAAAAATA 1821              A TT
         TT              AATATTTTTGTAAA CT  TTTTA
                    ||||||||||||| ||  |||||
                    TTATAAAAATATTT GG  AAAAT
                         A  GT
GAM343  GOLPH3   3'  TAAAAAAAGTTTTACTGCCATA 1981          TTTT
         TT              AATAT  GTAAAACTTTTTTTA
                    |||||   ||||||||||||||
                    TTATA   CATTTTGAAAAAAAT
                         CCGT
GAM343  KIAA0563 5'  TAAAAAAAGGAGCAAAAGTAT 1565              AAAA
                         ATATTTTTGT  CTTTTTTTA
                    ||||||||||  |||||||||
                    TATGAAAACG  GAAAAAAAT
                         AG__
GAM343  TAF2     3'  AGAAAGTTTGACAAAAATA  997             A
                         TATTTTTGT AAACTTTTT
                    ||||||||| |||||||||
                    ATAAAAACA TTTGAAAGA
                         G
GAM343  LOC147071 5' TAAAAAAAGGAGCAAAAGTAT 2965              AAAA
                         ATATTTTTGT  CTTTTTTTA
                    ||||||||||  |||||||||
                    TATGAAAACG  GAAAAAAAT
                         AG__
GAM343  LOC147639 5' AAAAGTGCTGCAAAAATATT  3110              AA
                         AATATTTTTGTA ACTTTT
                    |||||||||||| |||||
                    TTATAAAACGT TGAAAA
                         CG
GAM343  LOC201173 5' TAAAAAAAGGAGCAAAAGTAT 3405              AAAA
                         ATATTTTTGT  CTTTTTTTA
                    ||||||||||  |||||||||
                    TATGAAAACG  GAAAAAAAT
                         AG__
GAM343  LOC201220 5' TAAAAAAAGGAGCAAAAGTAT 3406              AAAA
                         ATATTTTTGT  CTTTTTTTA
                    ||||||||||  |||||||||
                    TATGAAAACG  GAAAAAAAT
                         AG__
GAM344  MARK1    3'  TATAATAAAACATGATTGCTTA 1857      TA   TAC
         A              TTA CGATC  GTTTTATTATA
                    ||| |||||  |||||||||||
                    AAT GTTAG  CAAAATAATAT
                         TC   TA_
GAM345  DKK1     3'  AAAATACTAGCTTATTTTCTGA 1417          _   TAA
                         TCAGAAAG AGGTT  TATTTT
                    ||||||||| |||||  |||||
```

<pre>
                        AGTCTTTT TTCGA ATAAAA
                          A   TC_
GAM345 KERA   3' AAAATATTGAATGCTTTCT 1349   AG

                        AGAAAG GTTTAATATTTT
                        IIIIII IIIIIIIIIII
                        TCTTTC TAAGTTATAAAA
                          G_
GAM345 PPP1R12A 3' AAAATACTACATCTTTCTGG 931   G TTAA

                        TCAGAAAGA GT   TATTTT
                        IIIIIIIII II   IIIIII
                        GGTCTTTCT CA   ATAAAA
                          A TC__
GAM345 S100B   3' AAAATTGAAAACCTCTTTC 1284   AAT

                        GAAAGAGGTTT ATTTT
                        IIIIIIIIIII IIIII
                        CTTTCTCCAAA TAAAA
                          AGT
GAM345 DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196   A GTT

                        ATCAGAA GAG   TAATATTTT
                        IIIIIII III   IIIIIIIII
                        TAGTCTT CTT   GTTATAAAA
                          _   AC_
GAM345 EML4   3' AAAATGTTTCCTCTTTCT 1876   TTT

                        AGAAAGAGG AATATTTT
                        IIIIIIIII IIIIIIII
                        TCTTTCTCC TTGTAAAA
                            T__
GAM345 FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990   AA GTTT

                        ATCAG AGAG   AATATTTT
                        IIIII IIII   IIIIIIII
                        TAGTC TCTC   TTATAAAA
                          CG   ATT_
GAM345 KIAA1054 3' AAAATGGTACCTCTTTC   2820   TTAA

                        GAAAGAGGT TATTTT
                        IIIIIIIII IIIIII
                        CTTTCTCCA GTAAAA
                          TG__
GAM345 SEMA3E   5' AAAATACAGCTTCTTCCTGA 1431   A   TAA

                        TCAG AAGAGGTT TATTTT
                        IIII IIIIIIIII IIIIII
                        AGTC TTCTTCGA ATAAAA
                          C   C__
GAM345 LOC130507 3' AAAATATTAAGATAACTTTCTG 3011   AGG_

                        CAGAAAG TTTAATATTTT
                        IIIIIII IIIIIIIIIII
                        GTCTTTC GAATTATAAAA
                          AATA
GAM345 LOC148145 5' AAAATATTAAACCTGGACCTGA 3296   AAAG
         T   ATCAG AGGTTTAATATTTT
                        IIIII   IIIIIIIIIIIII
</pre>

```
                            TAGTC  TCCAAATTATAAAA
                               CAGG
GAM346  DKK1      3' AAAATACTAGCTTATTTTCTGA 1417         _    TAA
                            TCAGAAAG AGGTT  TATTTT
                            |||||||| |||||  ||||||
                            AGTCTTTT TTCGA  ATAAAA
                               A     TC_
GAM346  KERA      3' AAAATATTGAATGCTTTCT  1349       AG
                            AGAAAG GTTTAATATTTT
                            |||||| |||||||||||
                            TCTTTC TAAGTTATAAAA
                               G_
GAM346  PPP1R12A  3' AAAATACTACATCTTTCTGG  931         G TTAA
                            TCAGAAAGA GT   TATTTT
                            ||||||||| ||   ||||||
                            GGTCTTTCT CA   ATAAAA
                               A      TC__
GAM346  S100B     3' AAAATTGAAAACCTCTTTC  1284         AAT
                            GAAAGAGGTTT ATTTT
                            ||||||||||| |||||
                            CTTTCTCCAAA TAAAA
                               AGT
GAM346  DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196     A  GTT
                            ATCAGAA GAG   TAATATTTT
                            ||||||| |||   |||||||||
                            TAGTCTT CTT   GTTATAAAA
                               _    AC_
GAM346  EML4      3' AAAATGTTTCCTCTTTCT  1876         TTT
                            AGAAAGAGG  AATATTTT
                            |||||||||  ||||||||
                            TCTTTCTCC  TTGTAAAA
                               T__
GAM346  FLJ21657  3' AAAATATTTTACTCTGCCTGAT 1990      AA   GTTT
                            ATCAG AGAG   AATATTTT
                            ||||| ||||   ||||||||
                            TAGTC TCTC   TTATAAAA
                               CG    ATT_
GAM346  KIAA1054  3' AAAATGGTACCTCTTTC  2820         TTAA
                            GAAAGAGGT  TATTTT
                            ||||||||| |||||
                            CTTTCTCCA  GTAAAA
                               TG__
GAM346  SEMA3E    5' AAAATACAGCTTCTTCCTGA  1431      A    TAA
                            TCAG AAGAGGTT  TATTTT
                            |||| ||||||||  ||||||
                            AGTC TTCTTCGA  ATAAAA
                               C    C__
GAM346  LOC130507 3' AAAATATTAAGATAACTTTCTG 3011       AGG_
                            CAGAAAG TTTAATATTTT
                            ||||||| |||||||||||
```

```
                    GTCTTTC  GAATTATAAAA
                              AATA
GAM346  LOC148145 5' AAAATATTAAACCTGGACCTGA 3296        AAAG
        T                 ATCAG  AGGTTTAATATTTT
                     |||||  ||||||||||||
                     TAGTC  TCCAAATTATAAAA
                              CAGG
GAM347  DKK1    3' AAAATACTAGCTTATTTTCTGA 1417         _    TAA
                   TCAGAAAG AGGTT  TATTTT
                   |||||||| |||||  ||||||
                   AGTCTTTT TTCGA  ATAAAA
                        A    TC_
GAM347  KERA    3' AAAATATTGAATGCTTTCT 1349        AG
                   AGAAAG GTTTAATATTTT
                   |||||| ||||||||||||
                   TCTTTC TAAGTTATAAAA
                         G_
GAM347  PPP1R12A 3' AAAATACTACATCTTTCTGG 931         G TTAA
                    TCAGAAAGA GT   TATTTT
                    |||||||| ||   ||||||
                    GGTCTTTCT CA   ATAAAA
                         A TC__
GAM347  S100B   3' AAAATTGAAAACCTCTTTC 1284         AAT
                   GAAAGAGGTTT ATTTT
                   ||||||||||| |||||
                   CTTTCTCCAAA TAAAA
                           AGT
GAM347  DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196        A GTT
                        ATCAGAA GAG   TAATATTTT
                        ||||||| ||| |||||||||
                        TAGTCTT CTT  GTTATAAAA
                             _ AC_
GAM347  EML4    3' AAAATGTTTCCTCTTTCT 1876         TTT
                   AGAAAGAGG AATATTTT
                   ||||||||| ||||||||
                   TCTTTCTCC TTGTAAAA
                           T__
GAM347  FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990      AA  GTTT
                    ATCAG AGAG   AATATTTT
                    ||||| |||| |||||||||
                    TAGTC TCTC   TTATAAAA
                        CG   ATT_
GAM347  KIAA1054 3' AAAATGGTACCTCTTTC 2820         TTAA
                    GAAAGAGGT   TATTTT
                    ||||||||| |||||
                    CTTTCTCCA  GTAAAA
                           TG__
GAM347  SEMA3E  5' AAAATACAGCTTCTTCCTGA 1431      A     TAA
                   TCAG AAGAGGTT  TATTTT
                   |||| |||||||| ||||||
```

```
                        AGTC TTCTTCGA   ATAAAA
                          C      C__
GAM347  LOC130507 3' AAAATATTAAGATAACTTTCTG 3011        AGG_
                        CAGAAAG   TTTAATATTTT
                        |||||||   |||||||||||
                        GTCTTTC   GAATTATAAAA
                            AATA
GAM347  LOC148145 5' AAAATATTAAACCTGGACCTGA 3296        AAAG
              T           ATCAG   AGGTTTAATATTTT
                        |||||   |||||||||||||
                        TAGTC   TCCAAATTATAAAA
                            CAGG
GAM348  DKK1      3' AAAATACTAGCTTATTTTCTGA 1417        _   TAA
                        TCAGAAAG AGGTT  TATTTT
                        |||||||| |||||  ||||||
                        AGTCTTTT TTCGA  ATAAAA
                          A    TC_
GAM348  KERA      3' AAAATATTGAATGCTTTCT 1349       AG
                        AGAAAG GTTTAATATTTT
                        |||||| |||||||||||
                        TCTTTC TAAGTTATAAAA
                            G_
GAM348  PPP1R12A 3' AAAATACTACATCTTTCTGG 931        G TTAA
                        TCAGAAAGA GT   TATTTT
                        ||||||||| ||   ||||||
                        GGTCTTTCT CA   ATAAAA
                          A    TC__
GAM348  S100B    3' AAAATTGAAAACCTCTTTC 1284        AAT
                        GAAAGAGGTTT ATTTT
                        ||||||||||| |||||
                        CTTTCTCCAAA TAAAA
                            AGT
GAM348  DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A GTT
                        ATCAGAA GAG  TAATATTTT
                        |||||||  |||  |||||||||
                        TAGTCTT CTT  GTTATAAAA
                            _  AC_
GAM348  EML4     3' AAAATGTTTCCTCTTTCT 1876        TTT
                        AGAAAGAGG  AATATTTT
                        |||||||||  ||||||||
                        TCTTTCTCC  TTGTAAAA
                            T__
GAM348  FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990      AA  GTTT
                        ATCAG  AGAG   AATATTTT
                        |||||  ||||   ||||||||
                        TAGTC  TCTC   TTATAAAA
                            CG  ATT_
GAM348  KIAA1054 3' AAAATGGTACCTCTTTC 2820        TTAA
                        GAAAGAGGT   TATTTT
                        |||||||||   ||||||
```

```
                              CTTTCTCCA  GTAAAA
                              TG__
GAM348  SEMA3E  5' AAAATACAGCTTCTTCCTGA 1431      A      TAA
                              TCAG AAGAGGTT  TATTTT
                              |||| |||||||||  ||||||
                              AGTC TTCTTCGA  ATAAAA
                              C        C__
GAM348  LOC130507 3' AAAATATTAAGATAACTTTCTG 3011          AGG_
                              CAGAAAG  TTTAATATTTT
                              |||||||  |||||||||||
                              GTCTTTC  GAATTATAAAA
                              AATA
GAM348  LOC148145 5' AAAATATTAAACCTGGACCTGA 3296       AAAG
            T              ATCAG  AGGTTTAATATTTT
                              ||||| ||||||||||||||
                              TAGTC  TCCAAATTATAAAA
                              CAGG
GAM349  DKK1    3' AAAATACTAGCTTATTTTCTGA 1417          _   TAA
                              TCAGAAAG AGGTT  TATTTT
                              |||||||| |||||  ||||||
                              AGTCTTTT TTCGA  ATAAAA
                              A    TC_
GAM349  KERA    3' AAAATATTGAATGCTTTCT 1349       AG
                              AGAAAG  GTTTAATATTTT
                              ||||||  ||||||||||||
                              TCTTTC  TAAGTTATAAAA
                              G_
GAM349  PPP1R12A 3' AAAATACTACATCTTTCTGG 931       G TTAA
                              TCAGAAAGA GT   TATTTT
                              ||||||||| ||   ||||||
                              GGTCTTTCT CA   ATAAAA
                              A TC__
GAM349  S100B   3' AAAATTGAAAACCTCTTTC 1284        AAT
                              GAAAGAGGTTT ATTTT
                              |||||||||||  |||||
                              CTTTCTCCAAA  TAAAA
                              AGT
GAM349  DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A  GTT
                              ATCAGAA GAG  TAATATTTT
                              ||||||| |||  |||||||||
                              TAGTCTT CTT  GTTATAAAA
                              _ AC_
GAM349  EML4    3' AAAATGTTTCCTCTTTCT 1876         TTT
                              AGAAAGAGG  AATATTTT
                              |||||||||  ||||||||
                              TCTTTCTCC  TTGTAAAA
                              T__
GAM349  FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990      AA  GTTT
                              ATCAG AGAG  AATATTTT
                              ||||| |||| ||||||||
```

```
                  TAGTC  TCTC   TTATAAAA
                    CG   ATT_
GAM349 KIAA1054 3' AAAATGGTACCTCTTTC  2820        TTAA
                   GAAAGAGGT   TATTTT
                   |||||||||   ||||||
                   CTTTCTCCA   GTAAAA
                      TG__
GAM349 SEMA3E  5' AAAATACAGCTTCTTCCTGA  1431    A    TAA
                  TCAG AAGAGGTT  TATTTT
                  |||| ||||||||  ||||||
                  AGTC TTCTTCGA  ATAAAA
                     C      C__
GAM349 LOC130507 3' AAAATATTAAGATAACTTTCTG  3011        AGG_
                   CAGAAAG   TTTAATATTTT
                   |||||||   |||||||||||
                   GTCTTTC   GAATTATAAAA
                     AATA
GAM349 LOC148145 5' AAAATATTAAACCTGGACCTGA  3296      AAAG
           T            ATCAG   AGGTTTAATATTTT
                        |||||   ||||||||||||||
                        TAGTC   TCCAAATTATAAAA
                          CAGG
GAM350 DKK1     3' AAAATACTAGCTTATTTTCTGA  1417        _   TAA
                  TCAGAAAG AGGTT  TATTTT
                  |||||||| |||||  ||||||
                  AGTCTTTT TTCGA  ATAAAA
                     A    TC_
GAM350 KERA     3' AAAATATTGAATGCTTTCT  1349      AG
                  AGAAAG GTTTAATATTTT
                  |||||| ||||||||||||
                  TCTTTC TAAGTTATAAAA
                    G_
GAM350 PPP1R12A 3' AAAATACTACATCTTTCTGG  931       G TTAA
                  TCAGAAAGA GT   TATTTT
                  ||||||||| ||   ||||||
                  GGTCTTTCT CA   ATAAAA
                    A TC__
GAM350 S100B    3' AAAATTGAAAACCTCTTTC  1284        AAT
                  GAAAGAGGTTT ATTTT
                  ||||||||||| |||||
                  CTTTCTCCAAA TAAAA
                     AGT
GAM350 DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT  2196     A GTT
                  ATCAGAA GAG   TAATATTTT
                  ||||||| |||   |||||||||
                  TAGTCTT CTT   GTTATAAAA
                    _   AC_
GAM350 EML4     3' AAAATGTTTCCTCTTTCT  1876      TTT
                  AGAAAGAGG  AATATTTT
                  |||||||||  ||||||||
```

```
                    TCTTTCTCC  TTGTAAAA
                        T__
GAM350  FLJ21657 3'  AAAATATTTTACTCTGCCTGAT 1990      AA   GTTT
                        ATCAG AGAG  AATATTTT
                        ||||| |||| ||||||||
                        TAGTC TCTC  TTATAAAA
                         CG   ATT_
GAM350  KIAA1054 3'  AAAATGGTACCTCTTTC    2820        TTAA
                        GAAAGAGGT  TATTTT
                        ||||||||| ||||||
                        CTTTCTCCA  GTAAAA
                            TG__
GAM350  SEMA3E   5'  AAAATACAGCTTCTTCCTGA 1431      A    TAA
                        TCAG AAGAGGTT  TATTTT
                        |||| |||||||| ||||||
                        AGTC TTCTTCGA  ATAAAA
                          C     C__
GAM350  LOC130507 3' AAAATATTAAGATAACTTCTG 3011        AGG_
                        CAGAAAG  TTTAATATTTT
                        |||||||  |||||||||||
                        GTCTTTC  GAATTATAAAA
                           AATA
GAM350  LOC148145 5' AAAATATTAAACCTGGACCTGA 3296      AAAG
             T                ATCAG  AGGTTTAATATTTT
                        |||||  ||||||||||||||
                        TAGTC  TCCAAATTATAAAA
                           CAGG
GAM351  DKK1     3'  AAAATACTAGCTTATTTTCTGA 1417          _   TAA
                        TCAGAAAG AGGTT  TATTTT
                        |||||||| ||||| ||||||
                        AGTCTTTT TTCGA  ATAAAA
                           A    TC_
GAM351  KERA     3'  AAAATATTGAATGCTTTCT  1349       AG
                        AGAAAG GTTTAATATTTT
                        |||||| |||||||||||
                        TCTTTC TAAGTTATAAAA
                           G_
GAM351  PPP1R12A 3'  AAAATACTACATCTTTCTGG  931          G TTAA
                        TCAGAAAGA GT   TATTTT
                        ||||||||| || ||||||
                        GGTCTTTCT CA   ATAAAA
                          A TC__
GAM351  S100B    3'  AAAATTGAAAACCTCTTTC  1284          AAT
                        GAAAGAGGTTT ATTTT
                        ||||||||||| |||||
                        CTTTCTCCAAA  TAAAA
                           AGT
GAM351  DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A  GTT
                        ATCAGAA GAG  TAATATTTT
                        ||||||| ||| |||||||||
```

```
                                    TAGTCTT CTT  GTTATAAAA
                                     _   AC_
GAM351  EML4      3' AAAATGTTTCCTCTTTCT  1876        TTT
                          AGAAAGAGG  AATATTTT
                          ||||||||| ||||||||
                          TCTTTCTCC  TTGTAAAA
                              T__
GAM351  FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990    AA   GTTT
                          ATCAG AGAG   AATATTTT
                          ||||| |||| ||||||||
                          TAGTC TCTC   TTATAAAA
                           CG   ATT_
GAM351  KIAA1054 3' AAAATGGTACCTCTTTC     2820        TTAA
                          GAAAGAGGT  TATTTT
                          ||||||||| |||||
                          CTTTCTCCA  GTAAAA
                              TG__
GAM351  SEMA3E   5' AAAATACAGCTTCTTCCTGA  1431    A     TAA
                          TCAG AAGAGGTT  TATTTT
                          |||| |||||||| ||||||
                          AGTC TTCTTCGA  ATAAAA
                           C        C__
GAM351  LOC130507 3' AAAATATTAAGATAACTTTCTG 3011       AGG_
                          CAGAAAG   TTTAATATTTT
                          ||||||| |||||||||||
                          GTCTTTC   GAATTATAAAA
                           AATA
GAM351  LOC148145 5' AAAATATTAAACCTGGACCTGA 3296       AAAG
             T            ATCAG   AGGTTTAATATTTT
                          ||||| ||||||||||||||
                          TAGTC   TCCAAATTATAAAA
                           CAGG
GAM352  DKK1     3' AAAATACTAGCTTATTTTCTGA  1417      _   TAA
                          TCAGAAAG AGGTT  TATTTT
                          |||||||| ||||| ||||||
                          AGTCTTTT TTCGA  ATAAAA
                              A    TC_
GAM352  KERA     3' AAAATATTGAATGCTTTCT  1349      AG
                          AGAAAG  GTTTAATATTTT
                          |||||| ||||||||||||
                          TCTTTC  TAAGTTATAAAA
                              G_
GAM352  PPP1R12A 3' AAAATACTACATCTTTCTGG  931        G TTAA
                          TCAGAAAGA GT   TATTTT
                          ||||||||| || |||||
                          GGTCTTTCT CA   ATAAAA
                              A TC__
GAM352  S100B    3' AAAATTGAAAACCTCTTTC  1284        AAT
                          GAAAGAGGTTT  ATTTT
                          ||||||||||| |||||
```

```
                        CTTTCTCCAAA  TAAAA
                                AGT
GAM352  DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196      A  GTT
                        ATCAGAA GAG  TAATATTTT
                        |||||||| |||  |||||||||
                        TAGTCTT CTT  GTTATAAAA
                             _  AC_
GAM352  EML4    3' AAAATGTTCCTCTTTCT 1876        TTT
                        AGAAAGAGG  AATATTTT
                        ||||||||| |||||||||
                        TCTTTCTCC  TTGTAAAA
                              T__
GAM352  FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990     AA  GTTT
                        ATCAG AGAG   AATATTT
                        ||||| ||||   ||||||||
                        TAGTC TCTC   TTATAAAA
                         CG   ATT_
GAM352  KIAA1054 3' AAAATGGTACCTCTTTC   2820        TTAA
                        GAAAGAGGT  TATTTT
                        ||||||||| |||||
                        CTTTCTCCA  GTAAAA
                             TG__
GAM352  SEMA3E  5' AAAATACAGCTTCTTCCTGA 1431     A    TAA
                        TCAG AAGAGGTT  TATTTT
                        |||| ||||||||  ||||||
                        AGTC TTCTTCGA  ATAAAA
                          C    C__
GAM352  LOC130507 3' AAAATATTAAGATAACTTTCTG 3011      AGG_
                        CAGAAAG  TTTAATATTTT
                        ||||||| ||||||||||||
                        GTCTTTC  GAATTATAAAA
                             AATA
GAM352  LOC148145 5' AAAATATTAAACCTGGACCTGA 3296     AAAG
         T              ATCAG  AGGTTTAATATTTT
                        ||||| ||||||||||||||
                        TAGTC  TCCAAATTATAAAA
                             CAGG
GAM353  EFG1    3' TGTCTATCTCAACTCTATT  3661      ATC  TC
                        AATAGAGTT  GAT  AGACA
                        ||||||||| |||  |||||
                        TTATCTCAA  CTA  TCTGT
                             CT_  __
GAM353  PHYH   3' TCTGCTATAACTCTTTCA  1281      T    CGATT
                        TGAA AGAGTTAT   CAGA
                        |||| ||||||||   ||||
                        ACTT TCTCAATA   GTCT
                          _     TC___
GAM353  SLC6A3  3' TGTCTGTTGACCAATCTCTATT 795         TTA__  TT
         CA               TGAATAGAG   TCGA  CAGACA
                        ||||||||| |||| ||||||
```

```
                          ACTTATCTC   AGTT GTCTGT
                        TAACC    __
GAM353  H2AV     3' TGCCTGACAATTAGCTCTATTC 2447           TCGAT   A
        A                TGAATAGAGTTA   TCAG CA
                     |||||||||||   |||| ||
                     ACTTATCTGAT   AGTC GT
                         TAAC_   C
GAM353  HMP19    3' GTCTGAACCGATATTTCT  3408      T   A
                     AGAG TATCG TTCAGAC
                     |||| ||||| |||||||
                     TCTT ATAGC AAGTCTG
                        T   C
GAM353  KIAA1726 3' TGTCTGAAAGCAACCCTACTC 2786    A  A  ATCGA
                     GA TAG GTT    TTCAGACA
                     || ||| |||   ||||||||
                     CT ATC CAA    AAGTCTGT
                        C   C   CGA__
GAM354  SOX11    3' GTCTCACTGTTTGATCAAACTT 992        A ATTTTT
           CT            AGAGGTTT AT   GTGAGAC
                     ||||||||| ||    |||||||
                     TCTTCAAA TA    CACTCTG
                         C GTTTGT
GAM354  CAP350   3' TCTTGTAATAGTTAAACCTC  1554         ATTT  TG
                     GAGGTTTAAT  TTG AGA
                     ||||||||||  ||| |||
                     CTCCAAATTG   AAT TCT
                        AT__  GT
GAM354  DKFZP564A022 3' TCTCACAAATATAAAACC  2174      A   TT
                     GGTTT ATATT  TGTGAGA
                     ||||| ||||| |||||||
                     CCAAA TATAA  ACACTCT
                         A    __
GAM354  FLJ11730 3' CTCACAAAGATAAACATC   2005    G  TAA
                     GA GTT  TATTTTTGTGAG
                     || ||| |||||||||||
                     CT CAA   ATAGAAACACTC
                         A    ___
GAM354  FLJ20686 5' CTCACAGTCCTACTGAACCTC 1765       A TTT
                     GAGGTTTA TA  TTGTGAG
                     |||||||| ||  |||||||
                     CTCCAAGT AT  GACACTC
                         C  CCT
GAM354  FRSB     3' GTCCCAGGGAGATATTAGACCT 1236            G  A
           CT            AGAGGTTTAATATTTTT TG GAC
                     |||||||||||||||| || |||
                     TCTCCAGATTATAGAGG AC CTG
                         G  C
GAM354  KIAA1600 3' ACAAAAAGACTAAACCTCT  2919        ATA
                     AGAGGTTTA TTTTTGT
                     ||||||||| |||||||
```

```
                        TCTCCAAAT  AAAAACA
                             CAG
GAM354  LOC124801 3' GTCTCACATTTGGCCCAAACCT 2996        AATATTTT
            C               GAGGTTT    TGTGAGAC
                        |||||||    ||||||||
                        CTCCAAA    ACACTCTG
                           CCCGGTTT
GAM354  LOC221035 3' TCCCAGTATTAAACCT    3593        TTTTG A
                        AGGTTTAATAT    TG GA
                        ||||||||||   || ||
                        TCCAAATTATG    AC CT
                        _____   C
GAM354  LOC51611 3' CGAAAATTAAACCTCT      1653        AT
                        AGAGGTTTAAT  TTTTG
                        |||||||||| |||||
                        TCTCCAAATTA AAAGC

                           __
GAM355  AXUD1    3' TTTATTCCATTTCTCTCT    2309        GA
                        AGAGAGAAA GAATAAA
                        |||||||| ||||||
                        TCTCTCTTT CTTATTT
                           AC
GAM355  BSN     3' ATTTTTCTTTTGTTTCTCTCT 1024      G   T
                        AGAGAGAAA AGAA AAAAAT
                        |||||||| |||| ||||||
                        TCTCTCTTT TTTT TTTTTA
                           G   C
GAM355  DPYSL2  3' AATATTTTCGTGTCTGTCTCTC 822        A  GA TA
            T              AGAGAGA AGA A AAAATATT
                        |||||| ||| | ||||||||
                        TCTCTCT TCT T TTTTATAA
                           G  G_ GC
GAM355  EVA1    3' AATGTGTTACTCTCTTTCCTT 1250      A      A  A
            C              GAG GAAAGAGA TAAA ATATT
                        ||| |||||||| |||| |||||
                        CTT CTTTCTCT ATTT TGTAA
                           C      C  G
GAM355  PTMS    3' TTTGCTCTCTTTCTCCCT     959     A      A
                        AG GAGAAAGAGA TAAA
                        || |||||||||| ||||
                        TC CTCTTTCTCT GTTT
                           C      C
GAM355  SELE    3' TTTTGTGGCTTTCTTTCT     748        AGA
                        AGAGAGAAAG ATAAAA
                        |||||||||| ||||||
                        TCTTTCTTTC TGTTTT
                           GG_
GAM355  SLC7A6  3' AATATTTTTGTACCTTTCTCCT 1076    A      AGA
                        AG GAGAAAG ATAAAAATATT
                        || ||||||| |||||||||||
```

```
                             TC CTCTTTC  TGTTTTTATAA
                             _       CA_
GAM355  TGFBR2    5' TTTCTTCTAGTTCTTTCT  1003        AG   T
                             AGAGAGAA  AGAA AAA
                             |||||||| |||| |||
                             TCTTTCTT  TCTT TTT
                                   GA    C
GAM355  DKFZP586N0721 5' TTTTATTCCCTTTCCTCT   1627      A   A
                             AGAG GAAAG GAATAAAA
                             |||| ||||| ||||||||
                             TCTC CTTTC CTTATTTT
                                _     C
GAM355  DKFZp761J139 5' TTTATTCTCTCTGTCTCT   2242      GAA
                             AGAGA  AGAGAATAAA
                             |||||  ||||||||||
                             TCTCT  TCTCTTATTT
                                    GTC
GAM355  FLJ10468  3' TTTTATTCTCCTTTC       1779      AAA
                             GAGAG  GAGAATAAAA
                             |||||  ||||||||||
                             CTTTC  CTCTTATTTT

                             ___
GAM355  FLJ20485  3' AATATTTTTAAAATCTCCTTTC 1874       AAA   A__
        T                    AGAGAG  GAGA  TAAAAATATT
                             ||||||  ||||  ||||||||||
                             TCTTTC  CTCT  ATTTTTATAA
                             ___     AAA
GAM355  H2BFQ     3' ATATTACTCTTTCTGTC    2523    G     AATAA
                             GA AGAAAGAG    AAATAT
                             || ||||||||    ||||||
                             CT TCTTCTC    TTTATA
                                G     A____
GAM355  KIAA0077 3' TTTTATTCTCTCTCCCTTT  2774     A A
                             AGAG GA AGAGAATAAAA
                             |||| || ||||||||||
                             TTTC CT TCTCTTATTTT
                                  C C
GAM355  KIAA0295 3' TTTTTTCCCTTTCTCTCT   2807        A   T
                             AGAGAGAAAG GAA AAA
                             |||||||||| ||| |||
                             TCTCTCTTC CTT TTT
                                   C  T
GAM355  KIAA0828 3' AATATTTTGCCTTCTTTCTTTC 3195         AATA
        T                    AGAGAGAAAGAG  AAAATATT
                             ||||||||||||  ||||||||
                             TCTTTCTTTCTT  TTTTATAA
                                   CCG_
GAM355  KIAA1203 3' AATATTTTTATTCTTGAGTTAT 2921      GAGAAA
        CT                   AGA   GAGAATAAAAATATT
                             |||   ||||||||||||||
```

```
                              TCT      TTCTTATTTTTATAA
                              ATTGAG
GAM355    OSBPL8    3' TTTTTATTATCCTCCTCTCT  1928        AAA  G
                              AGAGAG   GA AATAAAAA
                              |||||| || ||||||||
                              TCTCTC  CT TTATTTTT
                                CTC  A
GAM355    PAK6      3' AATATTTTTAGATTCTTCTGCT 1897      _   A  AA
                  C            GAG AGAA GAG  TAAAAATATT
                              ||| |||| ||| ||||||||||
                              CTC TCTT CTT ATTTTTATAA
                                G  _  AG
GAM355    POLR3F   3' AATATTTTCACTGTTCCTTCTT  2547          A A     ___
                 TCT              AGAGAGAA G GAATA  AAAATATT
                              ||||||||| | ||||| |||||||||
                              TCTTTCTT C CTTGT  TTTTATAA
                                       _ _   CAC
GAM355    RNF11    3' TTTATTCTCTTTCTTCT    1495      G
                              AGA AGAAAGAGAATAAA
                              ||| ||||||||||||||
                              TCT TCTTCTCTTATTT

                               _
GAM355    SLC16A6  5' TTTATTCTCTTCCCTTCT    1143       AGA
                              AGAG   AAGAGAATAAA
                              ||||   |||||||||||
                              TCTT   TTCTCTTATTT
                                CCC
GAM355    LOC144321 3' TTTTATTCCCTTCTCTC    3267       A A
                              GAGAGAA G GAATAAAA
                              ||||||| | |||||||||
                              CTCTCTT C CTTATTTT
                                 _ C
GAM355    LOC150951 5' ATATTTTTATTTTCTTCCT  3336      A
                              AG AAGAGAATAAAAATAT
                              || ||||||||||||||||
                              TC TTCTTTTATTTTTATA
                                C
GAM355    LOC199920 5' AATATTTTTATTCTTTGATTCT 3435        AA
                 T            GAGAG AGAGAATAAAAATATT
                              ||||| |||||||||||||||
                              TTCTT TTTCTTATTTTTATAA
                                AG
GAM355    LOC256435 3' AATATTTTTAAATGTTGTCTCT 3675          AAGAGAA
                 CT              AGAGAGA    TAAAAATATT
                              |||||||    |||||||||
                              TCTCTCT    ATTTTTATAA
                                GTTGTAA
GAM356    ADAMTS5   3' TATTTTCACAACTACTTTCTCT 1352          _ AATA_
                 CT              AGAGAGAAAG AG   AAAAATA
                              ||||||||| ||   ||||||
```

```
                          TCTCTCTTTC TC    TTTTAT
                            A  AACAC
GAM356   ADAT1    3'  TATTCCCAGCCTTTCTTTCTTC 1404              A____
                          GAAGAGAGAAAG   GAATA
                          ||||||||||   |||||
                          CTTCTTTCTTTC   CTTAT
                            CGACC
GAM356   ADCY2    3'  TTTTATTTTCCTGTCTTC   2711      G  AAA
                          GAAGA AG  GAGAATAAAA
                          ||||| ||  ||||||||||
                          CTTCT TC  CTTTTATTTT
                            G ___
GAM356   AHR      3'  ATTTTTGTTACTCTCTTC     840        _ A
                          GAAGAGAG AA GAGAAT
                          |||||||| || ||||||
                          CTTCTCTC TT TTTTTA
                            A  G
GAM356   BSN      3'  ATTTTTCTTTTGTTTCTCTCT 1025       G   T
                          AGAGAGAAA AGAA AAAAAT
                          ||||||||| |||| ||||||
                          TCTCTCTTT TTTT TTTTTA
                            G   C
GAM356   BSN      3'  TCTCCCCCTTTCTCTCTTC   1026             ____
                          GAAGAGAGAAA   GAGA
                          |||||||||||   ||||
                          CTTCTCTCTTT   CTCT
                            CCCC
GAM356   C7       3'  TATTCCTTATTTCTCTTT     756        _ A
                          GAAGAGAGA AAG GAATA
                          ||||||||| ||| |||||
                          TTTCTCTTT TTC CTTAT
                            A _
GAM356   CFTR     3'  TATTCCTTTTTCTCTCCTC   753     A      _
                          GA GAGAGAAAGAG AATA
                          || |||||||||||| ||||
                          CT CTCTCTTTTTC TTAT
                            C       C
GAM356   CHD2     3'  ATATTTTTTCTGATCCCCCACT 813     AA____   GAAT_    |||
                    CTCTCTTC          AGA   GA   AAAAATA  T
                          |||   ||   ||||||| |
                          TCT   CT   TTTTTAT  A
                            CACCCC AGTCT      |||
GAM356   CKN1     3'  TATTTTATTCTTTCTTC     703            AG
                          GAAGAGAGAA AGAATA
                          |||||||||| ||||||
                          CTTCTTTCTT TTTTAT
                            A_
GAM356   CTH      5'  TGTTCTTTTCCTCTCTTC    867            A
                          GAAGAGAG AAGAGAATA
                          |||||||| |||||||||
```

```
                              CTTCTCTC TTTTCTTGT
                                  C
GAM356  EVA1    3' ATTTTTATTTTTATGTCTCTC 1251        AA_
                        GAGAGA   GAGAATAAAAAT
                        ||||||   |||||||||||
                        CTCTCT   TTTTTATTTTTA
                                 GTA
GAM356  FBXL11  3' TTGTTCCCCTCTCTCTTT  1426          AAGA
                        GAAGAGAGA   GAATAA
                        |||||||||   ||||||
                        TTTCTCTCT   CTTGTT
                            CCCC
GAM356  GATA3   3' TATTTTCCTTCTCTCTC    893      A    A
                        GA GAGAGAA GAGAATA
                        || ||||||| |||||||
                        CT CTCTCTT CTTTTAT
                        _          C
GAM356  GDI2    5' TTTTCCTCTCTTTCTCTT   832          AT
                        GAGAGAAAGAGA AAAA
                        |||||||||||| ||||
                        TTCTCTTTCTCT TTTT
                                 CC
GAM356  HD      3' ATTCTCCCTTCTCTCTTT   899          A_
                        GAAGAGAGAA GAGAAT
                        |||||||||| ||||||
                        TTTCTCTCTT CTCTTA
                                 CC
GAM356  HTR2C   3' TATTTTTGCTCTCCCTCCCTTC 781     A AAA  A
                        GAAG GAG   GAGA TAAAAATA
                        |||| |||   |||| ||||||||
                        CTTC CTC   CTCT GTTTTTAT
                          C   C__   C
GAM356  LGR6    3' TTCTCTTCCCCTCTCTTC    3302        A__
                        GAAGAGAG  AAGAGAA
                        ||||||||  |||||||
                        CTTCTCTC  TTCTCTT
                                 CCC
GAM356  LRP8    3' TCTCTTATTTCTCTTTTC    2326        ___
                        GAAGAGAGAA  AGAGA
                        ||||||||||  |||||
                        CTTTTCTCTT  TCTCT
                                 TAT
GAM356  LRP8    3' TCTCTTATTTCTCTTTTC    1139        ___
                        GAAGAGAGAA  AGAGA
                        ||||||||||  |||||
                        CTTTTCTCTT  TCTCT
                                 TAT
GAM356  MEF2C   5' TTTTTTTTCTCTCTCTCTCTCT 926    _    A   T
             C                    GA AGAGAGA AGAGAA AAAAA
                                  || ||||||| |||||| |||||
```

```
                                  CT TCTCTCT TCTCTT TTTTT
                                   C       C       T
GAM356  MSR1    3' TATTTTTGGTTTCTCTCT  929            __
                       AGAGAGAAA GAGAATA
                       ||||||||| |||||||
                       TCTCTCTTT TTTTTAT
                               GG
GAM356  PCDH11X 3' TATTTTCACATTTTCTCTCT 2299           ____
                       AGAGAGAAA  GAGAATA
                       |||||||||  |||||||
                       TCTCTCTTT  CTTTTAT
                                TACA
GAM356  PCDH11X 3' TATTTTCACATTTTCTCTCT 2301           ____
                       AGAGAGAAA  GAGAATA
                       |||||||||  |||||||
                       TCTCTCTTT  CTTTTAT
                                TACA
GAM356  PCDH11Y 3' TATTTTCACATTTTCTCTCT 2303           ____
                       AGAGAGAAA  GAGAATA
                       |||||||||  |||||||
                       TCTCTCTTT  CTTTTAT
                                TACA
GAM356  PCMT1   3' TATCTTCTGCTCTTTCTTC  1205       A_  GA
                       GAAGAGAGA AGA ATA
                       ||||||||| ||| |||
                       CTTCTTTCT TCT TAT
                                CG  TC
GAM356  PCNA    3' TATTTTTTTTCTCTATTC   939      G
                       GAA AGAGAAAGAGAATA
                       ||| |||||||||||||
                       CTT TCTCTTTTTTTAT
                             A
GAM356  PRELP   3' ATTCGTTTTCTCTCTCTC   950     _    A
                       GA AGAGAGAAAG GAAT
                       || |||||||||| ||||
                       CT TCTCTCTTTT CTTA
                          C          G
GAM356  PTMS    3' TTTGCTCTCTTTCTCCCT   958    A      A
                       AG GAGAAAGAGA TAAA
                       || |||||||||| ||||
                       TC CTCTTTCTCT GTTT
                          C          C
GAM356  SLC4A4  3' TATTTTTATTCTCTTAAGTCTT 1054     GAGA
            T              GAAGA  AAGAGAATAAAAATA
                           |||||  |||||||||||||||
                           TTTCT  TTCTCTTATTTTTAT
                             GAA_
GAM356  TRPS1   5' TATTTCCTTTCTCTTTCTCTCT 1471        TAA
                       AGAGAGAAAGAGAA AAATA
                       |||||||||||||| |||||
```

```
                         TCTCTCTTCTCTT  TTTAT
                            TCC
GAM356   ARS2      5' TTTTGTTCGCCTCTCTTC  1650          AAAGA
                         GAAGAGAG    GAATAAAA
                         |||||||    ||||||||
                         CTTCTCTC    CTTGTTTT
                            CG___
GAM356   BRD4      3' TATTTTTAATTCTCTCTTC  2368          A_
                         GAAGAGAGAA GAGAATA
                         |||||||||| |||||||
                         CTTCTCTCTT TTTTTAT
                            AA
GAM356   CAPN13    3' TATTTTACCTGCCTCTCTTC 2485            AA __
                         GAAGAGAG AG AGAATA
                         |||||||| || ||||||
                         CTTCTCTC TC TTTTAT
                            CG CA
GAM356   CECR6     3' TTACCCTCTCCTCTCTTC  2218          AA  AA
                         GAAGAGAG AGAG TAA
                         |||||||| |||| |||
                         CTTCTCTC TCTC ATT
                            C_  CC
GAM356   DKFZP434I0714 5' TTTTTGTTTTTCCCCCTCTTC 3362       AGAAA
                         GAAGAG    GAGAATAAAAA
                         ||||||    |||||||||||
                         CTTCTC    TTTTGTTTTT
                            CCCC_
GAM356   DKFZP564G092 5' TATTCCTCTTTCTTTTC   1639        A A
                         GAAGAGAGA AG GAATA
                         ||||||||| || |||||
                         CTTTTCTTT TC CTTAT
                            C _
GAM356   DKFZp564K142 3' TATCCTCTTAACCTTCTCTTC 2231         A___   A
                         GAAGAGAG   AAGAG ATA
                         ||||||||   ||||| |||
                         CTTCTCTT   TTCTC TAT
                            CCAA   C
GAM356   DKFZp566D234 3' TATTTTTTTTCTCTGTC    2612     AG
                         GA AGAGAAAGAGAATA
                         || |||||||||||||||
                         CT TCTCTTTTTTTAT
                            G_
GAM356   DKFZP566I1024 3' TTTTAAAATCTATTCTCTC  2878        _  GAA
                         GAGAGAA AGA  TAAAA
                         ||||||| ||| |||||
                         CTCTCTT TCT  ATTTT
                            A  AAA
GAM356   EPI64     3' TATTTTGACATCTCTCTCTT 3681         A  GAATA
              C           GAAGAGAGA AGA   AAAATA
                         ||||||||| |||   ||||||
```

```
                   CTTCTCTCT TCT    TTTTAT
                     C  ACAG_
GAM356  FLJ00012  3' TATTTTTATCTCTATCTCCT  2985    A    A    A
                     AG GAGA AGAGA TAAAAATA
                     || |||| ||||| ||||||||
                     TC CTCT TCTCT ATTTTTAT
                       _      A      _
GAM356  FLJ10460  3' ATTTTTATTCTACCTTTC   1778      AAAG
                     GAGAG  AGAATAAAAAT
                     |||||  ||||||||||||
                     CTTTC  TCTTATTTTA
                          CA__
GAM356  FLJ10687  3' TTTATTCATTTCTCTCCTC   1793    A      GA
                     GA GAGAGAAA  GAATAAA
                     || ||||||||  |||||||
                     CT CTCTCTTT  CTTATTT
                        C       A_
GAM356  FLJ10738  3' TATTTTTACTCTCCCTCTTC  1799      AGAAA  A
                     GAAGAG   GAGA TAAAAATA
                     ||||||   |||| ||||||||
                     CTTCTC   CTCT ATTTTTAT
                        C___     C
GAM356  FLJ13158  3' TTCTCTCCCTTTCTCTTC   2109       A__
                     GAAGAGAGA  AGAGAA
                     |||||||||  ||||||
                     CTTCTCTTT  TCTCTT
                          CCC
GAM356  FLJ20294  5' TATTCCTGTCTCCTCTTT   1747        _  A A
                     GAAGAG AGA AG GAATA
                     |||||| ||| || |||||
                     TTTCTC TCT TC CTTAT
                        C  G  _
GAM356  FLJ21657  3' TATTCTACTTCTCTCTTC   1991         AG
                     GAAGAGAGAA AGAATA
                     |||||||||| ||||||
                     CTTCTCTCTT TCTTAT
                          CA
GAM356  GT650     3' TATTTCTGATTCTCCCTCTCTT 2341      AAA   AA_
            C                GAAGAGAG  GAGAAT  AAATA
                             |||||||| ||||||  |||||
                             CTTCTCTC  CTCTTA TTTAT
                                C__    GTC
GAM356  HEY2      3' TATTCTCTTTTTTTTCTC   1420    AG
                     GA AGAGAAAGAGAATA
                     || ||||||||||||||
                     CT TTTTTTTCTCTTAT
                        CT
GAM356  HIC2      3' ATTTTTTTTTCTCTCTCTTTTC 2717        A    T
                     GAAGAGAGA AGAGAA AAAAAT
                     ||||||||| |||||| ||||||
```

```
                    CTTTTCTCT TCTTTT TTTTTA
                        C      _
GAM356  HOOK3    3' ATTTTGAGGACTTTTTCTCTCT 2249          AATA_
                    AGAGAGAAAGAG    AAAAT
                    ||||||||||    |||||
                    TCTCTCTTTTC    TTTTA
                        AGGAG
GAM356  IL1RAPL1 5' TATTCTTATTTTCCCCTCTCTT 1488        AAA     A
                T          GAAGAGAG  GAGAATAA AATA
                           |||||||| |||||||| ||||
                           TTTCTCTC  CTTTTATT TTAT
                             CC_       C
GAM356  KALI     3' TTTTGTTCTTGTCCCTCTC  2347       AAA_
                    GAGAG   GAGAATAAAA
                    |||||   ||||||||||
                    CTCTC   TTCTTGTTTT
                      CCTG
GAM356  KIAA0077 3' TTTTATTCTCTCTCCCTTT  2773     A   AA
                    GAAG GAGA  GAGAATAAAA
                    |||| ||||  ||||||||||
                    TTTC CTCT  CTCTTATTTT
                        C    __
GAM356  KIAA0089 3' ATTTTTAGCCTCTTTTCTCTTC 2873        A  AA
                    GAAGAGAGAA GAG  TAAAAAT
                    |||||||||| ||| |||||||
                    CTTCTCTTTT CTC  ATTTTTA
                         _   CG
GAM356  KIAA0286 3' TATTTTCACCCTCTTTTC  2814        AAA
                    GAAGAGAG   GAGAATA
                    ||||||||   |||||||
                    CTTTTCTC   CTTTTAT
                         CCA
GAM356  KIAA0295 3' TTTTTTCCCTTTCTCTCT   2808       A   T
                    AGAGAGAAAG GAA AAA
                    |||||||||| ||| |||
                    TCTCTCTTTC CTT TTT
                         C   T
GAM356  KIAA0342 3' TATTCTCATTACTTCTCTTT 2890        _ _ A
                    GAAGAGA G AA GAGAATA
                    ||||||| | || |||||||
                    TTTCTCT C TT CTCTTAT
                         T A A
GAM356  KIAA0564 3' TATTTTTATTTTCTCCCTGCTC 2743      _ AA
                    GAG AG AGAGAATAAAAATA
                    ||| || ||||||||||||||
                    CTC TC TCTTTTATTTTTAT
                      G  CC
GAM356  KIAA0630 3' TATTTTTTAAAAGTCTTTCTCT 3465         GAAT__
            CT            AGAGAGAAAGA    AAAAATA
                          ||||||||||    |||||||
```

```
                        TCTCTCTTTCT    TTTTTAT
                             GAAAAT
GAM356  KIAA0662 3' TGTTCTCTCTCTCTTT  3215        A
                        GAAGAGAGA AGAGAATA
                        ||||||||| ||||||||
                        TTTCTCTCT TCTCTTGT
                             C
GAM356  KIAA0830 3' TTTGCTTCTCTTTCTCCT   2866    A         _
                        AG GAGAAAGAGAA TAAA
                        || |||||||||| ||||
                        TC CTCTTTCTCTT GTTT
                        _           C
GAM356  KIAA0964 3' ATTCTTATGTTTTTCTCTTTTC 1579         GA   A
                        GAAGAGAGAAAGA  ATAA AAT
                        |||||||||||||  |||| |||
                        CTTTTCTCTTTTT  TATT TTA
                             G_   C
GAM356  KIAA1076 3' TATTTTTTGCTTTCTCTC   2723        AGAAT
                        GAGAGAAAG    AAAAATA
                        |||||||||    |||||||
                        CTCTCTTTC    TTTTTAT
                             GT___
GAM356  KIAA1181 3' ATTCCTCTTCCTCTCTTC   2817      A    _
                        GAAGAGAG AAGAG AAT
                        |||||||| ||||| |||
                        CTTCTCTC TTCTC TTA
                             C     C
GAM356  KIAA1319 3' TATTTTTGTCTTCTTCCTTTC 1925      A   GA
                        GAGAG AAGA ATAAAAATA
                        ||||| |||| |||||||||
                        CTTTC TTCT TGTTTTTAT
                             C   TC
GAM356  KIAA1522 3' ATTCTCTGACCTTTCTCTCT  2708          _____
                        AGAGAGAA    AGAGAAT
                        ||||||||    |||||||
                        TCTCTCTT    TCTCTTA
                             TCCAG
GAM356  KIAA1906 3' ATTTTTATTCTCTGCTT    2971    AA
                        GAG AGAGAATAAAAAT
                        ||| |||||||||||||
                        TTC TCTCTTATTTTTA
                             G_
GAM356  MAPK6   5' TATTTTTCTTCTCCCTTT    952      A  AG
                        GAAG GAGAA AGAATA
                        |||| ||||| ||||||
                        TTTC CTCTT TTTTAT
                             C     CT
GAM356  MGC13138 3' TATTTTTATTCTTGTGACCCTC 2332        AGAAA_
                        GAG    GAGAATAAAAATA
                        |||    |||||||||||||
```

```
                              CTC    TTCTTATTTTTAT
                              CCAGTG
GAM356  MGC2742   5' TATTTCTTTTCTCTCTTC   2040           AG
                     GAAGAGAGAAAG  AATA
                     ||||||||||| ||||
                     CTTCTCTCTTTT TTAT
                              CT
GAM356  MGC32043  3' TATTCCTGTTTTCTCTTT   2486           _ A
                     GAAGAGAGAA AG GAATA
                     |||||||||| || |||||
                     TTTCTCTTTT TC CTTAT
                              G _
GAM356  NFAT5     3' TATTCCCTTTTTCTCTTC   2452          A
                     GAAGAGAGAAAG GAATA
                     ||||||||||| |||||
                     CTTCTCTTTTTC CTTAT
                              C
GAM356  OSBPL8    3' TTTTTATTATCCTCCTCTCTTC 1929      AAA G
                     GAAGAGAG  GA AATAAAAA
                     |||||||| || ||||||||
                     CTTCTCTC  CT TTATTTTT
                              CTC A
GAM356  RAB10     3' TGTTCTGCTTTTCCTCCTC   3337    A AG   _
                     GA GAG  AAAG AGAATA
                     || ||| |||| ||||||
                     CT CTC  TTTC TCTTGT
                        C  CT  G
GAM356  RANBP1    3' TATTTTCTTTTCCTCTCTTT  969         __
                     GAAGAGAG  AAAGAGAATA
                     ||||||||  ||||||||||
                     TTTCTCTC  TTTCTTTTAT
                              CT
GAM356  RASSF2    3' TATTTTCACAATCCTCTCTTC 1537      AAA___
                     GAAGAGAG    GAGAATA
                     ||||||||    |||||||
                     CTTCTCTC    CTTTTAT
                              CTAACA
GAM356  STK22D    3' TATTTTCATCAGCTTCTTCTCT 2226      AG AATA__
             CT         AGAGAGAA AG    AAAATA
                     |||||||| ||     ||||||
                     TCTCTCTT TC    TTTTAT
                              CT GACTAC
GAM356  SYNJ2     3' ATTTTTAGGTTTTCTCTTC   2606          AGAGAA
                     GAAGAGAGAA    TAAAAAT
                     ||||||||||    ||||||
                     CTTCTCTTTT    ATTTTTA
                              GG____
GAM356  TBLR1     3' TATTCTTTTTTTCCCTTC   2079        A
                     GAAG GAGAAAGAGAATA
                     |||| ||||||||||||
```

```
                           CTTC CTTTTTTTCTTAT
                              C
GAM356  TM9SF1    3' TATTGCTGTTCTCTCCCTTTCT 1296        AA      AA
            TC              GAAGAGAG AGAGAATA AATA
                           |||||||| ||||||||| ||||
                           CTTCTTTC TCTCTTGT TTAT
                              CC       CG
GAM356  ULK2     3' TATTCTATCCTCTCCTCTTC 1523       _ AAG_
                         GAAGAG AGA   AGAATA
                         |||||| ||| |||||||
                         CTTCTC TCT   TCTTAT
                          C   CCTA
GAM356  UNC5D    3' TTATTCTTTCTTCCTCTTC  2393       A  _
                        GAAGAG GAA AGAGAATAA
                        |||||| ||| |||||||||
                        CTTCTC CTT TTTCTTATT
                         _   C
GAM356  LOC121219 5' TTATTAACTCCTTCTCTCTTT 2988         A  __
                         GAAGAGAGAA GAG AATAA
                         ||||||||||| ||| |||||
                         TTTCTCTCTT CTC TTATT
                          C  AA
GAM356  LOC128077 3' ATTTGTTTTCTCTTTCTTTCCT 3006   A        TAA
            C               GA GAGAGAAAGAGAA  AAAT
                           || |||||||||||| ||||
                           CT CTTTCTTTCTCTT  TTTA
                           C         TTG
GAM356  LOC143451 3' TTCTCTCCTTCTCTCTTC   3058        __
                         GAAGAGAGAA AGAGAA
                         |||||||||| ||||||
                         CTTCTCTCTT TCTCTT
                              CC
GAM356  LOC145125 3' TTCTCTCCTTCTCTCTTC   3075        __
                         GAAGAGAGAA AGAGAA
                         |||||||||| ||||||
                         CTTCTCTCTT TCTCTT
                              CC
GAM356  LOC149351 3' ATTTTTCAGATCTTTCTCTTT 3131         GAAT
                         AGAGAGAAAGA  AAAAAT
                         ||||||||||| ||||||
                         TTTCTCTTTCT  TTTTTA
                          AGAC
GAM356  LOC149722 5' TATTCTTTCTTCTCTTC   3312         A
                         GAAGAGAGA AGAGAATA
                         ||||||||| |||||||||
                         CTTCTCTTT TTTCTTAT
                              C
GAM356  LOC149837 5' TATTCCTGTCTTTCTCTCT  3318         ___
                         AGAGAGAAAGA  GAATA
                         |||||||||| |||||
```

```
                         TCTCTCTTTCT  CTTAT
                          GTC
GAM356  LOC150054 3' TATTCTGTCTTTCTCCTC   3323     _   __
                         GAG AGAAAGA  GAATA
                         ||| |||||||  |||||
                         CTC TCTTTCT  CTTAT
                           C      GT
GAM356  LOC150150 5' TTTTGTGCCTCTCTTTCTTC 3324       AA  A_
                         GAAGAGAGA  GAG  ATAAAA
                         |||||||||  |||  ||||||
                         CTTCTTTCT  CTC  TGTTTT
                            __   CG
GAM356  LOC150225 3' TATTTTGTTTCCCTCTTC   3327       A  G
                         GAAGAG GAAA AGAATA
                         |||||| |||| ||||||
                         CTTCTC CTTT TTTTAT
                            C   G
GAM356  LOC152816 3' TATTTTTATCCTCAACCTCTT 3364      AAA  A
                         GAGAG  GAG ATAAAAATA
                         |||||  ||| |||||||||
                         TTCTC  CTC TATTTTAT
                           CAA   C
GAM356  LOC155038 3' ATTGCGTTTCTCTTTCTCCTTC 3198     A      TAAA
                         GAAG GAGAAAGAGAA   AAT
                         |||| |||||||||||   |||
                         CTTC CTCTTTCTCTT   TTA
                          _        TGCG
GAM356  LOC158629 3' TATTTTCTTTCCCTCTC   3394   A  A
                         GA GAG GAAAGAGAATA
                         || ||| |||||||||||
                         CT CTC CTTTCTTTTAT
                          _    C
GAM356  LOC158943 3' TATTTTCTTTTCCTCTCTTT 2572        __
                         GAAGAGAG  AAAGAGAATA
                         ||||||||  ||||||||||
                         TTTCTCTC  TTTCTTTTAT
                           CT
GAM356  LOC170082 3' ATTCTTTTCCCCTCTCTTTTC 3254          ____
                         GAAGAGAGA  AAGAGAAT
                         |||||||||  ||||||||
                         CTTTTCTCT  TTTTCTTA
                          CCCC
GAM356  LOC199920 5' TATTTTTATTCTTTGATTCTTC 3436      AGAA
                         GAAGAG   AGAGAATAAAAATA
                         ||||||   ||||||||||||||
                         CTTCTT   TTTCTTATTTTTAT
                          AG__
GAM356  LOC219667 3' ATTTTTGTTATCTCTCTTC   3516       AAGAG
                         GAAGAGAGA   AATAAAAAT
                         |||||||||   |||||||||
```

```
                        CTTCTCTCT    TTGTTTTTA
                        A____
GAM356  LOC220279 5' TATTTTCTTCCCCTACCTCTCT 3653        A_____
        TC              GAAGAGAG     AAGAGAATA
                        |||||||     ||||||||
                        CTTCTCTC    TTCTTTTAT
                          CATCCCC
GAM356  LOC221830 3' TATTTTCTTTTCTTTCTTC  3567          _
                        GAAGAGAGAAA GAGAATA
                        ||||||||||| |||||||
                        CTTCTTTCTTT CTTTTAT
                           T
GAM356  LOC222166 3' ATTTTACCTTCTCTCTTT   3635        AG_
                        GAAGAGAGAA  AGAAT
                        ||||||||||  |||||
                        TTTCTCTCTT  TTTTA
                           CCA
GAM356  LOC254440 3' TTCTCTCCTTCTCTCTTC   3729          __
                        GAAGAGAGAA  AGAGAA
                        ||||||||||  ||||||
                        CTTCTCTCTT  TCTCTT
                          CC
GAM356  LOC51123 3' ATTTTTATGCTGTTCCCTCTT 2571    A  AG  A
                        AAGAG GAA  AG ATAAAAAT
                        ||||| ||| || ||||||||
                        TTCTC CTT  TC TATTTTTA
                          C   G_  G
GAM356  LOC51596 5' TATTTTCCAAGTTTCTCTCTC 1651     A        ____
                        GA GAGAGAAA   GAGAATA
                        || |||||||||   |||||||
                        CT CTCTCTTT   CTTTTAT
                          _        GAAC
GAM356  LOC84570 5' TTTCGTTTTCCTCTCTCTTC 2257         AA   TA
                        GAAGAGAGA GAGAA AAA
                        ||||||||| ||||| |||
                        CTTCTCTCT CTTTT TTT
                           C_   GC
GAM356  LOC92710 5' TATTTTTATGCCTCTGTCTC 2885      A  A_
                        GAGA AGAG ATAAAAATA
                        |||| |||| |||||||||
                        CTCT TCTC TATTTTTAT
                          G   CG
GAM357  FANCF    3' GTCCCTTTAAAGCATTGA   1997         ATATAT
                        TCAATGTTTTAAA    GGAC
                        ||||||||||||    ||||
                        AGTTACGAAATTT    CCTG
                           C_____
GAM357  GPR65    5' TCCACCCTTTAAAAGCATTGA 2544     A TATA
                        TCAATGTTTT AAA   TGGA
                        |||||||||| |||   ||||
```

```
                         AGTTACGAAA TTT   ACCT
                         A   CCC_
GAM357  LMNB1    3' TGTCCATACACTTTGTTGCA 1226      TT   ATA
                         TGT  TAAA  TATGGACA
                         ||| ||||  ||||||||
                         ACG  GTTT  ATACCTGT
                         TT   CAC
GAM357  MEN1     5' CATAATATTTTAAAACATT  3600                _
                         AATGTTTTAAAATAT ATG
                         |||||||||||||| |||
                         TTACAAAATTTTATA TAC
                                        A
GAM357  PLAG1    3' TGTCCATATACCAGATTTAAAA 944              A____
            TATT          AATGTTTTAAA  TATATGGACA
                         |||||||||||   ||||||||||
                         TTATAAAATTT   ATATACCTGT
                              AGACC
GAM357  S100A11  3' TGTCACTTTTTTAAAACATGA 1231    A       TATATG
                         TCA TGTTTTAAAA   GACA
                         ||| ||||||||||    ||||
                         AGT ACAAAATTTT    CTGT
                         _        TTCA__
GAM357  SLC9A6   3' TCCAGTTAGAACATTGA      1290           AATATA
                         TCAATGTTTTAA   TGGA
                         |||||||||||    ||||
                         AGTTACAAGATT    ACCT
                              G_____
GAM357  SOD2     3' TCCATATACTTTGGGGACTTG 766      T   TA  _
                         CAA GTTT  AAA TATATGGA
                         ||| ||||  ||| ||||||||
                         GTT CAGG  TTT ATATACCT
                         _    GG   C
GAM357  BIRC2    5' TATATTTTTAAAACATTGA   2784              T
                         TCAATGTTTTAAAA ATATG
                         |||||||||||||| |||||
                         AGTTACAAAATTTT TATAT
                                    _
GAM357  CXorf1   5' TGTCCATAGAAAAAATATT  1145         AAAATA
                         AATGTTTT   TATGGACA
                         ||||||||   ||||||||
                         TTATAAAA   ATACCTGT
                              AAG___
GAM357  KIAA0367 3' TGTCCCACAATGCCTAAAACAT 2787           AAATATAT_
            TGA           TCAATGTTTTA   GGACA
                         |||||||||||    |||||
                         AGTTACAAAAT    CCTGT
                         CCGTAACAC
GAM357  KIAA1321 3' TCCTTGAGCTTTAAAGCATTGA 2627             ATATAT
                         TCAATGTTTTAAA   GGA
                         |||||||||||    |||
```

```
                        AGTTACGAAATTT    CCT
                               CGAGTT
GAM357  KIAA1718 3' TGTATTTTAAAATATTGA   2686
                        TCAATGTTTTAAAATATA
                        ||||||||||||||||||
                        AGTTATAAAATTTTATGT


GAM357  KIAA1789 5' TGTCCCTGCCCTAGAAACATTG 2781          AAAATATAT
               A           TCAATGTTTT     GGACA
                           |||||||||    |||||
                           AGTTACAAAG     CCTGT
                              ATCCGTC_
GAM357  PRO2964  3' CAAGTATTTTAAAACACTG  1842     A         A
                        CA TGTTTTAAAATAT TG
                        || ||||||||||||| ||
                        GT ACAAAATTTTATG AC
                           C         A
GAM357  SLC17A6  3' TGTCCATACACAGAAACAT  1912          AAAATA
                        ATGTTTT   TATGGACA
                        |||||||   |||||||||
                        TACAAAG   ATACCTGT
                           ACAC__
GAM357  TRAF3    5' CATTTTATTTTAAAACGTTGA 2542               T_
                        TCAATGTTTTAAAATA ATG
                        |||||||||||||||| |||
                        AGTTGCAAAATTTTAT TAC
                              TT
GAM357  LOC151361 3' TGTCTGTGTTTTTAAAAC   3344          T
                        GTTTTAAAA ATATGGACA
                        ||||||||| ||||||||||
                        CAAAATTTT TGTGTCTGT
                              _
GAM357  LOC158714 3' TCCACACATTTAAAACATTGA 3224             ATATA
                        TCAATGTTTTAAA   TGGA
                        |||||||||||||   ||||
                        AGTTACAAAATTT   ACCT
                            ACAC_
GAM357  LOC219667 3' TATACCTTAGAACATTGA  3518            AA
                        TCAATGTTTTAA TATA
                        |||||||||||| ||||
                        AGTTACAAGATT ATAT
                              CC
GAM357  LOC91565  3' TCCATTTTAAAACATT    2749          ATAT
                        AATGTTTTAAA   ATGGA
                        ||||||||||    |||||
                        TTACAAAATTT   TACCT
                            ____
GAM358  EHF      3' ATATTGTAGAAGGAAACACCAA 1411          T GGA
                        TTGGT GT  TCTTCTACAATAT
                        ||||| ||  |||||||||||||
```

```
                        AACCA CA  GGAAGATGTTATA
                         _  AA_
GAM358  C9orf5   3' ATATTGCAAAAAACTACAGCTA 2225          ATCTTCTA
        A                TTGGTTGTGG        CAATAT
                         |||||||||        ||||||
                         AATCGACATC        GTTATA
                         AAAAAAC_
GAM358  KIAA1546 3' TTGAAAAGACCACAACCAA  2805          A  CTA
                       TTGGTTGTGG TCTT  CAA
                       |||||||||| |||| |||
                       AACCAACACC AGAA  GTT
                        _  AA_
GAM358  LOC253263 3' TGAGAAAAACCCACAACTAA  3724          ATC_  A
                        TTGGTTGTGG   TTCT CA
                        ||||||||||   |||| ||
                        AATCAACACC   AAGA GT
                        CAAA  _
GAM359  BRCA1    3' GCCATGAGCACAAAATTATGGT 1380           AGGGTA
        A                  TATCATAA    TGCTCATGGC
                           ||||||||    ||||||||||
                           ATGGTATT    ACGAGTACCG
                           AAAAC_
GAM359  BRCA1    3' GCCATGAGCACAAAATTATGGT 1381           AGGGTA
        A                  TATCATAA    TGCTCATGGC
                           ||||||||    ||||||||||
                           ATGGTATT    ACGAGTACCG
                           AAAAC_
GAM359  BRCA1    3' GCCATGAGCACAAAATTATGGT 1382           AGGGTA
        A                  TATCATAA    TGCTCATGGC
                           ||||||||    ||||||||||
                           ATGGTATT    ACGAGTACCG
                           AAAAC_
GAM359  BRCA1    3' GCCATGAGCACAAAATTATGGT 1383           AGGGTA
        A                  TATCATAA    TGCTCATGGC
                           ||||||||    ||||||||||
                           ATGGTATT    ACGAGTACCG
                           AAAAC_
GAM359  BRCA1    3' GCCATGAGCACAAAATTATGGT 1384           AGGGTA
        A                  TATCATAA    TGCTCATGGC
                           ||||||||    ||||||||||
                           ATGGTATT    ACGAGTACCG
                           AAAAC_
GAM359  BRCA1    3' GCCATGAGCACAAAATTATGGT 1385           AGGGTA
        A                  TATCATAA    TGCTCATGGC
                           ||||||||    ||||||||||
                           ATGGTATT    ACGAGTACCG
                           AAAAC_
GAM359  BRCA1    3' GCCATGAGCACAAAATTATGGT 1386           AGGGTA
        A                  TATCATAA    TGCTCATGGC
                           ||||||||    ||||||||||
```

```
                              ATGGTATT    ACGAGTACCG
                                AAAAC_
GAM359   BRCA1    3' GCCATGAGCACAAAATTATGGT 1387          AGGGTA
         A                  TATCATAA    TGCTCATGGC
                            |||||||    ||||||||||
                              ATGGTATT    ACGAGTACCG
                                AAAAC_
GAM359   BRCA1    3' GCCATGAGCACAAAATTATGGT 1388          AGGGTA
         A                  TATCATAA    TGCTCATGGC
                            |||||||    ||||||||||
                              ATGGTATT    ACGAGTACCG
                                AAAAC_
GAM359   BRCA1    3' GCCATGAGCACAAAATTATGGT 1389          AGGGTA
         A                  TATCATAA    TGCTCATGGC
                            |||||||    ||||||||||
                              ATGGTATT    ACGAGTACCG
                                AAAAC_
GAM359   BRCA1    3' GCCATGAGCACAAAATTATGGT 1391          AGGGTA
         A                  TATCATAA    TGCTCATGGC
                            |||||||    ||||||||||
                              ATGGTATT    ACGAGTACCG
                                AAAAC_
GAM359   PPP1CB   3' GCCATTTGACACCCTTTATGAT 949              ATGCTC
         G                  TATCATAAAGGGT    ATGGC
                            ||||||||||||    |||||
                            GTAGTATTCCCA    TACCG
                                   CAGTT_
GAM359   TRPS1    3' CATGCACACCCTCTCTGATA 1470      TAA   A   TC
                          TATCA  AGGGT TGC  ATG
                          |||||  ||||| ||| |||
                          ATAGT  TCCCA ACG  TAC
                            CTC    C  __
GAM359   FLJ23323 3' GCCATGAATGGTGCCCTT 2077          GC_
                          AAGGGTAT  TCATGGC
                          ||||||||  |||||||
                          TTCCCGTG  AGTACCG
                               GTA
GAM359   KIAA0057 3' CCACAAGCATACCTATTAAGA 1421    A  A      CA
                          TC TAA GGGTATGCT  TGG
                          || ||| ||||||||| |||
                          AG ATT TCCATACGA  ACC
                             A  A       AC
GAM359   LOC145439 5' GCCATGAGCTGCATCTTTAT 3079          _  T
                          ATAAAGG GTA GCTCATGGC
                          ||||||| ||| |||||||||
                          TATTTCT CGT CGAGTACCG
                                A  _
GAM360   DKFZP434G1411 3' TAGGTTGATACATGTATCA 3554          AA
                          TGATACATGTATTAA  TA
                          |||||||||||||| ||
```

```
                          ACTATGTACATAGTT AT
                                 GG
GAM360  DKFZP564I052 3' GAAAGTATTCCTATCATGTAT 2760       T TAA
                          ATACATG AT   AATACTTTC
                          IIIIIII II   IIIIIIIII
                          TATGTAC TA   TTATGAAAG
                            _    TCC
GAM360  KLHL8   3' AAAGTATTTGTTACATAATCA 2639       AC   TTA
                   TGAT ATGTA  AAATACTTT
                   IIII IIIII  IIIIIIIII
                   ACTA TACAT  TTTATGAAA
                     A_    TG_
GAM360  XLKD1   3' AAAGTGCCATTAACAAATGTAT 1323       GTA  AA_
        CA                 TGATACAT TTAA TACTTT
                           IIIIIIIII IIII IIIIII
                           ACTATGTA AATT GTGAAA
                             AAC   ACC
GAM360  LOC51003 3' GAGGCACTTAATACATGTAT 1658            AATA
                     ATACATGTATTAA  CTT
                     IIIIIIIIIIIII  III
                     TATGTACATAATT  GAG
                           CACG
GAM361  GCNT2   5' TCTCGGGATGAAACGGAATCGA 831            _____ A
                   TCGATTCCGT    CC AGA
                   IIIIIIIIII    II III
                   AGCTAAGGCA    GG TCT
                     AAGTAG  C
GAM361  BLP1    3' TTACCTTGCAGACGGAATGA 2222     G     __   A
                   TC ATTCCGTC  CAAG TGA
                   II IIIIIIII  IIII III
                   AG TAAGGCAG  GTTC ATT
                    _    AC   C
GAM361  BLP1    3' TTACCTTGCAGACGGAATGA 2371     G     __   A
                   TC ATTCCGTC  CAAG TGA
                   II IIIIIIII  IIII III
                   AG TAAGGCAG  GTTC ATT
                    _    AC   C
GAM361  LOC143914 5' TCACTCAAACGGAATCGA  3062        CCA  A
                     TCGATTCCGT  AG TGA
                     IIIIIIIIII  II III
                     AGCTAAGGCA  TC ACT
                       AAC  _
GAM361  LOC253891 5' CACTGGGACGGAATCGG   3654        A A
                     TCGATTCCGTCC AG TG
                     IIIIIIIIIIII II II
                     GGCTAAGGCAGG TC AC
                          G  _
GAM362  ADSS   3' GAAACAAATGATGAAAACAT 2925     CCTGTT
                  ATGT    TCATTTGTTTC
                  IIII    IIIIIIIIII
```

```
                        TACA     AGTAAACAAAG
                       AAAGT_
GAM362  CASP6    3' GAAACAAAATCCTCAGGAAATT 2305      G    TTTCA
         A                 TAAT TCCTG    TTTGTTTC
                           |||| |||||    ||||||||
                           ATTA AGGAC    AAACAAAG
                             A    TCCTA
GAM362  CASP6    3' GAAACAAAATCCTCAGGAAATT 810       G    TTTCA
         A                 TAAT TCCTG    TTTGTTTC
                           |||| |||||    ||||||||
                           ATTA AGGAC    AAACAAAG
                             A    TCCTA
GAM362  CKTSF1B1 3' AAGTGGATAAACAGAACATT 1445        C    C  TG
                       AATGT CTGTTT ATT  TTT
                       ||||| |||||| |||  |||
                       TTACA GACAAA TAG  GAA
                         A     _    GT
GAM362  F2R      3' AAACAATGCAGTACAGGACAT 879             TTCAT_
                       ATGTCCTGT    TTGTTT
                       |||||||||    ||||||
                       TACAGGACA    AACAAA
                          TGACGT
GAM362  GPRK7    3' GGAAACAAATGTTTCTGACATT 2476            CTGTTT
                       AATGTC    CATTTGTTTCC
                       ||||||    |||||||||||
                       TTACAG    GTAAACAAAGG
                          TCTTT_
GAM362  NLGN1    3' AAACAAATGAGATGGAC      1591       T
                       GTCC GTTTCATTTGTTT
                       |||| |||||||||||||
                       CAGG TAGAGTAAACAAA
                         _
GAM362  APC10    5' GGAAACTGTAACAGGACATT 1574            T  TTT
                       AATGTCCTGTT CA  GTTTCC
                       ||||||||||| || ||||||
                       TTACAGGACAA GT  CAAAGG
                            T ___
GAM362  C20orf139 3' GGAACAAAAACAGGACATTA 3319              CAT
                       TAATGTCCTGTTT TTGTTTC
                       ||||||||||||| |||||||
                       ATTACAGGACAAA AACAAGG
                           ___
GAM362  FLJ11186 3' GAAGCCCGAAACAAGACATTA 1818        C    ATTT
                       TAATGTC TGTTTC  GTTTC
                       ||||||| ||||||  |||||
                       ATTACAG ACAAAG  CGAAG
                          A    CC__
GAM362  FLJ22116 5' GGAATTGCGGAAAACAGGAC 2073             CA   __
                       GTCCTGTTT TTTGT TTCC
                       ||||||||| ||||| ||||
```

```
                        CAGGACAAA  AGGCG  AAGG
                         __        TT
GAM362  FLJ32978  3'  AAACAAATGAAATCAACA   2487      CCT

                        TGT  GTTTCATTTGTTT
                        |||  ||||||||||||
                        ACA  TAAAGTAAACAAA
                          AC_
GAM362  KIAA1164  3'  GGAAACAAAACAAACAAAC 2862    CC   CA_

                        GT  TGTTT  TTTGTTCC
                        ||  |||||  |||||||||
                        CA  ACAAA  AAACAAAGG
                         AA    ACA
GAM362  KIAA1762  3'  AAAGAGAGAAACGGACA    2668      T   A   G

                        TGTCC GTTTC TTT TTT
                        ||||| ||||| ||| |||
                        ACAGG CAAAG AGA AAA
                          _    _  G
GAM362  KIAA1918  5'  GAAAGGAGACAGAACATTA  2969      C    ATTTG

                        TAATGT CTGTTTC   TTTC
                        |||||| |||||||    ||||
                        ATTACA GACAGAG    AAAG
                           A     G____
GAM362  POPX1     3'  GGAAACAAACTTCAGGTCA  1583     T  TTTCA

                        TG CCTG    TTTGTTCC
                        || ||||    |||||||||
                        AC GGAC    AAACAAAGG
                         T  TTC__
GAM362  PRO0800   3'  AAACAAAGAGACAGGAATTA 1852      G     A

                        TAAT TCCTGTTTC TTTGTTT
                        |||| ||||||||| |||||||
                        ATTA AGGACAGAG AAACAAA

                           _    _
GAM362  LOC142779 3'  GGAGTAACAAAATAGGACATTA 3050           CATT   __

                        TAATGTCCTGTTT  TGTT TCC
                        |||||||||||||   |||| |||
                        ATTACAGGATAAA   ACAA AGG
                           ____    TG
GAM362  LOC143274 5'  GGAAACAAACAAAAGGA    3053     G  CA

                        TCCT TTT TTTGTTCC
                        |||| ||| |||||||||
                        AGGA AAA AAACAAAGG
                          _  AC
GAM362  LOC154089 3'  AAACAAATACTGAGACAG   3186          ___

                        CTGTTTCA TTTGTTT
                        |||||||| |||||||
                        GACAGAGT AAACAAA
                          CAT
GAM362  LOC169679 3'  AGCATATGAAGACAGGACAT 3404          _  T

                        ATGTCCTGTTT CAT TGTT
                        ||||||||||| ||| ||||
```

```
                              TACAGGACAGA GTA ACGA
                              A   T
GAM362  LOC202052 5' GAAACAAATACCCAGAAGACA 3484        __   TTTC
                     TGTC CTG   ATTTGTTTC
                     |||| |||   |||||||||
                     ACAG GAC   TAAACAAAG
                       AA  CCA_
GAM362  LOC256021 3' GAAACGAGAACAATGACATTA 3708         C_   CAT
                     TAATGTC TGTTT  TTGTTTC
                     ||||||| |||||  |||||||
                     ATTACAG ACAAG  AGCAAAG
                          TA   ___
GAM362  LOC91650  5' AAACAAAACATCTCAGGACAT 2765         TTTCA_
                     ATGTCCTG    TTTGTTT
                     ||||||||    |||||||
                     TACAGGAC    AAACAAA
                         TCTACA
GAM362  LOC91752  5' AAGTCAAATAAAACAGGACA 2777          C   _
                     TGTCCTGTTT ATTTG TTT
                     |||||||||| ||||| |||
                     ACAGGACAAA TAAAC GAA
                              A   T
GAM363  ARCN1    3' CCCATTTCCTTCCAGTCA 844          GAAGT   CA
                     TGATTGGA   AGGAAA GG
                     ||||||||   |||||| ||
                     ACTGACCT   TCCTTT CC
                     _____      AC
GAM363  CTSK     3' TCCTACTTTGCTTCTCTCCACC 736      AT    _____
                 CA              TG TGGAGA   AGTAGGA
                     || ||||||    |||||||
                     AC ACCTCT    TCATCCT
                     CC    CTTCGTT
GAM363  HMG20A   3' TCCTATTTCCCTGCCATCA 1800        T___ A
                     TGAT  GG GAAGTAGGA
                     ||||  || |||||||||
                     ACTA  CC CTTTATCCT
                       CCGT _
GAM363  PRDM2    3' TCCTGTTTCCCACCCAG 1415         AGAA A
                     TTGG  GT GGAAACAGGA
                     ||||  || ||||||||||
                     GACC  CA CCTTTGTCCT
                       ____ C
GAM363  RNMT     3' CCTGCCTATCCTCTCCGATCA 1060       A_   AAA
                     TGATTGGAGA GTAGG  CAGG
                     |||||||||| |||||  ||||
                     ACTAGCCTCT TATCC  GTCC
                          CC   ___
GAM363  SCAP1    3' TCCCACTCCCTACTTCTGCCA 1052      _     AAACA
                     TGG AGAAGTAGG   GGA
                     ||| |||||||||   |||
```

```
                         ACC TCTTCATCC    CCT
                         G         CTCAC
GAM363  USH3A     5' CCTATTTTATTTCTCCATCA 2355     T       AAC
                         TGAT GGAGAAGTAGGA  AGG
                         |||| |||||||||||   |||
                         ACTA CCTCTTTATTTT  TCC
                             _         A__
GAM363  VAT1      3' TCCTGTTTCCCACCTCCTTCTC 1292        TA____
              C             GGAGAAG   GGAAACAGGA
                         |||||||   ||||||||||
                         CCTCTTC   CCTTTGTCCT
                            CTCCAC
GAM363  AIF1      5' CCTGCTGAAAACCCTCCAGTCA 2297          A_____
                         TGATTGGAG    AGTAGG
                         ||||||||||   ||||||
                         ACTGACCTC    TCGTCC
                            CCAAAAG
GAM363  CPLX1     3' CCTGTTTCTCCTCCATTCA 1317    T  AAGTA
                         TGA TGGAG   GGAAACAGG
                         ||| |||||   |||||||||
                         ACT ACCTC   TCTTTGTCC
                            T   C____
GAM363  CXYorf1   3' CCTGTTCCCCACCTCCCGGCTC 3228   _  A A A A
                         GA TTGG GA GT GG AACAGG
                         || |||| || || || ||||||
                         CT GGCC CT CA CC TTGTCC
                            C  _  C  C  C
GAM363  FLJ12221  3' CCCACCCTTGCTCTCCAATTA 2637       A   AAACA
                         TGATTGGAGA GTAGG   GG
                         |||||||||| |||||   ||
                         ATTAACCTCT CGTTC    CC
                            _   CCAC_
GAM363  FLJ20207  3' CCTGCCCTGCTTCCCCACCCA 1741   AT A    AAA
                         TG TGG GAAGTAGG  CAGG
                         || ||| |||||||||  ||||
                         AC ACC CTTCGTCC  GTCC
                            CC C      C__
GAM363  FLJ22215  3' CCTGCCCCCTACCCTGTTCTCC 3715        ____    AAA
                         GGAGAA  GTAGG  CAGG
                         ||||||  |||||  ||||
                         CCTCTT  CATCC  GTCC
                            GTCC     CCC
GAM363  FLJ31547  3' TCCCATAATTTCTCCCGCAATC 2511        ___    A___
              A             TGATT  GGAGAAGT  GGA
                         |||||  ||||||||   |||
                         ACTAA  CCTCTTTA   CCT
                            CGC       ATAC
GAM363  HSCBCIP1  3' TCCTACCTATGTCTTCTCCAAT 3449         ___    AAAC
                         ATTGGAGAAG  TAGG  AGGA
                         ||||||||||  ||||  ||||
```

```
                            TAACCTCTTC ATCC  TCCT
                         TGT  A___
GAM363  KIAA0515 5' TCCTACCAGAACTCCTCCGATC 2670        A  A__  AAAC
     A              TGATTGGAG AGT  GG  AGGA
                    |||||||| ||| ||  ||||
                    ACTAGCCTC TCA  CC   TCCT
                        C  AGA  A___
GAM363  KIAA1514 3' CCTGCTCAACTTCTCCA   1877        A  AAA
                    TGGAGAAGT GG  CAGG
                    ||||||||| ||  ||||
                    ACCTCTTCA CT  GTCC
                        A  C__
GAM363  KIAA1553 3' TCCTCACTTCTCCATCCA    3544     AT      _
                    TG TGGAGAAGT AGGA
                    || ||||||||| ||||
                    AC ACCTCTTCA TCCT
                       CT      C
GAM363  KIAA1656 3' CCCACTTCCTTCCAGTCA   2730        __   A
                    TGATTGGA GAAGT GG
                    |||||||| ||||| ||
                    ACTGACCT CTTCA CC
                        TC   C
GAM363  KIAA1877 3' CCTACCTTATTTCTCCAGCCA 2741   AT        AAAC
                    TG TGGAGAAGTAGG  AGG
                    || |||||||||||   |||
                    AC ACCTCTTTATTC  TCC
                       CG      CA__
GAM363  MTCH1    3' CCCGTCTACCCCTCCAGTCA  1493       AA   AAACA
                    TGATTGGAG GTAGG   GG
                    ||||||||| |||||   ||
                    ACTGACCTC CATCT   CC
                        CC  GC___
GAM363  N-PAC    3' CCGCCCTCACCCCTCCAATC  2902      AA _ AAACA
                    GATTGGAG GT AGG   GG
                    |||||||| || |||   ||
                    CTAACCTC CA TCC   CC
                        CC C CG___
GAM363  SEMA4B   5' CCTGTTTCCCACCTCC     2839     AA A
                    GGAG GT GGAAACAGG
                    |||| || |||||||||
                    CCTC CA CCTTTGTCC
                        __ C
GAM363  SPRY1    3' CCTGTTTCCCACCTTCTCT  2709       TA_
                    GGAGAAG GGAAACAGG
                    ||||||| |||||||||
                    TCTCTTC CCTTTGTCC
                        CAC
GAM363  WS-3     5' CCTGCCAGGCTCTCCAATC  1312        A A_ AAA
                    GATTGGAGA GT GG  CAGG
                    ||||||||| || ||  ||||
```

```
                        CTAACCTCT CG  CC  GTCC
                           _  GA ___
GAM363  LOC123242 5'  TCTGTACCTTCTCCATCCA  3030     AT       TAGGAA
                         TG TGGAGAAG    ACAGG
                         || |||||||||    |||||
                         AC ACCTCTTC    TGTCT
                          CT     CA____
GAM363  LOC127702 3'  CCTGCCCACAACTTCTCCAAAC 3024     A       A__ AAA
            A                TG TTGGAGAAGT  GG  CAGG
                         || ||||||||||| ||  ||||
                         AC AACCTCTTCA  CC  GTCC
                          A     ACA  C__
GAM363  LOC146745 5'  TCCTGCCACCATTTCTCCAACC 3099     A       A AAA
            A                TG TTGGAGAAGT GG  CAGGA
                         || ||||||||||| ||  |||||
                         AC AACCTCTTTA CC  GTCCT
                          C       _  ACC
GAM363  LOC147791 3'  CCCATTCCCTAACCTCCAATC 3294         AAG   A CA
                         GATTGGAG  TAGG AA GG
                         |||||||||  |||| || ||
                         CTAACCTC  ATCC TT CC
                            CA_   C AC
GAM363  LOC196892 3'  TCCTGGTGATTCTTCTCCAATC 3417              TAGGAAA
            A                TGATTGGAGAAG     CAGGA
                         |||||||||||||     |||||
                         ACTAACCTCTTC      GTCCT
                               TTAGTG_
GAM363  LOC200093 3'  CCTGTTCCCCACCTCCCGGCTC 2648      _  A A A A
                         GA TTGG GA GT GG AACAGG
                         || |||| || || || ||||||
                         CT GGCC CT CA CC TTGTCC
                          C  _  C C  C
GAM363  LOC201243 5'  TCCTGCCACCATTTCTCCAACC 3426     A       A AAA
            A                TG TTGGAGAAGT GG  CAGGA
                         || ||||||||||| ||  |||||
                         AC AACCTCTTTA CC  GTCCT
                          C       _  ACC
GAM363  LOC219404 3'  CCTGCTCCCTACTTCCTGGCA 3606    A TG A     AAA
                         TG T G GAAGTAGG  CAGG
                         || | | |||||||||  ||||
                         AC G C CTTCATCC  GTCC
                          _GT _     CTC
GAM363  LOC222066 3'  TCCTGCAAACCACCTTCTCCAA 3574            TA AAA_
            TCA                TGATTGGAGAAG GG  CAGGA
                         ||||||||||| ||  |||||
                         ACTAACCTCTTC CC  GTCCT
                              CA AAAC
GAM363  LOC253001 5'  TCTGTACCTTCTCCATCCA  3698     AT       TAGGAA
                         TG TGGAGAAG    ACAGG
                         || |||||||||    |||||
```

```
                        AC  ACCTCTTC     TGTCT
                        CT      CA____
GAM363  LOC91040 3'  CCTGTTCCCCACCTCCCGGCTC 2700      _   A  A  A  A
                        GA TTGG GA GT GG AACAGG
                        || |||| || || || ||||||
                        CT GGCC CT CA CC TTGTCC
                         C   _  C  C  C
```